

MA-I) //1.8e-32:71:100//BOS TAURUS (BOVINE) //P16874
 F-HEMBA1003568//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN) //4.1e-19:126:31//HOMO SAPIENS (HUMAN) //P14373
 F-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1 //3.9e-83:143:74//HOMO SAPIENS (HUMAN) //Q13330
 5 F-HEMBA1003571//HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D) //1.0:64:25//STAPHYLOCOCCUS AUREUS //P03860
 F-HEMBA1003579//CYTOTOXIN 1 (CYTOTOXIN V-II-1) (TOXIN V(II)1) //1.0:41:29//NAJA MELANOLEUCA (FOREST COBRA) (BLACK-LIPPED COBRA) //P01448
 10 F-HEMBA1003581//TALIN //3.7e-36:52:98//MUS MUSCULUS (MOUSE) //P26039
 F-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP) //1.6e-05:91:31//NICOTIANA SYLVESTRIS (WOOD TOBACCO) //P19682
 F-HEMBA1003595//HYPOTHETICAL 12.0 KD PROTEIN IN: DST1-HEM2 INTERGENIC REGION //1.0:55:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P53182
 15 F-HEMBA1003597
 F-HEMBA1003598//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11) //4.9e-10:85:41//ORYCTOLAGUS CUNICULUS (RABBIT) //P06333
 F-HEMBA1003615//PUTATIVE MINOR COAT PROTEIN (ORF43) //0.086:10:70//BACTERIOPHAGE PHI-LF //Q07482
 20 F-HEMBA1003617//HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I //4.4e-13:58:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q10169
 F-HEMBA1003621//LONG NEUROTOXIN 1 (NEUROTOXIN A) //0.096:40:37//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH) //P01387
 F-HEMBA1003622
 25 F-HEMBA1003630
 F-HEMBA1003637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!! //2.4e-13:47:74//HOMO SAPIENS (HUMAN) //P39188
 F-HEMBA1003640//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!! //0.87:25:64//HOMO SAPIENS (HUMAN) //P39193
 30 F-HEMBA1003645//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III //1.8e-10:157:26//CAENORHABDITIS ELEGANS //Q17963
 F-HEMBA1003646//SERINE-ARGININE PROTEIN 55 (SRP55) (ENHANCER OF DEFORMED) (52-KD BRACKETING PROTEIN) (B52 PROTEIN) //4.9e-05:207:27//DROSOPHILA MELANOGASTER (FRUIT FLY) //P26686
 F-HEMBA1003656
 35 F-HEMBA1003662//PROLINE-RICH PEPTIDE P-B //0.57:17:52//HOMO SAPIENS (HUMAN) //P02814
 F-HEMBA1003667//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! //6.0e-16:43:72//HOMO SAPIENS (HUMAN) //P39194
 F-HEMBA1003679
 F-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-) //3.9e-08:137:27//CAENORHABDITIS ELEGANS //P34629
 40 F-HEMBA1003684//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13) //2.1e-20:127:40//MUS MUSCULUS (MOUSE) //Q60821
 F-HEMBA1003690//HYPOTHETICAL PROTEIN KIAA0288 (HA6116) //3.0e-85:201:78//HOMO SAPIENS (HUMAN) //P56524
 45 F-HEMBA1003692//CELL DIVISION CONTROL PROTEIN 1 //0.13:69:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40986
 F-HEMBA1003711//CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E ANTIGEN) //0.021:153:26//HOMO SAPIENS (HUMAN) //P06731
 F-HEMBA1003714//ABAECIN //0.99:34:32//BOMBUS PASCUORUM //P81463
 50 F-HEMBA1003715
 F-HEMBA1003720//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //5.4e-34:155:56//HOMO SAPIENS (HUMAN) //P08547
 F-HEMBA1003725//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //1.3e-27:181:41//HOMO SAPIENS (HUMAN) //P08547
 55 F-HEMBA1003729//PTB-ASSOCIATED SPLICING FACTOR (PSF) //0.0037:103:33//HOMO SAPIENS (HUMAN) //P23246
 F-HEMBA1003733//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //5.0e-54:210:58//HOMO SAPIENS (HUMAN) //P08547

EP 1 074 617 A2

F-HEMBA1003742//MALE SPECIFIC SPERM PROTEIN MST84DB//0.066:72:33//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643
 F-HEMBA1003758
 F-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)//1.5e-51:220:52//MUS MUSCULUS (MOUSE)//Q61221
 5 F-HEMBA1003773
 F-HEMBA1003783
 F-HEMBA1003784
 F-HEMBA1003799//SHORT NEUROTOXIN 1 (TOXIN AA C)//0.95:27:37//ACANTHOPHIS ANTARCTICUS (COMMON DEATH ADDER)//P01434
 10 F-HEMBA1003803//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30]//0.46:96:34//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN)//P03338
 F-HEMBA1003804//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.019:30:50//HOMO SAPIENS (HUMAN)//P30808
 15 F-HEMBA1003805//HYPOTHETICAL 75.0 KD PROTEIN B0280.11 IN CHROMOSOME III//1.8e-20:109:47//CAENORHABDITIS ELEGANS//P42083
 F-HEMBA1003807
 F-HEMBA1003827//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//2.1e-09:23:78//OWENIA FUSIFORMIS//P21260
 20 F-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1)//2.0e-31:134:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40484
 F-HEMBA1003838//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.9e-22:39:76//HOMO SAPIENS (HUMAN)//P39192
 F-HEMBA1003856
 25 F-HEMBA1003864//HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REGION//1.5e-15:194:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36151
 F-HEMBA1003866//PROTEIN A39//0.0027:72:33//VACCINIA VIRUS (STRAIN COPENHAGEN)//P21062
 F-HEMBA1003879//80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80)//2.9e-16:22:100//HOMO SAPIENS (HUMAN)//Q09161
 30 F-HEMBA1003880//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.99:39:38//FELIS SILVESTRIS CATUS (CAT)//P48896
 F-HEMBA1003885//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.5e-28:47:76//HOMO SAPIENS (HUMAN)//P39193
 F-HEMBA1003893//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//1.7e-57:215:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53215
 35 F-HEMBA1003902
 F-HEMBA1003908
 F-HEMBA1003926//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.3e-10:60:63//HOMO SAPIENS (HUMAN)//P39186
 40 F-HEMBA1003937//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.1e-29:68:64//HOMO SAPIENS (HUMAN)//P39194
 F-HEMBA1003939//PROTEIN Q300//0.0025:24:62//MUS MUSCULUS (MOUSE)//Q02722
 F-HEMBA1003942//EXCITATORY INSECT TOXIN BJXTR-IT PRECURSOR (BJ-XTRIT)//0.084:67:31//BUTHOTUS JUDAICUS (SCORPION) (HOTTENTOTTA JUDAICA)//P56637
 45 F-HEMBA1003950//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (O71)//0.95:26:34//ESCHERICHIA COLI//P46878
 F-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT)//2.5e-17:89:46//MUS MUSCULUS (MOUSE)//P16372
 F-HEMBA1003958//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.2e-23:43:76//HOMO SAPIENS (HUMAN)//P08547
 50 F-HEMBA1003959
 F-HEMBA1003976//HYPOTHETICAL PROTEIN KIAA0076 (HA0936)//0.99:88:28//HOMO SAPIENS (HUMAN)//Q14999
 F-HEMBA1003978//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.98:19:57//HOMO SAPIENS (HUMAN)//P22531
 55 F-HEMBA1003985//LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS) (FRAGMENT)//1.0:40:32//MYCOBACTERIUM LEPRAE//P46861
 F-HEMBA1003987//HYPOTHETICAL PROTEIN UL66//0.27:65:33//HUMAN CYTOMEGALOVIRUS (STRAIN

AD169)//P16822
 F-HEMBA1003989//MALE SPECIFIC SPERM PROTEIN MST84DB//5.2e-05:64:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643
 F-HEMBA1004000//PROTEIN Q300//0.00042:17:82//MUS MUSCULUS (MOUSE)//Q02722
 5 F-HEMBA1004011//ALPHA-TYPE CALCITONIN GENE-RELATED PEPTIDE PRECURSOR (CGRP-1)//0.47:106:32//HOMO SAPIENS (HUMAN)//P06881
 F-HEMBA1004012//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN)//0.96:36:33//PARAMECIUM TETRAURELIA//P16001
 F-HEMBA1004015//HYPOTHETICAL 29.3 KD PROTEIN_B0280.6 IN CHROMOSOME III//0.00018:90:34//
 10 CAENORHABDITIS ELEGANS//P41997
 F-HEMBA1004024//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//5.1e-34:75:80//HOMO SAPIENS (HUMAN)//P39194
 F-HEMBA1004038
 F-HEMBA1004042
 15 F-HEMBA1004045//40S RIBOSOMAL PROTEIN S27A//1.0:20:55//ASPARGUS OFFICINALIS (GARDEN ASPARAGUS)//P31753
 F-HEMBA1004048//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.3e-06:158:35//MUS MUSCULUS (MOUSE)//P05143
 F-HEMBA1004049//32 KD HEAT SHOCK PROTEIN (4-1 PROTEIN)//0.098:106:32//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P54658
 20 F-HEMBA1004055//HYPOTHETICAL PROTEIN HI0258/259//0.87:133:23//HAEMOPHILUS INFLUENZAE//P43974
 F-HEMBA1004056//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//3.3e-25:39:64//HOMO SAPIENS (HUMAN)//P39191
 25 F-HEMBA1004074//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.9e-08:35:68//HOMO SAPIENS (HUMAN)//P39188
 F-HEMBA1004086
 F-HEMBA1004097//IMMEDIATE-EARLY PROTEIN IE4 (IE68) (FRAGMENT)//0.71:95:35//HERPES SIMPLEX VIRUS (TYPE 2)//P14379
 30 F-HEMBA1004111//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.7e-26:84:64//HOMO SAPIENS (HUMAN)//P39188
 F-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT)//2.8e-34:108:63//HOMO SAPIENS (HUMAN)//Q14141
 F-HEMBA1004132//HYPOTHETICAL PROTEIN HI1736//1.0:44:34//HAEMOPHILUS INFLUENZAE//P44300
 35 F-HEMBA1004133//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C//0.89:21:57//MYCOBACTERIUM TUBERCULOSIS//Q10826
 F-HEMBA1004138//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT)//0.016:39:41//MEDICAGO SATIVA (ALFALFA)//P11728
 F-HEMBA1004143//CYTOCHROME C OXIDASE POLYPEPTIDE VIII PRECURSOR (EC 1.9.3.1)//0.93:34:29//
 40 SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P04039
 F-HEMBA1004146//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.63:52:36//HOMO SAPIENS (HUMAN)//P02811
 F-HEMBA1004150//METALLOTHIONEIN-II (MT-II)//1.0:20:45//MUS MUSCULUS (MOUSE)//P02798
 F-HEMBA1004164//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.0e-13:57:71//HOMO SAPIENS (HUMAN)//
 45 P39195
 F-HEMBA1004168//V-TYPE SODIUM ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBUNIT F)//0.00035:90:34//ENTEROCOCCUS HIRAE//P43437
 F-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III//5.1e-14:115:31//
 50 CAENORHABDITIS ELEGANS//P34529
 F-HEMBA1004200
 F-HEMBA1004202//YPT1-RELATED PROTEIN 1//2.5e-24:96:52//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P11620
 F-HEMBA1004203//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//2.2e-09:48:64//HOMO SAPIENS (HUMAN)//
 55 P39193
 F-HEMBA1004207//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70)//0.98:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA)//P34779
 F-HEMBA1004225//METALLOTHIONEIN-II//1.0:30:33//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA)//P15114

EP 1 074 617 A2

F-HEMBA1004227//PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015)//5.9e-06:109:
 33//HOMO SAPIENS (HUMAN)//P49593
 F-HEMBA1004238//VERY HYPOTHETICAL XYLU PROTEIN//0.98:39:38//ESCHERICHIA COLI//P05056
 F-HEMBA1004241//SOX-13 PROTEIN (FRAGMENT)//0.66:36:38//MUS MUSCULUS (MOUSE)//Q04891
 5 F-HEMBA1004246
 F-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN
 CL-6)//1.0e-43:98:84//RATTUS NORVEGICUS (RAT)//Q08755
 F-HEMBA1004264//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//0.014:160:28//NEPHILA CLA-
 VIPES (ORB SPIDER)//P46804
 10 F-HEMBA1004267//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.8e-52:56:83//HOMO SAPIENS (HUMAN)//
 P39189
 F-HEMBA1004272
 F-HEMBA1004274//HYPOTHETICAL 13.0 KD PROTEIN F59B2.10 IN CHROMOSOME III//0.00084:33:54//
 CAENORHABDITIS ELEGANS//P34485
 15 F-HEMBA1004275//HYPOTHETICAL 56.5 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION//9.3e-06:125:
 27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40034
 F-HEMBA1004276//BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT)
 (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A)//3.7e-30:239:32//HOMO SA-
 PIENS (HUMAN)//Q10567
 20 F-HEMBA1004286//CUTICLE COLLAGEN 34//0.0027:71:38//CAENORHABDITIS ELEGANS//P34687
 F-HEMBA1004289//PTR3 PROTEIN (SSY3 PROTEIN)//1.0:76:28//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P43606
 F-HEMBA1004295//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.075:58:39//HO-
 MO SAPIENS (HUMAN)//P30808
 25 F-HEMBA1004306//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//0.020:132:30//ORGYIA PSEUDOTSUGATA
 MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341
 F-HEMBA1004312//EARLY PROTEIN I73R//0.99:65:32//AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)
 (ASFV)//P27946
 F-HEMBA1004321//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10)//4.3e-43:133:44//
 30 MUS MUSCULUS (MOUSE)//Q61967
 F-HEMBA1004323
 F-HEMBA1004327//SMALL PROLINE-RICH PROTEIN 2-1//0.027:48:43//HOMO SAPIENS (HUMAN)//P35326
 F-HEMBA1004330//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1)//0.46:70:34//HOMO SAPIENS (HU-
 MAN)//Q05925
 35 F-HEMBA1004334//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//7.7e-05:83:34//HOMO SAPIENS (HU-
 MAN)//P08547
 F-HEMBA1004335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.0e-24:41:80//HOMO SAPIENS (HUMAN)//
 P39195
 F-HEMBA1004341//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//2.8e-06:148:35//MUS MUSCULUS
 40 (MOUSE)//P05143
 F-HEMBA1004353//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.2e-29:57:80//HOMO SAPIENS (HUMAN)//
 P39195
 F-HEMBA1004354//CHL1 PROTEIN//0.017:40:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P22516
 45 F-HEMBA1004356
 F-HEMBA1004366//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.00045:49:46//HOMO SAPIENS (HU-
 MAN)//P08547
 F-HEMBA1004372//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME I//1.0:125:28//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10263
 50 F-HEMBA1004389//HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-FET4 INTERGENIC REGION//0.76:170:25//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04893
 F-HEMBA1004394
 F-HEMBA1004396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.2e-10:72:51//HOMO SAPIENS (HU-
 MAN)//P08547
 55 F-HEMBA1004405
 F-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CY-
 CLOPHILIN-10)//2.7e-29:146:48//CAENORHABDITIS ELEGANS//P52017
 F-HEMBA1004429//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/0.0019:47:59//HOMO SAPIENS (HU-

MAN)//P39191
 F-HEMBA1004433//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-20:47:68//HOMO SAPIENS (HUMAN)//
 P39192
 F-HEMBA1004460//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/6.2e-64:134:69//HOMO SAPIENS (HU-
 5 MAN)//P39193
 F-HEMBA1004461//METALLOTHIONEIN-LIKE PROTEIN 1//1.0:39:35//PISUM SATIVUM (GARDEN PEA)//
 P20830
 F-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-
 TEIN)//9.7e-43:101:48//MUS MUSCULUS (MOUSE)//Q61221
 10 F-HEMBA1004482//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34)//1.0:41:36//CANDIDA GLABRATA (YEAST)
 (TORULOPSIS GLABRATA)//P05040
 F-HEMBA1004499//TUBULIN BETA CHAIN//0.00021:55:36//CAENORHABDITIS ELEGANS//P52275
 F-HEMBA1004502
 F-HEMBA1004506//HYPOTHETICAL PROTEIN ORF-1137//5.3-11:119:35//MUS MUSCULUS (MOUSE)//
 15 P11260
 F-HEMBA1004507//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//0.00072:90:37//HOMO
 SAPIENS (HUMAN)//Q15428
 F-HEMBA1004509//HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION//6.3e-28:169:
 42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43589
 20 F-HEMBA1004534//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAMIN) (FILAMIN
 1)//1.3e-80:226:66//HOMO SAPIENS (HUMAN)//P21333
 F-HEMBA1004538//HYPOTHETICAL PROTEIN MJ0764//0.96:28:35//METHANOCOCCUS JANNASCHII//
 Q58174
 F-HEMBA1004542//METALLOTHIONEIN (MT)//0.78:36:41//GADUS MORHUA (ATLANTIC COD)//P51902
 25 F-HEMBA1004554
 F-HEMBA1004560//HYPOTHETICAL PROTEIN KIAA0281 (HA6725)//4.2e-15:56:69//HOMO SAPIENS (HU-
 MAN)//Q92556
 F-HEMBA1004573//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)//0.65:31:58//PLASMODIUM
 BERGHEI//P06915
 30 F-HEMBA1004577//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.9e-08:35:80//HOMO SAPIENS (HUMAN)//
 P39195
 F-HEMBA1004586//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.6e-08:64:54//HOMO SAPIENS (HU-
 MAN)//P39194
 F-HEMBA1004596//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C (HNRNP C) (HNRNP CORE
 35 PROTEIN C) (FRAGMENT)//0.00057:88:31//RATTUS NORVEGICUS (RAT)//P17132
 F-HEMBA1004604//COLLAGEN ALPHA 2(XI) CHAIN PRECURSOR (FRAGMENT)//0.045:37:45//MUS MUSCU-
 LUS (MOUSE)//Q64739
 F-HEMBA1004610//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-11:73:54//HOMO SAPIENS (HUMAN)//
 P39188
 40 F-HEMBA1004617
 F-HEMBA1004629
 F-HEMBA1004631//HYPOTHETICAL 7.8 KD PROTEIN IN WAPA-LICT INTERGENIC REGION//1.0:36:38//BA-
 CILLUS SUBTILIS//P42303
 F-HEMBA1004632//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING
 45 8.0 KD POLYPEPTIDE)//0.86:48:35//SYNECHOCOCCUS ELONGATUS NAEGELI//P20453
 F-HEMBA1004637//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III//1.7e-32:159:42//
 CAENORHABDITIS ELEGANS//P34535
 F-HEMBA1004638//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//2.8e-06:50:46//OWENIA FUSI-
 FORMIS//P21260
 50 F-HEMBA1004666//TOXIN S6C4//1.0:36:30//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S
 MAMBA)//P25682
 F-HEMBA1004669//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR
 SRP75)//1.6e-12:105:42//HOMO SAPIENS (HUMAN)//Q08170
 F-HEMBA1004670//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//2.5e-06:62:45//HOMO SAPIENS (HU-
 55 MAN)//P02452
 F-HEMBA1004672//HYPOTHETICAL PROTEIN MJ0437//0.95:37:29//METHANOCOCCUS JANNASCHII//
 Q57879
 F-HEMBA1004693//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN,

TYPE B) (NMMHC-B) //0.00035:217:23//HOMO SAPIENS (HUMAN) //P35580
 F-HEMBA1004697//IMMUNOGLOBULIN G BINDING PROTEIN H PRECURSOR (PROTEIN H) //0.058:118:30//
 STREPTOCOCCUS PYOGENES //P50470
 F-HEMBA1004705//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.8e-09:43:72//HOMO SAPIENS (HUMAN) //P39188
 5 F-HEMBA1004709//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.8e-18:50:84//HOMO SAPIENS (HUMAN) //P39189
 F-HEMBA1004711//ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2) //0.0027:148:30//HOMO SAPIENS (HUMAN) //000321
 10 F-HEMBA1004725//CUTICLE COLLAGEN 2 //0.0051:41:41//CAENORHABDITIS ELEGANS //P17656
 F-HEMBA1004730//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //1.4e-22:210:37//HOMO SAPIENS (HUMAN) //P08547
 F-HEMBA1004733//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.7e-07:50:62//HOMO SAPIENS (HUMAN) //P39188
 15 F-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42) //9.9e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS) //P42743
 F-HEMBA1004736//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //4.1e-60:210:61//HOMO SAPIENS (HUMAN) //P08547
 20 F-HEMBA1004748
 F-HEMBA1004751//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.8e-20:88:63//HOMO SAPIENS (HUMAN) //P39188
 F-HEMBA1004752//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN) //0.0043:126:34//XENOPUS LAEVIS (AFRICAN CLAWED FROG) //P17437
 25 F-HEMBA1004753//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.8e-28:47:78//HOMO SAPIENS (HUMAN) //P39193
 F-HEMBA1004756//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8:CAN1 INTERGENIC REGION //0.22:77:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P39981
 F-HEMBA1004758
 30 F-HEMBA1004763//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT) //1.1e-06:58:43//OWENIA FUSIFORMIS //P21260
 F-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //4.7e-65:298:53//HOMO SAPIENS (HUMAN) //P08547
 F-HEMBA1004770
 35 F-HEMBA1004771
 F-HEMBA1004776//GRANULIN 1 //0.78:28:42//CYPRINUS CARPIO (COMMON CARP) //P81013
 F-HEMBA1004778
 F-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT) //6.9e-20:74:63//HOMO SAPIENS (HUMAN) //P50851
 40 F-HEMBA1004803//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //1.4e-22:58:86//HOMO SAPIENS (HUMAN) //P08547
 F-HEMBA1004806//HYPOTHETICAL 24.3 KD PROTEIN IN PSBH-RPL11 INTERGENIC REGION (ORF182) //0.72:75:33//CYANOPHORA PARADOXA //P48324
 F-HEMBA1004807
 F-HEMBA1004816
 45 F-HEMBA1004820//HEMOLYMPH TRYPSIN INHIBITOR A (BPI-TYPE) (FRAGMENT) //1.0:50:38//MANDUCA SEXTA (TOBACCO HAWKMOTH) (TOBACCO HORNWORM) //P26226
 F-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68) //3.0e-76:171:91//CANIS FAMILIARIS (DOG) //Q00004
 F-HEMBA1004850//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS) //3.0e-05:64:43//BOS TAURUS (BOVINE) //P25508
 50 F-HEMBA1004863//TOXIN C13S1C1 PRECURSOR //0.38:52:30//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA) //P18329
 F-HEMBA1004864//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT) //0.89:24:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1) //P04612
 55 F-HEMBA1004865
 F-HEMBA1004880
 F-HEMBA1004889//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N) //0.66:23:47//HOMO SAPIENS (HUMAN) //P22532

F-HEMBA1004900
F-HEMBA1004909
F-HEMBA1004918//CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 (FRAGMENT)//0.56:37:32//SPINACIA OL-
ERACEA (SPINACH)//P09597
5 F-HEMBA1004923//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.5e-24:44:68//HOMO SAPIENS (HUMAN)//
P39188
F-HEMBA1004929//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (Å6L)//0.97:39:38//STRONGYLOCENTROTUS
PURPURATUS (PURPLE SEA URCHIN)//P15997
F-HEMBA1004930//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.6e-15:64:59//HOMO SAPIENS (HU-
10 MAN)//P08547
F-HEMBA1004933//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP)//0.34:58:41//HOMO SAPIENS
(HUMAN)//P50552
F-HEMBA1004934
F-HEMBA1004944
15 F-HEMBA1004954//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3)//0.58:78:30//PARA-
MECIUM TETRAURELIA//P15579
F-HEMBA1004956//HYPOTHETICAL 18.8 KD PROTEIN (ORF4)//0.98:57:31//PARAMECIUM TETRAURELIA//
P15605
F-HEMBA1004960//HYPOTHETICAL 12.6 KD PROTEIN-(ORFJ) (RETRON EC67)//1.0:58:27//ESCHERICHIA
20 COLI//P21324
F-HEMBA1004972
F-HEMBA1004973//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.90:55:30//HOMO SAPIENS
(HUMAN)//P22531
F-HEMBA1004977
25 F-HEMBA1004978
F-HEMBA1004980//MOTILIN PRECURSOR//0.088:79:31//MACACA MULATTA (RHESUS MACAQUE)//018811
F-HEMBA1004983//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES)//0.87:51:31//BUCHNERA
APHIDICOLA//Q59176
F-HEMBA1004995//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PRO-
30 TEIN 2) (XMEF2) (RSRFR2)//0.17:52:40//HOMO SAPIENS (HUMAN)//Q02080
F-HEMBA1005008//METALLOTHIONEIN (MT)//1.0:52:32//CRASSOSTREA VIRGINICA (EASTERN OYS-
TER)//P23038
F-HEMBA1005009//ACTIN//3.5e-27:171:38//CANDIDA ALBICANS (YEAST)//P14235
F-HEMBA1005019//HYPOTHETICAL PROTEIN HI1222//0.13:58:31//HAEMOPHILUS INFLUENZAE//P44129
35 F-HEMBA1005029//P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1)//0.76:72:31//GALLUS
GALLUS (CHICKEN)//P32250
F-HEMBA1005035//HOMEBOX PROTEIN HB9//0.0086:60:40//HOMO SAPIENS (HUMAN)//P50219
F-HEMBA1005039//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//0.47:49:32//HOMO SAPIENS
(HUMAN)//P22532
40 F-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16)//1.5e-19:39:100//MUS MUSCULUS
(MOUSE)//P35290
F-HEMBA1005050//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.074:34:44//BOS TAURUS (BOVINE)//
P25508
F-HEMBA1005062
45 F-HEMBA1005066//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//2.1e-44:126:65//HOMO SAPIENS (HU-
MAN)//P08547
F-HEMBA1005075//SUPPRESSOR PROTEIN SRP40//0.35:96:31//SACCHAROMYCES CEREVISIAE (BAK-
ER'S YEAST)//P32583
F-HEMBA1005079//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/3.6e-20:75:64//HOMO SAPIENS (HU-
50 MAN)//P39191
F-HEMBA1005083//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.00015:72:34//BOS TAURUS (BO-
VINE)//P25508
F-HEMBA1005101//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)//
4.8e-10:176:25//DROSOPHILA MELANOGASTER (FRUIT FLY)//P48809
55 F-HEMBA1005113
F-HEMBA1005123//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-24:99:60//HOMO SAPIENS (HU-
MAN)//P39194
F-HEMBA1005133//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION//0.11:22:54//

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40490
 F-HEMBA1005149//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.7e-16:59:71//HOMO SAPIENS (HUMAN)//
 P39188
 5 F-HEMBA1005152//GENOME POLYPROTEIN 2 [CONTAINS: HELPER COMPONENT PROTEINASE (EC
 3.4.22.-) (HC-PRO); 70 KD PROTEIN]//1.0:77:27//BARLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN II-
 1) (BAYMV)//Q01207
 F-HEMBA1005159//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0.40:53:33//APIS MEL-
 LIFERA (HONEYBEE)//P34859
 10 F-HEMBA1005185//MYOSIN IB HEAVY CHAIN//0.011:58:48//DICTYOSTELIUM DISCOIDEUM (SLIME
 MOLD)//P34092
 F-HEMBA1005201//HYPOTHETICAL 56.6 KD PROTEIN C16C9.03 IN CHROMOSOME I//3.9e-67:241:53//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09817
 F-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)//3.8e-124:257:95//CANIS
 FAMILIARIS (DOG)//Q00004
 15 F-HEMBA1005206//CUTICLE COLLAGEN 1//0.010:118:33//CAENORHABDITIS ELEGANS//P08124
 F-HEMBA1005219//PTB-ASSOCIATED SPLICING FACTOR (PSF)//0.99:85:40//HOMO SAPIENS (HUMAN)//
 P23246
 F-HEMBA1005223//HYPOTHETICAL GENE 1.05 PROTEIN//0.31:75:28//BACTERIOPHAGE T3//P07715
 20 F-HEMBA1005232//HYPOTHETICAL 7.8 KD PROTEIN//0.99:48:29//VACCINIA VIRUS (STRAIN WR), AND
 VACCINIA VIRUS (STRAIN COPENHAGEN)//P20544
 F-HEMBA1005241//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-28:138:55//HOMO SAPIENS (HU-
 MAN)//P39193
 F-HEMBA1005244//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.014:39:41//HOMO SAPIENS
 (HUMAN)//P22531
 25 F-HEMBA1005251//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.55:15:46//DICENTRARCHUS LABRAX
 (EUROPEAN SEA BASS)//Q36362
 F-HEMBA1005252//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II)//0.088:33:42//ZEA MAYS
 (MAIZE)//P43401
 F-HEMBA1005274
 30 F-HEMBA1005275//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.96:42:45//HOMO SAPIENS (HUMAN)//
 P39188
 F-HEMBA1005293//PROBABLE COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)//0.55:98:
 30//CAENORHABDITIS ELEGANS//Q20168
 F-HEMBA1005296//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)//0.095:75:34//HOMO SAPIENS (HU-
 35 MAN)//Q02817
 F-HEMBA1005304//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.4e-33:103:74//HOMO SAPIENS (HU-
 MAN)//P39189
 F-HEMBA1005311//PERIOD CLOCK PROTEIN (FRAGMENT)//0.99:45:31//DROSOPHILA SALTANS (FRUIT
 FLY)//Q04536
 40 F-HEMBA1005314//HYPOTHETICAL 6.3 KD PROTEIN T19C3.3 IN CHROMOSOME III//0.98:30:30//
 CAENORHABDITIS ELEGANS//Q10009
 F-HEMBA1005315//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.1e-05:35:51//HOMO SAPIENS (HU-
 MAN)//P08547
 F-HEMBA1005318//OLFACTORY RECEPTOR-LIKE PROTEIN COR8 (FRAGMENT)//0.57:44:38//GALLUS
 45 GALLUS (CHICKEN)//Q98913
 F-HEMBA1005331//IMMEDIATE-EARLY PROTEIN IE180//0.57:106:33//PSEUDORABIES VIRUS (STRAIN IN-
 DIANA-FUNKHAUSER / BECKER) (PRV)//P11675
 F-HEMBA1005338//CARTIAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1)//1.8e-55:199:59//GALLUS
 GALLUS (CHICKEN)//P05099
 50 F-HEMBA1005353//CHLOROPLAST 30S RIBOSOMAL PROTEIN S17//0.88:33:36//PORPHYRA PURPUREA//
 P51305
 F-HEMBA1005359//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//1.1e-68:255:48//HOMO SA-
 PIENS (HUMAN)//P51522
 F-HEMBA1005367//ALPHA-AMYLASE INHIBITOR AAI//1.0:25:40//AMARANTHUS HYPOCHONDRIACUS
 55 (PRINCE'S FEATHER)//P80403
 F-HEMBA1005372
 F-HEMBA1005374//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-34:92:75//HOMO SAPIENS (HU-
 MAN)//P39194

F-HEMBA1005382//APOLIPOPROTEIN C-II (APO-CII)//0.99:39:33//BOS TAURUS (BOVINE)//P19034
 F-HEMBA1005389//HYPOTHETICAL 70.0 KD PROTEIN IN DNAK 3'REGION (ORF4)//0.82:164:31//LACTO-
 COCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS)//P42377
 F-HEMBA1005394//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION//0.98:44:38//
 5 AUTOGRAPH CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41703
 F-HEMBA1005403//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2)//0.066:64:29//MUS MUSCULUS
 (MOUSE)//P07978
 F-HEMBA1005408//50S RIBOSOMAL PROTEIN L33//0.77:32:25//BACILLUS SUBTILIS//Q06798
 F-HEMBA1005410//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE
 10 (EC 2.7.7.49); ENDONUCLEASE]//0.0065:38:52//MUS MUSCULUS (MOUSE)//P11369
 F-HEMBA1005411//TOXIN S4C8//0.16:46:28//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMES-
 ON'S MAMBA)//P25683
 F-HEMBA1005423//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE
 4 INHIBITOR C) (P18-INK4C)//4.3e-09:29:96//HOMO SAPIENS (HUMAN)//P42773
 15 F-HEMBA1005426//TOXIN C10S2C2//0.99:49:34//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAM-
 BA)//P25684
 F-HEMBA1005443//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.9e-16:78:60//HOMO SAPIENS (HUMAN)//
 P39188
 F-HEMBA1005447//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.99:57:31//DASYPUS NOVEMCINCTUS
 20 (NINE-BANDED ARMADILLO)//O21329
 F-HEMBA1005468//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENTS)//0.68:41:
 31//ARTEMIA SALINA (BRINE SHRIMP)//P19040
 F-HEMBA1005469
 F-HEMBA1005472//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.5e-39:142:70//HOMO SAPIENS (HU-
 25 MAN)//P08547
 F-HEMBA1005474//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.8e-10:44:68//HOMO SAPIENS (HU-
 MAN)//P39194
 F-HEMBA1005475//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (U1 SNRNP 70 KD) (SNRNP70)//9.2e-
 14:179:33//HOMO SAPIENS (HUMAN)//P08621
 30 F-HEMBA1005497
 F-HEMBA1005500//60S RIBOSOMAL PROTEIN L37//0.11:53:33//SCHISTOSOMA MANSONI (BLOOD
 FLUKE)//O44125
 F-HEMBA1005506
 F-HEMBA1005508
 35 F-HEMBA1005511//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.5e-30:92:73//HOMO SAPIENS (HUMAN)//
 P39194
 F-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-)//2.0e-39:95:61//DROSOPHILA
 MELANOGASTER (FRUIT FLY)//O02193
 F-HEMBA1005517//PROLINE-RICH PROTEIN MP-2 PRECURSOR//2.1e-06:56:44//MUS MUSCULUS
 40 (MOUSE)//P05142
 F-HEMBA1005518//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//5.8e-05:192:33//BOS TAURUS (BO-
 VINE)//P02453
 F-HEMBA1005520//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.0e-18:87:57//HOMO SAPIENS (HUMAN)//
 P39188
 45 F-HEMBA1005526//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/5.1e-22:77:54//HOMO SAPIENS (HU-
 MAN)//P39191
 F-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1)//1.2e-81:157:98//MUS MUSCULUS (MOUSE)//
 Q60809
 F-HEMBA1005530//POLLEN ALLERGEN AMB P 5-A PRECURSOR (AMB P V-A)//0.98:19:47//AMBROSIA PSI-
 50 LOSTACHYA (WESTERN RAGWEED)//P43174
 F-HEMBA1005548//TRANSCRIPTION FACTOR MAF1//1.4e-72:137:97//RATTUS NORVEGICUS (RAT)//
 P54842
 F-HEMBA1005552//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.7e-29:47:78//HOMO SAPIENS (HUMAN)//
 P39193
 55 F-HEMBA1005558//HYPOTHETICAL 25.6 KD PROTEIN IN ABF2-CHL12 INTERGENIC REGION//1.6e-20:202:
 30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04272
 F-HEMBA1005568
 F-HEMBA1005570//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3)//1.0:80:31//

CAENORHABDITIS ELEGANS //P24885
 F-HEMBA1005576//TRANSMEMBRANE PROTEIN SEX PRECURSOR //8.5e-58:152:75//HOMO SAPIENS (HUMAN) //P51805
 F-HEMBA1005577//KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A //0.98:57:36//OVIS ARIES (SHEEP) //P02438
 5 F-HEMBA1005581//SLIT PROTEIN PRECURSOR //1.1e-62:254:41//DROSOPHILA MELANOGASTER (FRUIT FLY) //P24014
 F-HEMBA1005582//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED) //0.0091:189:29//RATTUS NORVEGICUS (RAT) //P28023
 10 F-HEMBA1005583//HYPOTHETICAL 41.2 KD PROTEIN IN CPS REGION (ORF7) //0.83:119:23//KLEBSIELLA PNEUMONIAE //Q48453
 F-HEMBA1005588//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! //1.9e-17:108:53//HOMO SAPIENS (HUMAN) //P39188
 F-HEMBA1005593//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N) //0.23:24:54//HOMO SAPIENS (HUMAN) //P22532
 15 F-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) //2.7e-39:257:39//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD) //P34036
 F-HEMBA1005606
 F-HEMBA1005609//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!! //3.2e-20:27:96//HOMO SAPIENS (HUMAN) //P39192
 20 F-HEMBA1005616//LATE CONTROL GENE B PROTEIN (GPB) //0.48:51:33//BACTERIOPHAGE 186 //P08711
 F-HEMBA1005621//MITOTIC MAD2 PROTEIN //1.2e-06:137:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40958
 F-HEMBA1005627//HYPOTHETICAL 17.1 KD PROTEIN IN PUBS 3'REGION //0.18:100:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P38898
 25 F-HEMBA1005631
 F-HEMBA1005632//HYPOTHETICAL 7.4 KD PROTEIN //0.32:59:32//VACCINIA VIRUS (STRAIN WR) //P04309
 F-HEMBA1005634//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! //2.6e-14:93:58//HOMO SAPIENS (HUMAN) //P39188
 30 F-HEMBA1005666//HYPOTHETICAL PROTEIN KIAA0129 //2.1e-05:126:25//HOMO SAPIENS (HUMAN) //Q14142
 F-HEMBA1005670
 F-HEMBA1005679//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //2.2e-08:40:72//HOMO SAPIENS (HUMAN) //P08547
 35 F-HEMBA1005680//SMALL PROLINE-RICH PROTEIN 2-1 //0.015:19:47//HOMO SAPIENS (HUMAN) //P35326
 F-HEMBA1005685
 F-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3) //4.2e-38:98:81//HOMO SAPIENS (HUMAN) //Q15768
 40 F-HEMBA1005705//PROTEIN Q300 //0.11:23:56//MUS MUSCULUS (MOUSE) //Q02722
 F-HEMBA1005717
 F-HEMBA1005732//BACTENECIN 7 PRECURSOR (BAC7) //0.22:55:41//OVIS ARIES (SHEEP) //P50415
 F-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) //4.5e-18:167:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P25296
 45 F-HEMBA1005746
 F-HEMBA1005755//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //7.4e-30:69:65//HOMO SAPIENS (HUMAN) //P08547
 F-HEMBA1005765//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! //2.8e-19:60:63//HOMO SAPIENS (HUMAN) //P39194
 50 F-HEMBA1005780//METALLOTHIONEIN-I (MT-1) //1.0:31:38//COLUMBA LIVIA (DOMESTIC PIGEON) //P15786
 F-HEMBA1005813
 F-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE) //1.0e-23:200:31//GALLUS GALLUS (CHICKEN) //P00789
 55 F-HEMBA1005822//PROTEIN Q300 //0.0016:21:80//MUS MUSCULUS (MOUSE) //Q02722
 F-HEMBA1005829//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! //9.6e-33:96:73//HOMO SAPIENS (HUMAN) //P39194
 F-HEMBA1005834//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //1.6e-22:103:46//NYCTICEBUS COU-

CANG (SLOW LORIS)//P08548
 F-HEMBA1005852//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//8.8e-06:95:35//MUS MUSCULUS (MOUSE)//P05143
 F-HEMBA1005853//HYPOTHETICAL PROTEIN
 5 MJ0647//0.39:28:39//METHANOCOCCUS JANNASCHII//Q58063
 F-HEMBA1005884
 F-HEMBA1005891//HYPOTHETICAL PROTEIN MTH137//0.95:51:27//METHANOBACTERIUM THERMOAUTOTROPHICUM//O26240
 10 F-HEMBA1005894//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-29:81:71//HOMO SAPIENS (HUMAN)//P39195
 F-HEMBA1005909//HYPOTHETICAL 8.2 KD PROTEIN B0353.1 IN CHROMOSOME III//0.98:19:52//CAENORHABDITIS ELEGANS//Q10958
 F-HEMBA1005911//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-27:86:70//HOMO SAPIENS (HUMAN)//P39188
 15 F-HEMBA1005921//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-38:99:81//HOMO SAPIENS (HUMAN)//P39194
 F-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//2.3e-17:76:51//HOMO SAPIENS (HUMAN)//P51522
 F-HEMBA1005934//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.024:54:40//HOMO SAPIENS (HUMAN)//P39189
 20 F-HEMBA1005962
 F-HEMBA1005963//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//1.7e-32:89:79//BOS TAURUS (BOVINE)//P53620
 F-HEMBA1005990//HYPOTHETICAL BHLF1 PROTEIN//3.0e-09:180:36//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181
 25 F-HEMBA1005991//HYPOTHETICAL PROTEIN KIAA0032//3.0e-17:107:43//HOMO SAPIENS (HUMAN)//Q15034
 F-HEMBA1005999
 F-HEMBA1006002
 30 F-HEMBA1006005//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B)//0.0017:45:44//MUS MUSCULUS (MOUSE)//Q62267
 F-HEMBA1006031//BASIC PROLINE-RICH PEPTIDE IB-1//0.00016:84:39//HOMO SAPIENS (HUMAN)//P04281
 F-HEMBA1006035//DNAK PROTEIN 1 (HEAT SHOCK PROTEIN 70) (HSP70)//0.43:100:27//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//Q55154
 35 F-HEMBA1006036//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.2e-64:150:74//HOMO SAPIENS (HUMAN)//P39194
 F-HEMBA1006042
 F-HEMBA1006067//METALLOTHIONEIN A (MT-A)//0.86:34:41//THERMARCES CERBERUS//P52721
 40 F-HEMBA1006081
 F-HEMBA1006090//SODIUM/GLUCOSE COTRANSPORTER 3 (NA(+)/GLUCOSE COTRANSPORTER 3) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER)//0.87:35:54//SUS SCROFA (PIG)//P31636
 F-HEMBA1006091//EARLY NODULIN 20 PRECURSOR (N-20)//0.027:87:32//MEDICAGO TRUNCATULA (BARREL MEDIC)//P93329
 45 F-HEMBA1006100//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.1e-09:58:60//HOMO SAPIENS (HUMAN)//P39195
 F-HEMBA1006108//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION//5.6e-16:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53867
 F-HEMBA1006121//HOMEBOX PROTEIN CDX-1 (CAUDAL-TYPE HOMEBOX PROTEIN 1)//3.4e-05:106:37//HOMO SAPIENS (HUMAN)//P47902
 50 F-HEMBA1006124//50S RIBOSOMAL PROTEIN L33//1.0:12:83//BACILLUS STEAROTHERMOPHILUS//P23375
 F-HEMBA1006130//SEL-10 PROTEIN//7.7e-05:129:28//CAENORHABDITIS ELEGANS//Q93794
 F-HEMBA1006138//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.8e-13:41:73//HOMO SAPIENS (HUMAN)//P39194
 55 F-HEMBA1006142//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.3e-39:101:77//HOMO SAPIENS (HUMAN)//P39192
 F-HEMBA1006155//GENE 33 POLYPEPTIDE//0.21:70:31//RATTUS NORVEGICUS (RAT)//P05432

F-HEMBA1006158
 F-HEMBA1006173//PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.48) (STEP) (NEURAL-SPECIFIC PROTEIN-TYROSINE PHOSPHATASE) (FRAGMENT)//0.017:20:95//HOMO SAPIENS (HUMAN)//P54829
 5 F-HEMBA1006182//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.37:31:61//HOMO SAPIENS (HUMAN)//P39188
 F-HEMBA1006198//HOMEBOX PROTEIN HOX-B3 (HOX-2.7) (MH-23)//0.85:61:29//MUS MUSCULUS (MOUSE)//P09026
 F-HEMBA1006235//50S RIBOSOMAL PROTEIN L33//1.0:26:38//AQUIFEX AEOLICUS//O67756
 10 F-HEMBA1006248//MALE SPECIFIC SPERM PROTEIN MST84DB//0.0041:64:37//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643
 F-HEMBA1006252//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR DE-3//1.0:22:40//DOLICHOS AXILLARIS (MACROTYLOMA AXILLARE)//P01057
 F-HEMBA1006253//DISINTEGRIN ERISTICOPHIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)//0.95:19:47//ERISTOCOPHIS MACMAHONI (LEAF-NOSED VIPER)//P22826
 15 F-HEMBA1006259
 F-HEMBA1006268//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//7.0e-05:32:65//HOMO SAPIENS (HUMAN)//P39192
 F-HEMBA1006272//RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 2)//4.8e-112:248:78//HOMO SAPIENS (HUMAN)//P10264
 20 F-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT)//2.5e-71:164:75//HOMO SAPIENS (HUMAN)//P51003
 F-HEMBA1006283//50S RIBOSOMAL PROTEIN L32//0.81:27:44//THERMUS AQUATICUS (SUBSP. THERMOPHILUS)//P80339
 25 F-HEMBA1006284//CUTICLE COLLAGEN 2//0.36:42:40//CAENORHABDITIS ELEGANS//P17656
 F-HEMBA1006291//HYPOTHETICAL 43.3 KD PROTEIN IN EVGS-GLK INTERGENIC REGION//2.4e-37:143:31//ESCHERICHIA COLI//P76518
 F-HEMBA1006293//MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR//0.20:134:29//RATTUS NORVEGICUS (RAT)//Q63345
 30 F-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//2.1e-43:187:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38821
 F-HEMBA1006310//SIGNAL TRANSDUCER CD24 PRECURSOR (HEAT STABLE ANTIGEN) (HSA) (NECTADRIN)//0.71:46:39//RATTUS NORVEGICUS (RAT)//Q07490
 F-HEMBA1006328//RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48) (NUCLEOCAPSID PHOSPHOPROTEIN)//0.44:141:24//HUMAN PARAINFLUENZA 1 VIRUS (STRAIN CI-5/73)//P32531
 35 F-HEMBA1006334//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627//0.98:26:46//ARCHAE-OGLOBUS FULGIDUS//028646
 F-HEMBA1006344//EZRIN (P81) (CYTOVILLIN) (VILLIN-2)//8.8e-08:91:36//MUS MUSCULUS (MOUSE)//P26040
 F-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-)//9.1e-48:149:50//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q2193
 40 F-HEMBA1006349//METALLOTHIONEIN-LIKE PROTEIN 1//0.015:59:33//CASUARINA GLAUCA (SWAMP OAK)//Q39511
 F-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//6.8e-96:261:66//HOMO SAPIENS (HUMAN)//P28160
 45 F-HEMBA1006364//PUTATIVE ENDONUCLEASE C1F12.06C (EC 3.1.-)//0.97:60:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10348
 F-HEMBA1006377//EARLY NODULIN 20 PRECURSOR (N-20)//0.00023:110:35//MEDICAGO TRUNCATULA (BARREL MEDIC)//P93329
 F-HEMBA1006380
 50 F-HEMBA1006381//METALLOTHIONEIN-II//1.0:26:38//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA)//P15114
 F-HEMBA1006398//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//3.3e-26:123:52//HOMO SAPIENS (HUMAN)//P08547
 F-HEMBA1006416
 55 F-HEMBA1006419//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-24:102:50//HOMO SAPIENS (HUMAN)//P39189
 F-HEMBA1006421//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.1e-21:101:57//HOMO SAPIENS (HUMAN)//P39188

EP 1 074 617 A2

F-HEMBA1006424//HYPOTHETICAL PROTEIN IORF1.//0.85:55:30//BOVINE CORONAVIRUS (STRAIN ME-BUS), AND BOVINE CORONAVIRUS (STRAIN QUEBEC).//P22053
F-HEMBA1006426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.8e-36:78:74//HOMO SAPIENS (HUMAN).//P39195
5 F-HEMBA1006438//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//1.0:38:36//GUILLARDIA THETA (CRYPTO-MONAS PHI).//O78421
F-HEMBA1006445//RAS-LIKE PROTEIN 3.//1.9e-06:40:47//RHIZOMUCOR RACEMOSUS (MUCOR CIRCINELLOIDES F. LUSITANICUS).//P22280
F-HEMBA1006446
10 F-HEMBA1006461//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/4.1e-18:68:67//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1006467
F-HEMBA1006471
F-HEMBA1006474//40 KD PROTEIN.//1.1e-37:231:38//BORNA DISEASE VIRUS (BDV).//Q01552
15 F-HEMBA1006483//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-38:77:74//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1006485//HYPOTHETICAL 9.3 KD PROTEIN IN NAD3-NAD7 INTERGENIC REGION (ORF 79).//0.91:30:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38465
F-HEMBA1006486//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-12:78:51//HOMO SAPIENS (HUMAN).//P08547
20 F-HEMBA1006489//FUN34 PROTEIN.//0.94:58:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32907
F-HEMBA1006492//NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MWFE) (CI-MWFE).//0.87:44:36//HOMO SAPIENS (HUMAN).//O15239
25 F-HEMBA1006494//FERREDOXIN-LIKE PROTEIN IN NIF REGION.//0.11:46:26//RHIZOBIUM LEGUMINOSARUM (BIOVAR TRIFOLI).//P42711
F-HEMBA1006497
F-HEMBA1006502//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.15:26:73//HOMO SAPIENS (HUMAN).//P39188
30 F-HEMBA1006507//DIAPHANOUS PROTEIN.//0.0055:129:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608
F-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//1.1e-32:177:41//ESCHERICHIA COLI.//P25716
F-HEMBA1006530//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.052:84:26//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P15583
35 F-HEMBA1006535//INHIBITOR OF APOPTOSIS PROTEIN 1 (MIAP1) (MIAP-1).//6.6e-05:53:39//MUS MUSCULUS (MOUSE).//O08863
F-HEMBA1006540//PRESYNAPTIC PROTEIN SAP97 (SYNAPSE-ASSOCIATED PROTEIN 97) (DISCS, LARGE HOMOLOG 1).//2.1e-07:206:23//RATTUS NORVEGICUS (RAT).//Q62696
40 F-HEMBA1006546//PROBABLE E5 PROTEIN.//0.11:70:32//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553
F-HEMBA1006559//SUPPRESSOR PROTEIN SRP40.//0.015:221:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-HEMBA1006562//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).//1.5e-07:122:33//HOMO SAPIENS (HUMAN).//P10163
45 F-HEMBA1006566//CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (CDC2 HOMOLOG EG1 PROTEIN KINASE).//0.63:53:37//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P23437
F-HEMBA1006569//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//4.4e-06:88:39//BOS TAURUS (BOVINE).//P02465
F-HEMBA1006579
50 F-HEMBA1006583//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.011:61:40//MUS MUSCULUS (MOUSE).//P05142
F-HEMBA1006595//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.6e-34:93:77//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1006597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.9e-26:75:74//HOMO SAPIENS (HUMAN).//P39195
55 F-HEMBA1006612//SUPPRESSOR PROTEIN SRP40.//0.026:221:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-HEMBA1006617//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.6e-20:73:63//HOMO SAPIENS (HUMAN).//

P39188
 F-HEMBA1006624//HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION//2.6e-31:209:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40506
 F-HEMBA1006631//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION//1.5e-15:131:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53331
 5 F-HEMBA1006635
 F-HEMBA1006639//POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN 1) (PABP 1)//2.2e-11:48:75//MUS MUSCULUS (MOUSE)//P29341
 F-HEMBA1006643//LONG NEUROTOXIN CR1 PRECURSOR (KAPPA NEUROTOXIN)//0.28:48:27//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT)//P15817
 10 F-HEMBA1006648//ZINC FINGER PROTEIN 12 (ZINC FINGER PROTEIN KOX3) (FRAGMENT)//0.26:17:47//HOMO SAPIENS (HUMAN)//P17014
 F-HEMBA1006652//60S RIBOSOMAL PROTEIN L7//2.4e-44:206:47//MUS MUSCULUS (MOUSE)//P14148
 F-HEMBA1006653
 15 F-HEMBA1006659
 F-HEMBA1006665//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.018:43:58//HOMO SAPIENS (HUMAN)//P08547
 F-HEMBA1006674//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130)//2.9e-05:154:33//HOMO SAPIENS (HUMAN)//O00268
 20 F-HEMBA1006676//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//3.6e-09:52:51//OWENIA FUSIFORMIS//P21260
 F-HEMBA1006682
 F-HEMBA1006695//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.1e-06:35:65//HOMO SAPIENS (HUMAN)//P39188
 25 F-HEMBA1006696
 F-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 INTERGENIC REGION//3.4e-19:104:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53196
 F-HEMBA1006709//RETINOIC ACID RECEPTOR RXR-BETA//0.24:111:36//HOMO SAPIENS (HUMAN)//P28702
 30 F-HEMBA1006717
 F-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT)//5.8e-09:111:40//HOMO SAPIENS (HUMAN)//Q01485
 F-HEMBA1006744//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.8e-32:84:78//HOMO SAPIENS (HUMAN)//P39191
 35 F-HEMBA1006754//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.3e-75:220:62//HOMO SAPIENS (HUMAN)//P08547
 F-HEMBA1006758//VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VECADHERIN) (CADHERIN-5) (7B4 ANTIGEN) (CD144 ANTIGEN)//0.024:110:29//HOMO SAPIENS (HUMAN)//P33151
 F-HEMBA1006767
 40 F-HEMBA1006779//MITOCHONDRIAL RIBOSOMAL PROTEIN S12//0.67:19:42//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE)//Q34940
 F-HEMBA1006780
 F-HEMBA1006789//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.056:98:30//MUS MUSCULUS (MOUSE)//P05143
 45 F-HEMBA1006795//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//2.9e-11:143:30//NYCTICEBUS COUCANG (SLOW LORIS)//P08548
 F-HEMBA1006796//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)//0.16:38:42//MUS MUSCULUS (MOUSE)//P70315
 F-HEMBA1006807//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III//4.4e-75:184:77//CAENORHABDITIS ELEGANS//P34568
 50 F-HEMBA1006821//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.011:20:85//HOMO SAPIENS (HUMAN)//P39194
 F-HEMBA1006824//PROTEIN B11//0.44:27:44//VACCINIA VIRUS (STRAIN WR)//Q01229
 F-HEMBA1006832//HYPOTHETICAL 34.6 KD PROTEIN C13G5.2 IN CHROMOSOME III//1.0:46:36//CAENORHABDITIS ELEGANS//P34327
 55 F-HEMBA1006849
 F-HEMBA1006865//ACROSIN INHIBITORS IIA AND IIB (BUSI-II)//1.0:41:31//BOS TAURUS (BOVINE)//P01001
 F-HEMBA1006877//OXYSTEROL-BINDING PROTEIN//3.7e-26:239:36//ORYCTOLAGUS CUNICULUS (RAB-

BIT).//P16258
 F-HEMBA1006885//HYPOTHETICAL 27.2 KD PROTEIN F09E5.8 IN CHROMOSOME II.//4.5e-38:185:43//
 CAENORHABDITIS ELEGANS.//P52057
 F-HEMBA1006900
 5 F-HEMBA1006914//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2).//
 5.2e-27:269:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52488
 F-HEMBA1006921//CYTOTOXIN 3 (COMPONENT 3.20).//0.99:32:37//NAJA MELANOLEUCA (FOREST CO-
 BRA) (BLACK-LIPPED COBRA).//P01473
 F-HEMBA1006926//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//0.0024:148:
 10 33//RATTUS NORVEGICUS (RAT).//P54258
 F-HEMBA1006929//HYPOTHETICAL PROTEIN MJ0525.//0.95:35:20//METHANOCOCCUS JANNASCHII.//
 Q57945
 F-HEMBA1006936//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-
 3)(PRP-2/PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C)[CONTAINS: PEPTIDE P-C].//0.074:116:31//HOMO
 15 SAPIENS (HUMAN).//P02810
 F-HEMBA1006938
 F-HEMBA1006941//THIOREDOXIN H-TYPE 1 (TRX-H1).//2.1e-13:90:33//NICOTIANA TABACUM (COMMON
 TOBACCO).//P29449
 F-HEMBA1006949
 20 F-HEMBA1006973//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.75:29:55//BOS TAURUS (BOVINE).//
 P25508
 F-HEMBA1006976//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANS-
 FERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST)
 (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4).//3.9e-108:117:95//HOMO SAPIENS (HUMAN).//Q11206
 25 F-HEMBA1006993
 F-HEMBA1006996//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//
 0.12:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779
 F-HEMBA1007002//PLATELET GLYCOPROTEIN IX PRECURSOR (GP1X) (CD42A).//0.00096:60:33//HOMO SA-
 PIENS (HUMAN).//P14770
 30 F-HEMBA1007017//HYPOTHETICAL 7.2 KD PROTEIN IN CYAY-DAPF INTERGENIC REGION.//1.0:25:56//ES-
 CHERICHIA COLI.//P39166
 F-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN
 A) (DLC-A).//8.5e-120:278:80//GALLUS GALLUS (CHICKEN).//Q90828
 F-HEMBA1007045//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.1e-12:158:29//
 35 XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
 F-HEMBA1007051
 F-HEMBA1007052//60S RIBOSOMAL PROTEIN L37-B (L35) (YP55).//0.94:37:35//SACCHAROMYCES CERE-
 VISIAE (BAKER'S YEAST).//P51402
 F-HEMBA1007062//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:55:29//RHINOCEROS UNICORNIS
 40 (GREATER INDIAN RHINOCEROS).//Q96063
 F-HEMBA1007066//ECLOSION HORMONE PRECURSOR (ECDYSIS ACTIVATOR) (EH).//0.58:49:38//BOM-
 BYX MORI (SILK MOTH).//P25331
 F-HEMBA1007073//PUTATIVE SMALL MEMBRANE PROTEIN (ORF 4).//0.86:46:34//CANINE ENTERIC
 CORONAVIRUS (STRAIN INSAVC-1) (CCV).//P36696
 45 F-HEMBA1007078//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.6e-29:56:67//HOMO SAPIENS (HUMAN).//
 P39193
 F-HEMBA1007080//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.028:122:30//XENO-
 PUS LAEVIS (AFRICAN CLAWED FROG).//P17437
 F-HEMBA1007085//RTOA PROTEIN (RATIO-A).//7.4e-11:221:31//DICTYOSTELIUM DISCOIDEUM (SLIME
 50 MOLD).//P54681
 F-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//3.3e-29:173:36//METHANOCOCCUS JANNASCHII.//
 Q57626
 F-HEMBA1007112
 F-HEMBA1007113
 55 F-HEMBA1007121//INOSITOL POLYPHOSPHATE 1-PHOSPHATASE (EC 3.1.3.57) (IPP).//5.4e-07:90:28//HO-
 MO SAPIENS (HUMAN).//P49441
 F-HEMBA1007129//HIRUSTASIN.//0.88:37:32//HIRUDO MEDICINALIS (MEDICINAL LEECH) //P80302
 F-HEMBA1007147//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REGION.//0.92:23:34//

EP 1 074 617 A2

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53182
F-HEMBA1007149//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17)//0.0078:17:70//ESCHERICHIA COLI//P05834
5 F-HEMBA1007151//WDNM1 PROTEIN PRECURSOR//0.25:45:37//MUS MUSCULUS (MOUSE)//Q62477
F-HEMBA1007174//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION//6.9e-18:97:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47160
F-HEMBA1007178//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!9.8e-06:38:65//HOMO SAPIENS (HUMAN)//P39195
10 F-HEMBA1007194//GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM PRECURSOR (EC 1.1.1.49) (G6PD)//1.0:80:32//NICOTIANA TABACUM (COMMON TOBACCO)//Q43793
F-HEMBA1007203//PROTEIN A22//1.0:115:26//VARIOLA VIRUS//P33845
F-HEMBA1007206
F-HEMBA1007224//HYPOTHETICAL 35.7 KD PROTEIN C41C4.6 IN CHROMOSOME II//2.4e-05:92:30//CAENORHABDITIS ELEGANS//Q09275
15 F-HEMBA1007243//HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) (HGPRT) (HGPRTASE) (HPRT B)//3.1e-74:205:67//MUS MUSCULUS (MOUSE)//P00493
F-HEMBA1007251//VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23)//0.52:108:30//DROSOPHILA MELANOGASTER (FRUIT FLY)//P13238
F-HEMBA1007256
20 F-HEMBA1007267//CALICIN (FRAGMENT)//0.060:88:31//HOMO SAPIENS (HUMAN)//Q13939
F-HEMBA1007273//HYPOTHETICAL 8.1 KD PROTEIN (ORF65)//0.95:40:37//GUILLARDIA THETA (CRYPTOMONAS PHI)//O78421
F-HEMBA1007279//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!4.6e-24:98:64//HOMO SAPIENS (HUMAN)//P39188
25 F-HEMBA1007281
F-HEMBA1007288//HYPOTHETICAL 13.5 KD PROTEIN IN ZMS1-MNS1 INTERGENIC REGION//0.88:11:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47162
F-HEMBA1007300//CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17) (CGB-PDE)//2.7e-43:220:41//BOS TAURUS (BOVINE)//Q28156
30 F-HEMBA1007301//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR//3.3e-22:115:33//HOMO SAPIENS (HUMAN)//P02461
F-HEMBA1007319
F-HEMBA1007320//HYPOTHETICAL 28.0 KD PROTEIN IN GLOB-RNHA INTERGENIC REGION//1.0:48:37//ESCHERICHIA COLI//P75672
35 F-HEMBA1007322//THREONINE DEHYDRATASE OPERON ACTIVATOR PROTEIN//1.0:59:33//ESCHERICHIA COLI//P11866
F-HEMBA1007327
F-HEMBA1007341//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!9.1e-12:37:62//HOMO SAPIENS (HUMAN)//P39188
40 F-HEMBA1007342//PROBABLE E5 PROTEIN//0.89:96:29//PYGMY CHIMPANZEE PAPILLOMAVIRUS TYPE 1//Q02268
F-HEMBA1007347//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2)//0.92:62:43//OVIS ARIES (SHEEP)//Q29400
F-HEMBA1000005//WEAK NEUROTOXIN 5//0.98:30:33//NAJA NAJA (INDIAN COBRA)//P29179
45 F-HEMBA1000008//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!2.7e-35:73:84//HOMO SAPIENS (HUMAN)//P39195
F-HEMBA1000018//HYPOTHETICAL BHLF1 PROTEIN//0.39:90:37//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181
F-HEMBA1000024//VIRE LOCUS 9 KD VIRULENCE PROTEIN//0.66:36:41//AGROBACTERIUM TUMEFACIENS//P08061
50 F-HEMBA1000025//MUSCARINIC TOXIN ALPHA (MT-ALPHA)//0.46:32:40//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA)//P80494
F-HEMBA1000030//SUPPRESSOR PROTEIN SRP40//6.7e-07:50:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583
55 F-HEMBA1000036//HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III//2.5e-07:120:29//CAENORHABDITIS ELEGANS//P46576
F-HEMBA1000037//HYPOTHETICAL 59.9 KD PROTEIN-IN SGA1-KTR7 INTERGENIC REGION//1.7e-05:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40492

EP 1 074 617 A2

F-HEMBB1000039//VERY HYPOTHETICAL 11.9 KD PROTEIN C4H3.12C IN CHROMOSOME I//1.0:61:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10219
F-HEMBB1000044
5 F-HEMBB1000048//HYPOTHETICAL 15.7 KD PROTEIN IN IDH-DEOR INTERGENIC REGION.//1.0:63:31//BACILLUS SUBTILIS //P54942
F-HEMBB1000050//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-14:34:79//HOMO SAPIENS (HUMAN)//P39194
F-HEMBB1000054//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.9e-31:45:73//HOMO SAPIENS (HUMAN)//P39193
10 F-HEMBB1000055//MUSCARINIC TOXIN ALPHA (MT-ALPHA)//1.0:14:57//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA)//P80494
F-HEMBB1000059//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.0e-21:82:59//HOMO SAPIENS (HUMAN)//P39195
15 F-HEMBB1000083//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN; WE-14]//0.87:172:28//RATTUS NORVEGICUS (RAT)//P10354
F-HEMBB1000089//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83)//1.0:42:33//ESCHERICHIA COLI//P46879
F-HEMBB1000099//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/7.7e-08:31:87//HOMO SAPIENS (HUMAN)//P39189
20 F-HEMBB1000103//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.4e-38:136:58//HOMO SAPIENS (HUMAN)//P08547
F-HEMBB1000113//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.9e-13:57:64//HOMO SAPIENS (HUMAN)//P39188
F-HEMBB1000119//MAF PROTEIN//3.6e-32:195:43//BACILLUS SUBTILIS//Q02169
25 F-HEMBB1000136//HYPOTHETICAL 12.7 KD PROTEIN IN PCS60-ABD1 INTERGENIC REGION//0.65:71:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38327
F-HEMBB1000141//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD)//0.00014:34:64//HOMO SAPIENS (HUMAN)//P20931
F-HEMBB1000144//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.0e-26:81:69//HOMO SAPIENS (HUMAN)//P39191
30 F-HEMBB1000173//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.2e-29:91:71//HOMO SAPIENS (HUMAN)//P39188
F-HEMBB1000175//ANTIMICROBIAL PEPTIDE ENAP-1 (FRAGMENT)//0.97:41:36//EQUUS CABALLUS (HORSE)//P80930
35 F-HEMBB1000198//HYPOTHETICAL 7.7 KD PROTEIN YCF33 (ORF67)//0.91:21:52//PORPHYRA PURPUREA//P51329
F-HEMBB1000215//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.4e-08:39:76//HOMO SAPIENS (HUMAN)//P39192
F-HEMBB1000217//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG)//2.9e-32:174:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q06624
40 F-HEMBB1000218//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.73:31:38//MICROTUS PENNSYLVANICUS (MEADOW VOLE)//P24949
F-HEMBB1000226//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II//6.5e-26:191:34//CAENORHABDITIS ELEGANS//Q09217
45 F-HEMBB1000240
F-HEMBB1000244//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-05:44:61//HOMO SAPIENS (HUMAN)//P39188
F-HEMBB1000250
F-HEMBB1000258
50 F-HEMBB1000264//CUTICLE COLLAGEN SQT-1 //0.15:89:33//CAENORHABDITIS ELEGANS//P12114
F-HEMBB1000266//TRANSLATION INITIATION FACTOR IF-2//2.7e-06:167:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39730
F-HEMBB1000272//CYTOCHROME C OXIDASE POLYPEPTIDE VIB (EC 1.9.3.1) (AED)//0.75:30:43//BOS TAURUS (BOVINE)//P00429
55 F-HEMBB1000274//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP)//1.0:38:36//SUS SCROFA (PIG)//P35323
F-HEMBB1000284//CALTRIN (CALCIUM TRANSPORT INHIBITOR)//1.0:56:30//MUS MUSCULUS (MOUSE)//Q09098

F-HEMBB1000307
 F-HEMBB1000312
 F-HEMBB1000317//THROMBOSPONDIN 1 PRECURSOR//3.2e-32:135:43//HOMO SAPIENS (HUMAN)//
 P07996
 5 F-HEMBB1000318//PUTATIVE SMALL MEMBRANE PROTEIN (NONSTRUCTURAL PROTEIN NS3) (NON-
 STRUCTURAL 9.5 KD PROTEIN)//0.41:51:31//HUMAN CORONAVIRUS (STRAIN OC43)//Q04854
 F-HEMBB1000335//ZINC FINGER PROTEIN 13 (ZFP-13) (KROX-8 PROTEIN) (FRAGMENT)//0.82:33:45//MUS
 MUSCULUS (MOUSE)//P10754
 F-HEMBB1000336//ALDEHYDE OXIDASE (EC 1.2.3.1) (FRAGMENTS)//0.80:44:40//ORYCTOLAGUS CUNIC-
 10 ULUS (RABBIT)//P80456
 F-HEMBB1000337//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR
 SRP75)//0.94:118:22//HOMO SAPIENS (HUMAN)//Q08170
 F-HEMBB1000338//MALE SPECIFIC SPERM PROTEIN MST84DA//0.042:33:39//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01642
 15 F-HEMBB1000339//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-14:54:55//HOMO SAPIENS (HUMAN)//
 P39188
 F-HEMBB1000341//GENE 74 PROTEIN (GP74)//1.0:39:33//MYCOBACTERIOPHAGE L5//Q05289
 F-HEMBB1000343
 F-HEMBB1000354//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-15:83:56//HOMO SAPIENS (HUMAN)//
 20 P39188
 F-HEMBB1000369//PROTEIN Q300//0.99:27:40//MUS MUSCULUS (MOUSE)//Q02722
 F-HEMBB1000374//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.7e-34:56:78//HOMO SAPIENS (HUMAN)//
 P39189
 F-HEMBB1000376
 25 F-HEMBB1000391//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.0013:79:35//BOS TAURUS (BO-
 VINE)//P25508
 F-HEMBB1000399//CHECKPOINT PROTEIN RAD17//2.8e-15:187:31//SCHIZOSACCHAROMYCES POMBE
 (FISSION YEAST)//P50531
 F-HEMBB1000402//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT)//0.027:60:
 30 38//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE)//P15583
 F-HEMBB1000404//CYANELLE 50S RIBOSOMAL PROTEIN L28//0.94:29:27//CYANOPHORA PARADOXA//
 P48129
 F-HEMBB1000420//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)//0.023:97:35//HOMO SA-
 PIENS (HUMAN)//Q15427
 35 F-HEMBB1000434//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.8e-20:111:54//HOMO SAPIENS (HU-
 MAN)//P39194
 F-HEMBB1000438//HYPOTHETICAL 7.9 KD PROTEIN IN GP55-NRDG INTERGENIC REGION//0.93:24:50//
 BACTERIOPHAGE T4//P07076
 F-HEMBB1000441//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-23:85:70//HOMO SAPIENS (HUMAN)//
 40 P39188
 F-HEMBB1000449//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.88:27:51//HOMO SAPIENS (HUMAN)//
 P39195
 F-HEMBB1000455
 F-HEMBB1000472
 45 F-HEMBB1000480//PROTEIN STBC//1.0:52:30//ESCHERICHIA COLI//P11905
 F-HEMBB1000487//SHORT NEUROTOXIN 1 (NEUROTOXIN, ALPHA) (NEUROTOXIN II)//0.93:29:34//NAJA
 OXIANA (CENTRAL ASIAN COBRA) (OXUS COBRA)//P01427
 F-HEMBB1000490//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.3e-16:50:80//HOMO SAPIENS (HUMAN)//
 P39195
 50 F-HEMBB1000491
 F-HEMBB1000493//3A PROTEIN//1.0:51:35//AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAU-
 DETTE) (IBV)//P30237
 F-HEMBB1000510//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//9.7e-27:132:45//HOMO SAPIENS (HU-
 MAN)//P08547
 55 F-HEMBB1000518//CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1)//0.021:47:40//LEISHMANIA
 TARENTOLAE (SAUROLEISHMANIA TARENTOLAE)//P14546
 F-HEMBB1000523
 F-HEMBB1000530//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN)//9.8e-14:43:83//GALLUS

GALLUS (CHICKEN)//P32018
 F-HEMBB1000550//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3)//0.19:97:30//TRYPA-
 NOSTOMA BRUCEI BRUCEI//P04540
 F-HEMBB1000554//MATERNAL B9.10 PROTEIN (P30 B9.10)//0.94:82:25//XENOPUS LAEVIS (AFRICAN
 5 CLAWED FROG)//P40744
 F-HEMBB1000556//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)
 (TAFII-130) (TAFII130)//0.043:201:29//HOMO SAPIENS (HUMAN)//000268
 F-HEMBB1000564//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:5:2:34//METRIDIVM SENILE
 (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE)//O47493
 10 F-HEMBB1000573//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.3e-10:52:73//HOMO SAPIENS (HU-
 MAN)//P39191
 F-HEMBB1000575//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.8e-26:76:76//HOMO SAPIENS (HUMAN)//
 P39192
 F-HEMBB1000586//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3)
 15 (COMPLEX I-MLRQ) (CI-MLRQ)//0.74:23:52//HOMO SAPIENS (HUMAN)//O00483
 F-HEMBB1000589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.9e-25:61:75//HOMO SAPIENS (HUMAN)//
 P39193
 F-HEMBB1000591//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:34:35//PETROMYZON MARINUS
 (SEA LAMPREY)//Q35537
 20 F-HEMBB1000592//SMALL PROLINE-RICH PROTEIN 2-1//0.0016:49:42//HOMO SAPIENS (HUMAN)//P35326
 F-HEMBB1000593//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS)//0.0070:189:32//GALLUS GALLUS
 (CHICKEN)//P12105
 F-HEMBB1000598//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//5.7e-10:110:41//NYCTICEBUS COU-
 CANG (SLOW LORIS)//P08548
 25 F-HEMBB1000623//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III//0.0022:98:28//
 CAENORHABDITIS ELEGANS//P34284
 F-HEMBB1000630
 F-HEMBB1000631//ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOCEPTOR) (SUBTYPE
 C4)//8.8e-06:59:40//HOMO SAPIENS (HUMAN)//P18825
 30 F-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP)//7.3e-13:173:28//MUS MUSCU-
 LUS (MOUSE)//P27671
 F-HEMBB1000637//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.6e-41:94:82//HOMO SAPIENS (HUMAN)//
 P39193
 F-HEMBB1000638//INVOLUCRIN//1.9e-06:144:29//HOMO SAPIENS (HUMAN)//P07476
 35 F-HEMBB1000643//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.3e-30:77:76//HOMO SAPIENS (HUMAN)//
 P39195
 F-HEMBB1000649//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.5e-37:58:81//HOMO SAPIENS (HUMAN)//
 P39189
 F-HEMBB1000652//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-37:61:77//HOMO SAPIENS (HUMAN)//
 40 P39193
 F-HEMBB1000665//HYPOTHETICAL PROTEIN BBD24//0.83:38:36//BORRELIA BURGDORFERI (LYME DIS-
 EASE SPIROCHETE)//P70845
 F-HEMBB1000671//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.8e-51:74:71//HOMO SAPIENS (HU-
 MAN)//P08547
 45 F-HEMBB1000673//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB) (ST-H)//0.012:
 37:37//ESCHERICHIA COLI//P07965
 F-HEMBB1000684//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.1e-21:66:72//HOMO SAPIENS (HUMAN)//
 P39193
 F-HEMBB1000693//HUNTINGTIN ASSOCIATED PROTEIN 1 (HAP1)//5.2e-26:121:49//RATTUS NORVEGICUS
 50 (RAT)//P54256
 F-HEMBB1000705
 F-HEMBB1000706
 F-HEMBB1000709//HYPOTHETICAL 5.8 KD PROTEIN//1.0:29:44//CLOVER YELLOW MOSAIC VIRUS
 (CYMV)//P16485
 55 F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8B//7.4e-105:205:98//RATTUS NORVEGICUS (RAT)//
 P70550
 F-HEMBB1000726//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.4e-25:85:70//HOMO SAPIENS (HU-
 MAN)//P39194

EP 1 074 617 A2

F-HEMBB1000738//50S RIBOSOMAL PROTEIN L33//1.0:41:31//THERMUS AQUATICUS (SUBSP. THERMOPHILUS)//P35871
F-HEMBB1000749//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.3e-29:42:85//HOMO SAPIENS (HUMAN)//P39194
5 F-HEMBB1000763//NIFU PROTEIN//0.089:63:36//FRANKIA ALNI//P46045
F-HEMBB1000770//CALTRIN-LIKE PROTEIN II//0.98:13:69//CAVIA PORCELLUS (GUINEA PIG)//P22075
F-HEMBB1000774//HIGH MOBILITY GROUP PROTEIN HMG-Y//0.029:53:32//MUS MUSCULUS (MOUSE)//P17095
F-HEMBB1000781//MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (MEKK 2)//3.5e-75:144:98//MUS MUSCULUS (MOUSE)//Q61083
10 F-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION//2.6e-49:232:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39956
F-HEMBB1000790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.9e-16:93:51//HOMO SAPIENS (HUMAN)//P39188
15 F-HEMBB1000794
F-HEMBB1000807//MUSCARINIC ACETYLCHOLINE RECEPTOR M3//0.54:111:27//GALLUS GALLUS (CHICKEN)//P49578
F-HEMBB1000810
F-HEMBB1000821
20 F-HEMBB1000822//HYPOTHETICAL 10 KD PROTEIN (ORF 6)//0.10:50:34//NARCISSUS MOSAIC VIRUS (NMV)//P15099
F-HEMBB1000826//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD)//0.00025:73:39//HOMO SAPIENS (HUMAN)//P20931
F-HEMBB1000827//HYPOTHETICAL 7.4 KD PROTEIN//0.89:23:52//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)//P19302
25 F-HEMBB1000831//MALE SPECIFIC SPERM PROTEIN MST87F//0.98:35:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//P08175
F-HEMBB1000835//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//7.8e-31:96:46//HOMO SAPIENS (HUMAN)//P08547
30 F-HEMBB1000840//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.00012:102:36//NYCTICEBUS COUCANG (SLOW LORIS)//P08548
F-HEMBB1000848//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//7.3e-97:239:70//HOMO SAPIENS (HUMAN)//P08547
F-HEMBB1000852
35 F-HEMBB1000870
F-HEMBB1000876//METALLOTHIONEIN (MT)//0.99:14:64//PERCA FLUVIATILIS (PERCH)//P52725
F-HEMBB1000883//HYPOTHETICAL 7.8 KD PROTEIN (ORF62)//0.34:60:33//GUILLARDIA THETA (CRYPTOMONAS PHI)//O78459
F-HEMBB1000887//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE//1.0:26:42//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI)//Q48251
40 F-HEMBB1000888
F-HEMBB1000890
F-HEMBB1000893
F-HEMBB1000908//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.0074:45:51//HOMO SAPIENS (HUMAN)//P39188
45 F-HEMBB1000910//PROBABLE E5 PROTEIN//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58//P26552
F-HEMBB1000913//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.29:56:46//HOMO SAPIENS (HUMAN)//P39195
F-HEMBB1000915//CYTOCHROME B (EC 1.10.2.2)//2.5e-24:62:90//HOMO SAPIENS (HUMAN)//P00156
50 F-HEMBB1000917//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.9e-26:53:66//HOMO SAPIENS (HUMAN)//P39193
F-HEMBB1000927//NEURONAL CALCIUM SENSOR 1 (NCS-1) (FREQUENIN)//3.9e-44:182:45//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q91614
F-HEMBB1000947//SMALL PROLINE-RICH PROTEIN 2-1//0.24:69:27//HOMO SAPIENS (HUMAN)//P35326
55 F-HEMBB1000959//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.0e-31:89:68//HOMO SAPIENS (HUMAN)//P39195
F-HEMBB1000973//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR//0.96:66:36//BOS TAURUS (BOVINE)//O18739

EP 1 074 617 A2

F-HEMBB1000975//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG)//0.00042:77:41//HOMO SAPIENS (HUMAN)//P04196
F-HEMBB1000981
F-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN)//1.0e-18:
5 178:30//MUS MUSCULUS (MOUSE)//P28575
F-HEMBB1000991
F-HEMBB1000996//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3)//0.58:
34:35//ESCHERICHIA COLI//P33669
F-HEMBB1001004//PROBABLE E4 PROTEIN//0.24:110:35//HUMAN PAPILLOMAVIRUS TYPE 5B//P26550
10 F-HEMBB1001008
F-HEMBB1001011//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.
16)//3.2e-17:104:47//HOMO SAPIENS (HUMAN)//P17097
F-HEMBB1001014//EOTAXIN PRECURSOR (EOSINOPHIL CHEMOTACTIC PROTEIN)//1.0:58:39//RATTUS
NORVEGICUS (RAT)//P97545
15 F-HEMBB1001020//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.4e-07:36:75//HOMO SAPIENS (HUMAN)//
P39189
F-HEMBB1001024
F-HEMBB1001037//FERREDOXIN//1.0:52:25//MOORELLA THERMOACETICA (CLOSTRIDIUM THER-
MOACETICUM)//P00203
20 F-HEMBB1001047
F-HEMBB1001051//PROTEIN FAN (FACTOR ASSOCIATED WITH N-SMASE ACTIVATION)//3.4e-21:50:100//
HOMO SAPIENS (HUMAN)//Q92636
F-HEMBB1001056//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//0.0099:115:35//ORGYIA PSEUDOTSUGATA
MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341
25 F-HEMBB1001058//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-33:95:76//HOMO SAPIENS (HUMAN)//
P39192
F-HEMBB1001060//HYPOTHETICAL 8.2 KD PROTEIN ZC21.7 IN CHROMOSOME III//1.0:38:36//
CAENORHABDITIS ELEGANS//P34591
F-HEMBB1001063
30 F-HEMBB1001068
F-HEMBB1001096//NOXIUSTOXIN (NTX) (TOXIN II.11)//0.99:36:38//CENTRUROIDES NOXIUS (MEXICAN
SCORPION)//P08815
F-HEMBB1001102//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I//1.1e-27:115:36//
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09701
35 F-HEMBB1001105//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//0.80:70:40//
HOMO SAPIENS (HUMAN)//P28067
F-HEMBB1001112//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//1.1e-126:287:85//RATTUS
NORVEGICUS (RAT)//P38378
F-HEMBB1001114//HYPOTHETICAL 9.6 KD PROTEIN (ORF2)//0.84:62:27//BACTERIOPHAGE L2//P42537
40 F-HEMBB1001117
F-HEMBB1001119//COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR//1.6e-21:50:98//HOMO SAPIENS (HU-
MAN)//Q99715
F-HEMBB1001126//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II//1.7e-50:184:53//
CAENORHABDITIS ELEGANS//Q09296
45 F-HEMBB1001133//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.4e-09:53:62//HOMO SAPIENS (HUMAN)//
P39192
F-HEMBB1001137//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAG-
MENT)//2.0e-05:206:27//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414
F-HEMBB1001142//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.1e-05:46:56//HOMO SAPIENS (HUMAN)//
50 P39193
F-HEMBB1001151//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I//2.3e-23:109:44//
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10149
F-HEMBB1001153//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR//0.75:76:34//ASCARIS SUUM (PIG
ROUNDWORM) (ASCARIS LUMBRICOIDES)//P27393
55 F-HEMBB1001169//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-16:71:59//HOMO SAPIENS (HUMAN)//
P39195
F-HEMBB1001175//ANKYRIN//3.2e-12:169:31//MUS MUSCULUS (MOUSE)//Q02357
F-HEMBB1001177//PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG//9.4e-07:148:27//HOMO SAPIENS (HU-

MAN)//Q15269
 F-HEMBB1001182//HYPOTHETICAL 36.0 KD PROTEIN//1.3e-09:110:31//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//P54858
 F-HEMBB1001199
 5 F-HEMBB1001208//HYPOTHETICAL PROTEIN LAMBDA-SP5//0.053:23:47//MUS MUSCULUS (MOUSE)//
 P15974
 F-HEMBB1001209
 F-HEMBB1001210//HYPOTHETICAL PROTEIN LAMBDA-SP5//0.14:40:37//MUS MUSCULUS (MOUSE)//
 P15974
 10 F-HEMBB1001218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-19:49:67//HOMO SAPIENS (HU-
 MAN)//P39194
 F-HEMBB1001221//CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR (EC 1.9.3.1)//0.11:
 44:38//HOMO SAPIENS (HUMAN)//P14406
 F-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65)//2.0e-45:192:53//MUS MUSCULUS
 15 (MOUSE)//P46938
 F-HEMBB1001242//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN
 CHROMOSOME I//5.5e-37:226:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09876
 F-HEMBB1001249//OXALOACETATE DECARBOXYLASE GAMMA CHAIN (EC 4.1.1.3)//1.0:23:43//KLEBSIEL-
 LA PNEUMONIAE//P13155
 20 F-HEMBB1001253//METALLOTHIONEIN-IH (MT-1H) (METALLOTHIONEIN-0) (MT-0)//0.14:16:43//HOMO SA-
 PIENS (HUMAN)//P80294
 F-HEMBB1001254//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-12:40:75//HOMO SAPIENS (HUMAN)//
 P39195
 F-HEMBB1001267//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0e-12:33:78//HOMO SAPIENS (HUMAN)//
 25 P39193
 F-HEMBB1001271//HYPOTHETICAL 25.1 KD PROTEIN B0302.5 IN CHROMOSOME X//1.0:58:37//
 CAENORHABDITIS ELEGANS//Q10928
 F-HEMBB1001282//ANKYRIN HOMOLOG PRECURSOR//9.5e-13:206:31//CHROMATIUM VINOSUM//Q06527
 F-HEMBB1001288//COPPER HOMEOSTASIS PROTEIN .CUTC//4.6e-42:163:51//ESCHERICHIA COLI//
 30 P46719
 F-HEMBB1001289//HYPOTHETICAL PROTEIN ORF-1137//1.0e-05:106:26//MUS MUSCULUS (MOUSE)//
 P11260
 F-HEMBB1001294//GTP-BINDING PROTEIN TC10//1.3e-34:58:94//HOMO SAPIENS (HUMAN)//P17081
 F-HEMBB1001302//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3)//0.24:
 35 49:46//HOMO SAPIENS (HUMAN)//Q99626
 F-HEMBB1001304//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT)//1.0:
 17:70//LYCOPERSICON ESCULENTUM (TOMATO)//Q01157
 F-HEMBB1001314//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR//0.21:104:27//DROSOPHILA ERECTA
 (FRUIT FLY)//P13730
 40 F-HEMBB1001315//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.3e-24:53:71//HOMO SAPIENS (HUMAN)//
 P39195
 F-HEMBB1001317//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I//0.24:90:31//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09782
 F-HEMBB1001326//HYPOTHETICAL PROTEIN LAMBDA-SP5//0.36:26:50//MUS MUSCULUS (MOUSE)//
 45 P15974
 F-HEMBB1001331//HYPOTHETICAL BHLF1 PROTEIN//1.0:127:33//EPSTEIN-BARR VIRUS (STRAIN B95-8)
 (HUMAN HERPESVIRUS 4)//P03181
 F-HEMBB1001335//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT)//0.85:44:29//SCIARA CO-
 PROPHILA (FUNGUS GNAT)//Q01799
 50 F-HEMBB1001337//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.2e-20:62:62//HOMO SAPIENS (HU-
 MAN)//P39194
 F-HEMBB1001339//HYPOTHETICAL 17.3 KD PROTEIN CY1A11.16C//8.2e-07:123:34//MYCOBACTERIUM
 TUBERCULOSIS//Q50606
 F-HEMBB1001346//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.2e-14:60:45//HOMO SAPIENS (HU-
 55 MAN)//P08547
 F-HEMBB1001348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.6e-14:61:62//HOMO SAPIENS (HUMAN)//
 P39188
 F-HEMBB1001356

F-HEMBB1001364
 F-HEMBB1001366/HISTIDINE-RICH PROTEIN//0.87:26:42//PLASMODIUM FALCIPARUM (ISOLATE FCM17 /
 SENEGAL)//P14586
 F-HEMBB1001367//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/8.6e-40:146:61//HOMO SAPIENS (HU-
 5 MAN)//P39192
 F-HEMBB1001369
 F-HEMBB1001380//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.9e-25:49:83//HOMO SAPIENS (HUMAN)//
 P39193
 F-HEMBB1001384//BH3 INTERACTING DOMAIN DEATH AGONIST (BID)//0.80:95:29//MUS MUSCULUS
 10 (MOUSE)//P70444
 F-HEMBB1001387//PEA2 PROTEIN (PPF2 PROTEIN)//0.022:117:34//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P40091
 F-HEMBB1001394//ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE
 CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA
 15 A SUBUNIT)//0.38:85:31//MUS MUSCULUS (MOUSE)//P17426
 F-HEMBB1001410
 F-HEMBB1001424//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR//0.99:37:21//
 ORYZA SATIVA (RICE)//P12162
 F-HEMBB1001426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.0035:40:60//HOMO SAPIENS (HUMAN)//
 20 P39195
 F-HEMBB1001429//CYTOSOL AMINOPEPTIDASE (EC 3.4.11.1) (LEUCINE AMINOPEPTIDASE) (LAP) (LEU-
 CYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (EC 3.4.11.5) (PROLYL AMINOPEPTIDASE)//1.1e-
 99:21:86//BOS TAURUS (BOVINE)//P00727
 F-HEMBB1001436//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.4e-30:57:78//HOMO SAPIENS (HUMAN)//
 25 P39195
 F-HEMBB1001443//[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE PRECURSOR (PDP) (EC
 3.1.3.43) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT (PDPC))//2.5e-79:155:97//
 BOS TAURUS (BOVINE)//P35816
 F-HEMBB1001449
 F-HEMBB1001454//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAG-
 30 MENT)//1.1e-05:196:31//HOMO SAPIENS (HUMAN)//P10161
 F-HEMBB1001458//24 KD ANTIGEN (FRAGMENT)//0.94:18:50//PLASMODIUM CHABAUDI//P14592
 F-HEMBB1001463
 F-HEMBB1001464//PPF2L ANTIGEN (FRAGMENT)//1.0:45:28//PLASMODIUM FALCIPARUM (ISOLATE PALO
 35 ALTO / UGANDA)//P07765
 F-HEMBB1001482//GASTRULA ZINC FINGER PROTEIN XLGF16.1 (FRAGMENT)//4.2e-10:37:43//XENO-
 PUS LAEVIS (AFRICAN CLAWED FROG)//P18712 F-HEMBB1001500
 F-HEMBB1001521//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.4e-39:59:72//HOMO SAPIENS (HUMAN)//
 P39188
 F-HEMBB1001527//HOMEODOMAIN PROTEIN HOX-B5 (XLHBOX-4) (XHOX-1B) (FRAGMENT)//0.21:131:25//
 40 XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P09019
 F-HEMBB1001531//GENE 32 PROTEIN (GP32)//0.88:95:30//MYCOBACTERIOPHAGE L5//Q05241
 F-HEMBB1001535//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:31:38//LUMBRICUS TERRESTRIS
 (COMMON EARTHWORM)//Q34942
 45 F-HEMBB1001536
 F-HEMBB1001537//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/0.0063:52:50//HOMO SAPIENS (HU-
 MAN)//P39191
 F-HEMBB1001555//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.9e-23:69:63//HOMO SAPIENS (HUMAN)//
 P39188
 50 F-HEMBB1001562//RABPHILIN-3A//0.087:147:27//RATTUS NORVEGICUS (RAT)//P47709
 F-HEMBB1001564//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//5.9e-27:107:54//HOMO SAPIENS (HU-
 MAN)//P08547
 F-HEMBB1001565//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.9e-12:51:54//HOMO SAPIENS (HU-
 MAN)//P39194
 55 F-HEMBB1001585
 F-HEMBB1001586
 F-HEMBB1001588//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REGION//0.0031:31:48//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36140

F-HEMBB1001603
 F-HEMBB1001618//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE
 (EC 2.7.7.49); ENDONUCLEASE]//0.00076:47:44//MUS MUSCULUS (MOUSE)//P11369
 F-HEMBB1001619//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//1.0:52:32//HOMO SAPIENS
 5 (HUMAN)//P22531
 F-HEMBB1001630
 F-HEMBB1001635//METALLOTHIONEIN-LIKE PROTEIN TYPE 2 A//1.0:27:44//LYCOPERSICON ESCULEN-
 TUM (TOMATO)//Q40157
 F-HEMBB1001637//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//0.0042:26:73//HOMO SAPIENS (HUMAN)//
 10 P39188
 F-HEMBB1001641
 F-HEMBB1001653//SURVIVAL MOTOR NEURON PROTEIN 1//0.51:36:47//CANIS FAMILIARIS (DOG)//
 O02771
 F-HEMBB1001665//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1)//0.0030:135:34//HOMO SAPIENS (HU-
 15 MAN)//Q05925
 F-HEMBB1001668//PROBABLE 60S RIBOSOMAL PROTEIN L39//0.99:25:44//CAENORHABDITIS ELEGANS//
 P52814
 F-HEMBB1001673//HYPOTHETICAL 46.1 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//0.0054:128:
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38823
 20 F-HEMBB1001684//SUPPRESSOR PROTEIN SRP40//0.56:81:34//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P32583
 F-HEMBB1001685//CYTOCHROME C OXIDASE POLYPEPTIDE VIII-HEART PRECURSOR (EC 1.9.3.1) (VIIIb)
 (IX)//1.0:21:47//BOS TAURUS (BOVINE)//P10175
 F-HEMBB1001695//MYOSIN IC HEAVY CHAIN//8.9e-05:86:40//ACANTHAMOEBA CASTELLANII (AMOEBA)//
 25 P10569
 F-HEMBB1001704//!!!! ALU SUBFAMILY SX WARNING ENTRY!!!!//9.0e-08:35:71//HOMO SAPIENS (HUMAN)//
 P39195
 F-HEMBB1001706//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUA-
 MOUS CELL MARKER) (SPRP)//0.91:39:41//SUS SCROFA (PIG)//P35323
 30 F-HEMBB1001707//FERREDOXIN-LIKE PROTEIN IN NIF REGION//1.0:43:23//BRADYRHIZOBIUM JAPONI-
 CUM//P27394
 F-HEMBB1001717//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENT)//1.0:71:25//
 LEMUR CATTAL (RING-TAILED LEMUR)//Q34878
 F-HEMBB1001735//!!!! ALU SUBFAMILY SQ WARNING ENTRY!!!!//9.0e-35:97:74//HOMO SAPIENS (HU-
 35 MAN)//P39194
 F-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) (EIF3
 P116) (EIF3 P110)//0.00069:180:28//HOMO SAPIENS (HUMAN)//P55884
 F-HEMBB1001747
 F-HEMBB1001749//!!!! ALU SUBFAMILY SX WARNING ENTRY!!!!//1.8e-43:75:70//HOMO SAPIENS (HUMAN)//
 40 P39195
 F-HEMBB1001753//PROTEIN Q300//0.00091:16:81//MUS MUSCULUS (MOUSE)//Q02722
 F-HEMBB1001756//CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 (XE-P9)//0.94:35:42//XENO-
 PUS LAEVIS (AFRICAN CLAWED FROG)//Q91879
 F-HEMBB1001760
 45 F-HEMBB1001762//GENE 35 PROTEIN (GP35)//0.76:21:47//MYCOBACTERIOPHAGE L5//Q05245
 F-HEMBB1001785
 F-HEMBB1001797//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35//0.99:41:31//PORPHYRA PURPUREA//
 P51270
 F-HEMBB1001802
 50 F-HEMBB1001812//!!!! ALU SUBFAMILY SP WARNING ENTRY!!!!//2.2e-39:54:77//HOMO SAPIENS (HUMAN)//
 P39193
 F-HEMBB1001816//!!!! ALU SUBFAMILY SQ WARNING ENTRY!!!!//1.1e-19:97:57//HOMO SAPIENS (HU-
 MAN)//P39194
 F-HEMBB1001831//HYPOTHETICAL 45.6 KD PROTEIN IN COX5A-ALG11 INTERGENIC REGION//0.62:204:
 23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53951
 55 F-HEMBB1001834//GLYCINE-RICH RNA-BINDING PROTEIN 1 (FRAGMENT)//0.0014:40:45//SORGHUM VUL-
 GARE (SORGHUM)//Q99069
 F-HEMBB1001836//!!!! ALU SUBFAMILY SB2 WARNING ENTRY!!!!//7.1e-14:85:61//HOMO SAPIENS (HU-

MAN)//P39191
 F-HEMBB1001839//PROBABLE E4 PROTEIN//0.61:49:34//HUMAN PAPILLOMAVIRUS TYPE 6C//P20969
 F-HEMBB1001850
 F-HEMBB1001863//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-30:57:68//HOMO SAPIENS (HUMAN)//P39194
 5 F-HEMBB1001867
 F-HEMBB1001868//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//0.00036:47:53//NICOTIANA TABACUM (COMMON TOBACCO)//P13983
 F-HEMBB1001869//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.0e-11:95:45//HOMO SAPIENS (HUMAN)//P39188
 10 F-HEMBB1001872//HYPOTHETICAL 8.2 KD PROTEIN IN LEF8-FP INTERGENIC REGION//1.0:34:38//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41459
 F-HEMBB1001874
 F-HEMBB1001875
 15 F-HEMBB1001880
 F-HEMBB1001899//GENE 11 PROTEIN//1.0:45:31//SPIROPLASMA VIRUS SPV1-R8A2 B//P15902
 F-HEMBB1001905//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION//8.8e-54:216:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48234
 F-HEMBB1001906
 20 F-HEMBB1001908//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN//6.3e-51:138:80//HOMO SAPIENS (HUMAN)//Q92794
 F-HEMBB1001910
 F-HEMBB1001911
 F-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)//2.3e-27:71:70//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24574
 25 F-HEMBB1001921//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//9.8e-13:75:53//HOMO SAPIENS (HUMAN)//P08547
 F-HEMBB1001922
 30 F-HEMBB1001925//EPITHELIAL MEMBRANE PROTEIN-1 (EMP-1) (TUMOR-ASSOCIATED MEMBRANE PROTEIN)//1.0:55:30//MUS MUSCULUS (MOUSE)//P47801
 F-HEMBB1001930//HYPOTHETICAL 9.6 KD PROTEIN K10D2.7 IN CHROMOSOME III//0.43:49:26//CAENORHABDITIS ELEGANS//Q09412
 F-HEMBB1001944//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.1e-34:63:85//HOMO SAPIENS (HUMAN)//P39189
 35 F-HEMBB1001945//NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP)//0.28:45:40//AMARANTHUS CAUDATUS (LOVE-LIES-BLEEDING) (INCA-WHEAT)//P80450
 F-HEMBB1001947//PROTEIN UL24//0.48:42:47//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)//P10208
 F-HEMBB1001950//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION (O378)//1.6e-24:162:36//ESCHERICHIA COLI//P52062
 40 F-HEMBB1001952
 F-HEMBB1001953
 F-HEMBB1001957//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.7e-11:51:60//HOMO SAPIENS (HUMAN)//P39188
 45 F-HEMBB1001962//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.6e-24:163:42//HOMO SAPIENS (HUMAN)//P39188
 F-HEMBB1001967//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.1e-35:55:80//HOMO SAPIENS (HUMAN)//P39189
 F-HEMBB1001973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-37:108:75//HOMO SAPIENS (HUMAN)//P39192
 50 F-HEMBB1001983//LYSIS PROTEIN (E PROTEIN) (GPE)//0.84:45:37//BACTERIOPHAGE ALPHA-3//P31280
 F-HEMBB1001988
 F-HEMBB1001990
 F-HEMBB1001996//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.4e-14:98:40//HOMO SAPIENS (HUMAN)//P08547
 55 F-HEMBB1001997//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.1e-19:38:73//HOMO SAPIENS (HUMAN)//P39188
 F-HEMBB1002002//CYTOCHROME C BIOGENESIS PROTEIN CCSA//1.0:150:25//PORPHYRA PURPUREA//

P51369
 F-HEMBB1002005//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.6e-12:94:40//HOMO SAPIENS (HUMAN)//
 P39195
 F-HEMBB1002009
 5 F-HEMBB1002015//HYPOTHETICAL 7.7 KD PROTEIN IN MRR-TSR INTERGENIC REGION (F67)//1.0:17:47//
 ESCHERICHIA COLI//P39395
 F-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1)//2.4e-50:139:55//BLABERUS DIS-
 COIDALIS (TROPICAL COCKROACH)//P29981
 10 F-HEMBB1002043//HYPOTHETICAL 9.5 KD PROTEIN IN DHFR 3'REGION (ORF3)//0.052:40:42//HERPESVI-
 RUS SAIMIRI (SUBGROUP C / STRAIN 488)//P22577
 F-HEMBB1002044//CELLULOSE COMPLEMENTING PROTEIN//0.45:87:33//ACETOBACTER XYLINUM (AC-
 ETOBACTER PASTEURIANUS)//P37697
 F-HEMBB1002045//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.78:18:55//HOMO SAPIENS (HUMAN)//
 P03928
 15 F-HEMBB1002049
 F-HEMBB1002050//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC
 PEPTIDE P-F] (FRAGMENT)//1.0e-06:188:27//HOMO SAPIENS (HUMAN)//P02812
 F-HEMBB1002068//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4)//0.0023:56:44//GALLUS GALLUS (CHICK-
 EN)//P17277
 20 F-HEMBB1002069//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//
 0.0074:134:33//NICOTIANA TABACUM (COMMON TOBACCO)//P13983
 F-HEMBB1002092//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEM-
 BRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E]//2.4e-07:75:40//BABOON ENDOGENOUS VI-
 RUS (STRAIN M7)//P10269
 25 F-HEMBB1002094//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/1.9e-24:63:82//HOMO SAPIENS (HU-
 MAN)//P39191
 F-HEMBB1002115//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II)//0.94:26:42//ZEA MAYS
 (MAIZE)//P43401
 F-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4//4.6e-57:176:67//RATTUS NORVEGICUS (RAT)//
 30 P56163
 F-HEMBB1002139//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35//1.0:17:52//PORPHYRA PURPUREA//
 P51270
 F-HEMBB1002142//EARLY NODULIN 20 PRECURSOR (N-20)//0.087:52:36//MEDICAGO TRUNCATULA (BAR-
 REL MEDIC)//P93329
 35 F-HEMBB1002152//HYPOTHETICAL 12.3 KD PROTEIN IN RPL3-RPL33 INTERGENIC REGION (ORF102)//
 5.8e-05:61:37//CYANOPHORA PARADOXA//P15811
 F-HEMBB1002189//HYPOTHETICAL PROTEIN UL125//1.0:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN
 AD169)//P16835
 F-HEMBB1002190
 40 F-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN
 KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK)//1.2e-27:59:100//
 HOMO SAPIENS (HUMAN)//Q06418
 F-HEMBB1002217//ZINC FINGER PROTEIN 184 (FRAGMENT)//6.6e-22:106:50//HOMO SAPIENS (HUMAN)//
 Q99676
 45 F-HEMBB1002218//PROTEIN Q300//0.85:19:52//MUS MUSCULUS (MOUSE)//Q02722
 F-HEMBB1002232//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.6e-21:56:71//HOMO SAPIENS (HUMAN)//
 P39195
 F-HEMBB1002247
 F-HEMBB1002249//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.2e-29:93:69//HOMO SAPIENS (HU-
 MAN)//P39194
 50 F-HEMBB1002254//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-29:101:67//HOMO SAPIENS (HU-
 MAN)//P39194
 F-HEMBB1002255//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3)//1.0:73:28//PARA-
 MECIUM TETRAURELIA//P15579
 55 F-HEMBB1002266//GLUTAMIC ACID-RICH PROTEIN PRECURSOR//0.0079:151:26//PLASMODIUM FALCI-
 PARUM (ISOLATE FC27 / PAPUA NEW GUINEA)//P13816
 F-HEMBB1002280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//5.2e-15:182:36//NYCTICEBUS COU-
 CANG (SLOW LORIS)//P08548

F-HEMBB1002300
 F-HEMBB1002306//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.00011:26:84//HOMO SAPIENS (HUMAN)//P39195
 F-HEMBB1002327//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.1e-11:41:85//HOMO SAPIENS (HUMAN)//P39189
 5 F-HEMBB1002329//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION//9.9e-17:232:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40032
 F-HEMBB1002340
 F-HEMBB1002342//HYPOTHETICAL 32.5 KD PROTEIN IN MSH6-BMH2 INTERGENIC REGION//3.6e-40:102:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03835
 10 F-HEMBB1002358//THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE)//6.1e-30:63:96//HOMO SAPIENS (HUMAN)//P23919
 F-HEMBB1002359//HYPOTHETICAL 7.1 KD PROTEIN C6G9.01C IN CHROMOSOME I//0.97:28:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q92346
 15 F-HEMBB1002364//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT)//0.47:119:25//HOMO SAPIENS (HUMAN)//P12895
 F-HEMBB1002371//HYPOTHETICAL 15.5 KD PROTEIN C2F7.12 IN CHROMOSOME I PRECURSOR//3.0e-05:111:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09703
 F-HEMBB1002381//PUTATIVE CUTICLE COLLAGEN C09G5.4//0.34:105:34//CAENORHABDITIS ELEGANS//Q09455
 20 F-HEMBB1002383//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.049:103:32//AQUIFEX AEOLICUS//066566
 F-HEMBB1002387//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK PROTEIN 11)//0.18:75:28//RICKETTSIA TSUTSUGAMUSHI//P16626
 25 F-HEMBB1002409//HIGH MOBILITY GROUP PROTEIN HMG-Y//0.014:61:36//MUS MUSCULUS (MOUSE)//P17095
 F-HEMBB1002415
 F-HEMBB1002425//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.8e-18:55:70//HOMO SAPIENS (HUMAN)//P39194
 30 F-HEMBB1002442//LIN-10 PROTEIN//5.1e-15:121:31//CAENORHABDITIS ELEGANS//P34692
 F-HEMBB1002453//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.2e-32:54:75//HOMO SAPIENS (HUMAN)//P39189
 F-HEMBB1002457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-07:31:64//HOMO SAPIENS (HUMAN)//P39188
 35 F-HEMBB1002458//MALE SPECIFIC SPERM PROTEIN MST84DA//0.92:28:53//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01642
 F-HEMBB1002477//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT)//0.0066:198:27//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414
 40 F-HEMBB1002489//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)//0.030:182:28//HOMO SAPIENS (HUMAN)//Q15427
 F-HEMBB1002492
 F-HEMBB1002495//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-08:41:75//HOMO SAPIENS (HUMAN)//P39192
 F-HEMBB1002502//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT)//0.00030:31:77//HOMO SAPIENS (HUMAN)//P12895
 45 F-HEMBB1002509
 F-HEMBB1002510
 F-HEMBB1002520//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.8e-36:162:50//NYCTICEBUS COUCANG (SLOW LORIS)//P08548
 50 F-HEMBB1002522//7 KD PROTEIN (ORF 4)//0.77:32:40//CHRYSAANTHEMUM VIRUS B (CVB)//P37990
 F-HEMBB1002531
 F-HEMBB1002534//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.1e-36:80:73//HOMO SAPIENS (HUMAN)//P39195
 F-HEMBB1002545
 55 F-HEMBB1002550//HOMEODOMAIN PROTEIN HOX-D11 (HOX-4.6) (HOX-5.5)//3.8e-05:83:34//MUS MUSCULUS (MOUSE)//P23813
 F-HEMBB1002556
 F-HEMBB1002579//SPLICING FACTOR U2AF 35 KD SUBUNIT (U2 AUXILIARY FACTOR 35 KD SUBUNIT) (U2

SNRNP AUXILIARY FACTOR SMALL SUBUNIT) (FRAGMENT).//5.0e-06:27:77//SUS SCROFA (PIG).//Q29350
 F-HEMBB1002582//PROTEINASE INHIBITOR.//1.0:27:40//SOLANUM MELONGENA (EGGPLANT) (AUBER-
 GINE).//P01078
 F-HEMBB1002590//HYPOTHETICAL PROTEIN IN MMSB 3'REGION (ORF1) (FRAGMENT).//1.9e-20:90:54//
 5 PSEUDOMONAS AERUGINOSA.//P28812
 F-HEMBB1002596
 F-HEMBB1002600//NOVEL ANTIGEN 2 (NAG-2).//1.9e-60:187:59//HOMO SAPIENS (HUMAN).//O14817
 F-HEMBB1002601//M PROTEIN, SEROTYPE 6 PRECURSOR.//1.0:71:35//STREPTOCOCCUS PYOGENES.//
 P08089
 10 F-HEMBB1002603
 F-HEMBB1002607//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-
 MENT).//0.0032:142:33//HOMO SAPIENS (HUMAN).//P10162
 F-HEMBB1002610//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:79:49//HOMO SAPIENS (HU-
 MAN).//P08547
 15 F-HEMBB1002613//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.9e-08:41:60//HOMO SAPIENS (HUMAN).//
 P39188
 F-HEMBB1002614//HYPOTHETICAL 9.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS (STRAIN COPENHA-
 GEN).//P20553
 F-HEMBB1002617//INSECT TOXIN 1 (BOT IT1).//1.0:44:29//BUTHUS OCCITANUS TUNETANUS (COMMON
 20 EUROPEAN SCORPION).//P55902
 F-HEMBB1002623//HYPOTHETICAL 9.7 KD PROTEIN (ORF88) (PUTATIVE DNA-BINDING PROTEIN).//0.42:
 31:54//BACTERIOPHAGE P4.//P12552
 F-HEMBB1002635//STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE
 3) (MAP KINASE P49 3F12).//6.2e-17:44:95//HOMO SAPIENS (HUMAN).//P53779
 25 F-HEMBB1002664//SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEIN B (SM-B) (SNRNP-B)
 (SM11) (FRAGMENT).//1.0:57:36//RATTUS NORVEGICUS (RAT).//P17136
 F-HEMBB1002677//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.9e-06:194:34//NYCTICEBUS COU-
 CANG (SLOW LORIS).//P08548
 F-HEMBB1002683//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.96:56:
 30 35//LEMUR CATT (RING-TAILED LEMUR).//Q34879
 F-HEMBB1002684//SILLUCIN.//1.0:16:50//RHIZOMUCOR PUSILLUS.//P02885
 F-HEMBB1002686
 F-HEMBB1002692
 F-HEMBB1002697//HELIX-DESTABILIZING PROTEIN (SINGLE-STRANDED DNA BINDING PROTEIN) (GPV).//
 35 0.57:36:38//BACTERIOPHAGE FD, BACTERIOPHAGE F1, AND BACTERIOPHAGE M13.//P03669
 F-HEMBB1002699
 F-HEMBB1002702
 F-HEMBB1002705//HYPOTHETICAL 34.8 KD PROTEIN C4H3.04C IN CHROMOSOME I.//3.6e-40:180:37//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10212
 40 F-HEMBB1002712
 F-MAMMA1000009//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-32:95:75//HOMO SAPIENS (HU-
 MAN).//P39189
 F-MAMMA1000019
 F-MAMMA1000020//DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING] 5 (EC 1.14.13.8) (HEPATIC
 45 FLAVIN-CONTAINING MONOOXYGENASE 5) (FMO 5) (DIMETHYLANILINE OXIDASE 5).//5.2e-12:24:100//HO-
 MO SAPIENS (HUMAN).//P49326
 F-MAMMA1000025//BETA-2-MICROGLOBULIN PRECURSOR.//1.0:73:26//BRACHYDANIO RERIO (ZE-
 BRAFISH) (ZEBRA DANIO).//Q04475
 F-MAMMA1000043//HYPOTHETICAL PXBL-I PROTEIN (FRAGMENT).//0.057:130:31//BOVINE LEUKEMIA VI-
 50 RUS (JAPANESE ISOLATE BLV-1) (BLV).//P03412
 F-MAMMA1000045
 F-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//7.5e-44:138:55//MUS MUSCULUS
 (MOUSE).//P47226
 F-MAMMA1000057//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-39:92:69//HOMO SAPIENS (HU-
 55 MAN).//P39194
 F-MAMMA1000069//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0044:96:34//ORGYIA PSEUDOTSUGATA
 MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341
 F-MAMMA1000084//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.4e-28:94:73//HOMO SAPIENS (HU-

MAN)//P39195
 F-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--
 TRNA LIGASE) (CYSRS)//6.6e-38:90:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09860
 F-MAMMA1000092//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.4e-30:43:86//HOMO SAPIENS (HU-
 5 MAN)//P39192
 F-MAMMA1000103//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.038:17:52//HOMO SAPIENS
 (HUMAN)//P22531
 F-MAMMA1000117//50S RIBOSOMAL PROTEIN L24E (HL21/HL22)//0.90:25:48//HALOARcula MARISMOR-
 TUI (HALOBACTERIUM MARISMORTUI)//P14116
 10 F-MAMMA1000129//HYPOTHETICAL BHLF1 PROTEIN//0.0016:75:40//EPSTEIN-BARR VIRUS (STRAIN
 B95-8) (HUMAN HERPESVIRUS 4)//P03181
 F-MAMMA1000133
 F-MAMMA1000134//HYPOTHETICAL PROTEIN MJ0647//1.0:41:41//METHANOCOCCUS JANNASCHII//
 Q58063
 15 F-MAMMA1000139//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-3 SUBUNIT//0.99:
 69:28//BOS TAURUS (BOVINE), AND MUS MUSCULUS (MOUSE)//P29798
 F-MAMMA1000143//CALPAIN INHIBITOR (CALPASTATIN) (FRAGMENT)//0.023:111:27//MUS MUSCULUS
 (MOUSE)//P51125
 F-MAMMA1000155//PUTATIVE CUTICLE COLLAGEN C09G5.5//0.018:125:34//CAENORHABDITIS ELE-
 20 GANS//Q09456
 F-MAMMA1000163//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR (PERI-
 PLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN)//0.11:88:25//SHEWANEL-
 LA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS)//Q54463
 F-MAMMA1000171
 25 F-MAMMA1000173//DREBRIN E//7.6e-41:197:43//HOMO SAPIENS (HUMAN)//Q16643
 F-MAMMA1000175//GAMMA-THIONIN HOMOLOG PPT PRECURSOR//0.92:39:38//PETUNIA INTEGRIFOLIA
 (VIOLET-FLOWERED PETUNIA) (PETUNIA INFLATA)//Q40901
 F-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//2.4e-106:249:61//HOMO SA-
 PIENS (HUMAN)//P51523
 30 F-MAMMA1000198//MALE SPECIFIC SPERM PROTEIN MST84DD//0.0014:35:42//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01645
 F-MAMMA1000221
 F-MAMMA1000227//6.8 KD MITOCHONDRIAL PROTEOLIPID//1.0:30:40//MUS MUSCULUS (MOUSE)//
 P56379
 35 F-MAMMA1000241//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K)//1.0:40:37//PORPHYRA PUR-
 PUREA//P51370
 F-MAMMA1000251//HYPOTHETICAL 6.8 KD PROTEIN IN FIC-PPIA INTERGENIC REGION//0.99:29:48//SAL-
 MONELLA TYPHIMURIUM//P37771
 F-MAMMA1000254//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION//1.0:20:50//SACCHAROMYCES
 40 CEREVISIAE (BAKER'S YEAST)//P53820
 F-MAMMA1000257//HYPOTHETICAL 50.0 KD PROTEIN IN HEML 3'REGION (ORF2)//0.22:50:44//PSEU-
 DOMONAS AERUGINOSA//Q51470
 F-MAMMA1000264//GASTRIN-RELEASING PEPTIDE RECEPTOR (GRP-R) (GRP-PREFERRING BOMBESIN
 RECEPTOR)//0.80:39:43//HOMO SAPIENS (HUMAN)//P30550
 45 F-MAMMA1000266
 F-MAMMA1000270//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.5e-42:95:84//HOMO SAPIENS (HU-
 MAN)//P39189
 F-MAMMA1000277//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN]//
 0.0062:90:34//MUS MUSCULUS (MOUSE)//P28481
 50 F-MAMMA1000278//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT)//0.00096:59:33//HORDEUM VULGARE
 (BARLEY)//P17991
 F-MAMMA1000279//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.4e-17:56:76//HOMO SAPIENS (HU-
 MAN)//P39195
 F-MAMMA1000284//ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2)//
 0.017:146:30//MUS MUSCULUS (MOUSE)//Q61324
 55 F-MAMMA1000287//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-32:84:58//HOMO SAPIENS (HU-
 MAN)//P39189
 F-MAMMA1000302//C-HORDEIN (CLONE PC-919) (FRAGMENT)//1.0:42:33//HORDEUM VULGARE (BAR-

LEY)//P17992
 F-MAMMA1000307//PROBABLE E4 PROTEIN//0.21:71:30//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1)//
 P24832
 F-MAMMA1000309//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN)//0.0026:
 5 141:36//HOMO SAPIENS (HUMAN)//P27658
 F-MAMMA1000312
 F-MAMMA1000313//DNA REPAIR PROTEIN RAD51 HOMOLOG (25 KD PROTEIN) (FRAGMENT)//0.76:52:32//
 STAPHYLOCOCCUS AUREUS//P31337
 F-MAMMA1000331
 10 F-MAMMA1000339//50S RIBOSOMAL PROTEIN L29P//0.78:32:46//METHANOBACTERIUM THERMOAU-
 TOTROPHICUM//O26117
 F-MAMMA1000340//HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION//1.0:29:58//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36039
 F-MAMMA1000348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.5e-09:63:60//HOMO SAPIENS (HUMAN)//
 15 P39188
 F-MAMMA1000356//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.3e-05:42:52//HOMO SAPIENS (HUMAN)//
 P39188
 F-MAMMA1000360
 F-MAMMA1000361//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.4e-33:84:72//HOMO SAPIENS (HU-
 20 MAN)//P39189
 F-MAMMA1000372//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.6e-21:53:71//HOMO SAPIENS (HU-
 MAN)//P39193
 F-MAMMA1000385
 F-MAMMA1000388//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTI-
 25 VATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN)//0.40:72:36//HOMO SAPIENS (HUMAN)//P43489
 F-MAMMA1000395//RABPHILIN-3A (FRAGMENT)//0.032:125:25//MUS MUSCULUS (MOUSE)//P47708
 F-MAMMA1000402//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//3.1e-28:266:40//HOMO SAPIENS (HU-
 MAN)//P08547
 F-MAMMA1000410//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3)
 30 (COMPLEX I-13KD-B) (CI-13KD-B) (B13)//5.9e-06:32:68//HOMO SAPIENS (HUMAN)//Q16718
 F-MAMMA1000413//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE
 (EC 2.7.7.49); ENDONUCLEASE]//6.7e-05:93:31//MUS MUSCULUS (MOUSE)//P11369
 F-MAMMA1000414
 F-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III//4.1e-28:119:53//
 35 CAENORHABDITIS ELEGANS//Q09232
 F-MAMMA1000421//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-23:68:76//HOMO SAPIENS (HU-
 MAN)//P39194
 F-MAMMA1000422//METALLOTHIONEIN (MT)//0.037:42:42//GADUS MORHUA (ATLANTIC COD)//P51902
 F-MAMMA1000423
 40 F-MAMMA1000424//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.048:23:73//HOMO SAPIENS (HUMAN)//
 P39189
 F-MAMMA1000429//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5//2.7e-05:110:30//SAC-
 CHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q92331
 F-MAMMA1000431//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.4e-15:85:58//HOMO SAPIENS (HU-
 45 MAN)//P39194
 F-MAMMA1000444//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.3e-25:65:76//HOMO SAPIENS (HU-
 MAN)//P39194
 F-MAMMA1000446//ZYXIN//0.79:155:29//GALLUS GALLUS (CHICKEN)//Q04584
 F-MAMMA1000458//HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I//0.0048:46:43//
 50 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09713
 F-MAMMA1000468//PERIOD CLOCK PROTEIN (FRAGMENT)//0.50:20:55//DROSOPHILA ROBUSTA (FRUIT
 FLY)//Q03296
 F-MAMMA1000472//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-17:106:55//HOMO SAPIENS (HUMAN)//
 P39188
 55 F-MAMMA1000478//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.9e-35:80:68//HOMO SAPIENS (HU-
 MAN)//P39195
 F-MAMMA1000483//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.8e-24:74:77//HOMO SAPIENS (HU-
 MAN)//P39193

F-MAMMA1000490//TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112) (PTK-RL-18) (RESTING LYMPHOCYTE KINASE)//0.43:21:57//MUS MUSCULUS (MOUSE)//P42682
 F-MAMMA1000500//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)//0.61:33:54//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1)//P12506
 5 F-MAMMA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-32:43:83//HOMO SAPIENS (HUMAN)//P39194
 F-MAMMA1000516
 F-MAMMA1000522//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.0015:113:32//HOMO SAPIENS (HUMAN)//P08547
 10 F-MAMMA1000524//HYPOTHETICAL HOST RANGE 8.5 KD PROTEIN//1.0:63:31//VACCINIA VIRUS (STRAIN WR)//P17359
 F-MAMMA1000559//METALLOTHIONEIN-I (MT-I) (MT-IB/MT-IA)//0.31:16:50//CALLINECTES SAPIDUS (BLUE CRAB)//P55949
 F-MAMMA1000565//FERREDOXIN-TYPE PROTEIN NAPF//0.98:37:35//ESCHERICHIA COLI//P33939
 15 F-MAMMA1000567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.5e-37:95:76//HOMO SAPIENS (HUMAN)//P39195
 F-MAMMA1000576//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/4.1e-07:34:64//HOMO SAPIENS (HUMAN)//P39191
 F-MAMMA1000583
 20 F-MAMMA1000585//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-28:89:75//HOMO SAPIENS (HUMAN)//P39194
 F-MAMMA1000594//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-24:38:71//HOMO SAPIENS (HUMAN)//P39195
 F-MAMMA1000597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.1e-25:74:77//HOMO SAPIENS (HUMAN)//P39195
 25 F-MAMMA1000605//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-18:83:50//HOMO SAPIENS (HUMAN)//P39195
 F-MAMMA1000612//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION//4.0e-42:166:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P41318
 30 F-MAMMA1000616
 F-MAMMA1000621
 F-MAMMA1000623//METALLOTHIONEIN-IK (MT-1K)//0.0045:25:48//HOMO SAPIENS (HUMAN)//P80296
 F-MAMMA1000625//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.00078:79:35//MUS MUSCULUS (MOUSE)//P05143
 35 F-MAMMA1000643//HYPOTHETICAL 9.3 KD PROTEIN//1.0:25:28//MAGUARI VIRUS//P16607
 F-MAMMA1000664
 F-MAMMA1000669//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.2e-05:186:30//HOMO SAPIENS (HUMAN)//P08547
 F-MAMMA1000670//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.6e-06:195:30//MUS MUSCULUS (MOUSE)//P05143
 40 F-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-)//3.8e-28:184:35//AEDES AEGYPTI (YELLOW FEVER MOSQUITO)//P42660
 F-MAMMA1000684//DNA-BINDING PROTEIN (VMW21)//1.1e-07:55:56//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)//P04487
 45 F-MAMMA1000696//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-31:97:74//HOMO SAPIENS (HUMAN)//P39194
 F-MAMMA1000707//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA)//0.31:19:42//CALLINECTES SAPIDUS (BLUE CRAB)//P55950
 F-MAMMA1000713//XYLULOSE KINASE (EC 2.7.1.17) (XYLUKINASE)//1.6e-05:88:35//LACTOBACILLUS PENTOSUS//P21939
 50 F-MAMMA1000714//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE)//0.44:126:30//RATTUS NORVEGICUS (RAT)//P16636
 F-MAMMA1000718//METALLOTHIONEIN-IIIE (MT-2E)//1.0:51:31//ORYCTOLAGUS CUNICULUS (RABBIT)//P80292
 55 F-MAMMA1000720//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.3e-28:60:71//HOMO SAPIENS (HUMAN)//P39193
 F-MAMMA1000723//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//3.7e-14:63:53//HOMO SAPIENS (HUMAN)//P08547

EP 1 074 617 A2

F-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)//1.8e-43:258:43//HOMO SAPIENS (HUMAN)//O14647
F-MAMMA1000732//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.9e-12:76:55//HOMO SAPIENS (HUMAN)//P39188
5 F-MAMMA1000733
F-MAMMA1000734//NPL1 PROTEIN (SEC63 PROTEIN)//2.5e-18:181:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P14906
F-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I//5.4e-52:196:58//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P87115
10 F-MAMMA1000744//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/6.3e-36:144:47//HOMO SAPIENS (HUMAN)//P39190
F-MAMMA1000746
F-MAMMA1000752
F-MAMMA1000760//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/6.6e-29:75:72//HOMO SAPIENS (HUMAN)//P39195
15 F-MAMMA1000761//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-09:59:64//HOMO SAPIENS (HUMAN)//P39194
F-MAMMA1000775
F-MAMMA1000776//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.3e-35:99:74//HOMO SAPIENS (HUMAN)//P39193
20 F-MAMMA1000778//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-19:65:70//HOMO SAPIENS (HUMAN)//P39195
F-MAMMA1000782
F-MAMMA1000798//HYPOTHETICAL PROTEIN ORF-1137//0.015:59:37//MUS MUSCULUS (MOUSE)//P11260
25 F-MAMMA1000802//MYOSIN IC HEAVY CHAIN//0.35:94:41//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569
F-MAMMA1000824//ACTIN 1//0.046:60:31//ZEA MAYS (MAIZE)//P02582
F-MAMMA1000831//PROBABLE NI/FE-HYDROGENASE 1 B-TYPE CYTOCHROME SUBUNIT//1.0:30:46//ESCHERICHIA COLI//P19929
30 F-MAMMA1000839//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-28:80:58//HOMO SAPIENS (HUMAN)//P39188
F-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4)//1.5e-39:130:36//METHANOBACTERIUM THERMOAUTOTROPHICUM//O27540
35 F-MAMMA1000842//C-HORDEIN (CLONE PC-919) (FRAGMENT)//0.064:43:41//HORDEUM VULGARE (BARLEY)//P17992
F-MAMMA1000843
F-MAMMA1000845//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3)//0.43:58:34//DROSOPHILA YAKUBA (FRUIT FLY)//P03895
40 F-MAMMA1000851//CUTICLE COLLAGEN 34//0.019:107:29//CAENORHABDITIS ELEGANS//P34687
F-MAMMA1000855//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//0.00098:149:32//HOMO SAPIENS (HUMAN)//Q15428
F-MAMMA1000856//METALLOTHIONEIN (MT)//0.63:39:41//POTAMON POTAMIOS//P55952
F-MAMMA1000859//GLYCOPROTEIN X PRECURSOR//0.014:192:28//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1)//P28968
45 F-MAMMA1000862//DISINTEGRIN KISTRIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)//1.0:66:27//AGKISTRODON RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA)//P17494
F-MAMMA1000863//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.4e-16:41:68//HOMO SAPIENS (HUMAN)//P39188
50 F-MAMMA1000865//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT)//0.030:100:32//HOMO SAPIENS (HUMAN)//P81489
F-MAMMA1000867//APTOTOXIN IX (PARALYTIC PEPTIDE IX) (PP IX)//0.98:43:32//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER)//P49272
F-MAMMA1000875//PROLINE-RICH PEPTIDE P-B//0.18:21:47//HOMO SAPIENS (HUMAN)//P02814
55 F-MAMMA1000876//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-22:85:71//HOMO SAPIENS (HUMAN)//P39189
F-MAMMA1000877//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.2e-38:62:74//HOMO SAPIENS (HUMAN)//P39188

EP 1 074 617 A2

F-MAMMA1000880//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.49:79:32//BOS TAURUS (BOVINE)//
P25508
F-MAMMA1000883//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X//0.87:15:60//
CAENORHABDITIS ELEGANS//Q11116
5 F-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN
H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN
SENSITIVE GLYCOPROTEIN 120) (PK-120)//5.3e-17:130:40//HOMO SAPIENS (HUMAN)//Q14624
F-MAMMA1000905
F-MAMMA1000906
10 F-MAMMA1000908//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//8.0e-17:70:62//HOMO SAPIENS (HU-
MAN)//P08547
F-MAMMA1000914//HYPOTHETICAL 6.2 KD PROTEIN//0.97:36:36//THERMOPROTEUS TENAX VIRUS 1
(STRAIN KRA1) (TTV1)//P19299
F-MAMMA1000921
15 F-MAMMA1000931//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.6e-10:49:65//HOMO SAPIENS (HUMAN)//
P39188
F-MAMMA1000940//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32//0.42:22:54//RECLINOMONAS
AMERICANA//Q21281
F-MAMMA1000941//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.3e-25:55:69//HOMO SAPIENS (HUMAN)//
20 P39188
F-MAMMA1000942//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.3e-08:36:75//HOMO SAPIENS (HU-
MAN)//P39194
F-MAMMA1000943
F-MAMMA1000956//SMALL HISTIDINE-ALANINE-RICH PROTEIN PRECURSOR (SHARP) (ANTIGEN 57)//
25 0.041:122:25//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA)//P04930
F-MAMMA1000957//HEAT-STABLE ENTEROTOXIN A2 PRECURSOR (STA2)//0.024:37:37//ESCHERICHIA
COLI//Q47185
F-MAMMA1000962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//6.0e-39:61:78//HOMO SAPIENS (HU-
MAN)//P39189
30 F-MAMMA1000968//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//0.0054:29:72//HOMO SAPIENS (HUMAN)//
P39194
F-MAMMA1000975//CUTICLE COLLAGEN DPY-2 PRECURSOR//1.0:93:30//CAENORHABDITIS ELEGANS//
P35799
F-MAMMA1000979//PROLINE-RICH PEPTIDE P-B//0.012:12:66//HOMO SAPIENS (HUMAN)//P02814
35 F-MAMMA1000987//HYPOTHETICAL PROTEIN LAMBDA-SP34//1.0:47:40//MUS MUSCULUS (MOUSE)//
P15973
F-MAMMA1000998
F-MAMMA1001003//PROBABLE E5 PROTEIN//1.0:52:42//HUMAN PAPILLOMAVIRUS TYPE 33//P06426
F-MAMMA1001008//PROGASTRICIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C) (FRAGMENT)//3.2e-14:
40 131:35//MACACA FUSCATA FUSCATA (JAPANESE MACAQUE)//P03955
F-MAMMA1001021//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.016:61:42//STREPTO-
MYCES FRADIAE//P20186
F-MAMMA1001024
F-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R)
45 (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT)//2.4e-20:234:29//GALLUS GALLUS (CHICKEN)//
Q90674
F-MAMMA1001035//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.7e-15:52:78//HOMO SAPIENS (HU-
MAN)//P39193
F-MAMMA1001038//NEUROTOXIN II (TOXIN RP-II) (SODIUM CHANNEL TOXIN II)//0.53:25:48//RADIANTHUS
50 PAUMOTENSIS (SEA ANEMONE) (HETERACTIS PAUMOTENSIS)//P01534
F-MAMMA1001041//SPECTRIN BETA CHAIN, ERYTHROCYTE//6.3e-18:112:43//MUS MUSCULUS
(MOUSE)//P15508
F-MAMMA1001050
F-MAMMA1001059//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06//1.3e-34:187:47//SCHIZOSAC-
55 CHAROMYCES POMBE (FISSION YEAST)//Q09747
F-MAMMA1001067//PROTEIN Q300//0.36:12:75//MUS MUSCULUS (MOUSE)//Q02722
F-MAMMA1001073//HEPATOCTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 1 (HFH-1)//1.0:70:37//RAT-
TUS NORVEGICUS (RAT)//Q63244

F-MAMMA1001074//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.00067:163:32//HOMO SAPIENS (HUMAN)//P08547
 F-MAMMA1001075//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1)//0.53:72:34//HOMO SAPIENS (HUMAN)//P29374
 5 F-MAMMA1001078//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//5.0e-79:184:73//HOMO SAPIENS (HUMAN)//P08547
 F-MAMMA1001080//IG HEAVY CHAIN PRECURSOR V-III REGION (VH26)//1.7e-27:82:71//HOMO SAPIENS (HUMAN)//P01764
 F-MAMMA1001082
 10 F-MAMMA1001091//HYPOTHETICAL BHLF1 PROTEIN//3.1e-05:198:32//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181
 F-MAMMA1001092//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//7.1e-21:65:72//HOMO SAPIENS (HUMAN)//P08547
 F-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN)//1.0e-18:68:48//DROSOPHILA MELANOGASTER (FRUIT FLY)//P51521
 15 F-MAMMA1001110//PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR//0.080:108:37//MUS MUSCULUS (MOUSE)//P02463
 F-MAMMA1001126//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.3e-07:66:45//HOMO SAPIENS (HUMAN)//P39189
 20 F-MAMMA1001133//HYPOTHETICAL 13.2 KD PROTEIN IN RPS4A-BAT2 INTERGENIC REGION//0.96:43:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47174
 F-MAMMA1001139//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II//5.4e-42:81:62//CAENORHABDITIS ELEGANS//Q09201
 F-MAMMA1001143//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00014:36:66//HOMO SAPIENS (HUMAN)//P39188
 25 F-MAMMA1001145
 F-MAMMA1001154//CSBA PROTEIN//1.0:39:38//BACILLUS SUBTILIS//P37953
 F-MAMMA1001161//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.2e-23:53:64//HOMO SAPIENS (HUMAN)//P39188
 30 F-MAMMA1001162//CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27)//0.69:86:31//MUS MUSCULUS (MOUSE)//P41272
 F-MAMMA1001181//HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME III//0.00010:74:47//CAENORHABDITIS ELEGANS//Q18486
 F-MAMMA1001186//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.0e-32:44:86//HOMO SAPIENS (HUMAN)//P39194
 35 F-MAMMA1001191//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (FRAGMENT)//0.096:40:40//MACROPUS EUGENII (TAMMAR WALLABY)//Q28466
 F-MAMMA1001198//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN)//2.5e-75:204:70//HOMO SAPIENS (HUMAN)//P42566
 40 F-MAMMA1001202//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA)//0.52:46:32//CALLINECTES SAPIDUS (BLUE CRAB)//P55950
 F-MAMMA1001203//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//7.3e-11:82:58//HOMO SAPIENS (HUMAN)//P39192
 F-MAMMA1001206//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.9e-17:67:71//HOMO SAPIENS (HUMAN)//P39188
 45 F-MAMMA1001215//9 KD PROTEIN//1.0:51:33//HOMO SAPIENS (HUMAN)//P13994
 F-MAMMA1001220//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//3.4e-37:55:87//HOMO SAPIENS (HUMAN)//P39189
 F-MAMMA1001222//HYPOTHETICAL 73.6 KD PROTEIN CY49.21//3.7e-06:168:38//MYCOBACTERIUM TUBERCULOSIS//Q10690
 50 F-MAMMA1001243
 F-MAMMA1001244//TRP OPERON LEADER PEPTIDE//1.0:18:55//SERRATIA MARCESCENS//P03055
 F-MAMMA1001249//HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3'REGION (ORF57)//0.57:23:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA)//P34774
 55 F-MAMMA1001256//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.3e-07:79:44//HOMO SAPIENS (HUMAN)//P39188
 F-MAMMA1001259//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-)//0.046:86:32//MYCOPLASMA GENITALIUM//P47486

F-MAMMA1001260//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE //2.7e-05:219:27//HOMO SAPIENS (HUMAN) //P13535
 F-MAMMA1001268//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //9.7e-27:89:67//HOMO SAPIENS (HUMAN) //P08547
 5 F-MAMMA1001271//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN) //4.0e-06:126:38//HOMO SAPIENS (HUMAN) //P54259
 F-MAMMA1001274//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.4e-29:57:66//HOMO SAPIENS (HUMAN) //P39194
 F-MAMMA1001280//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17) //0.27:24:54//ESCHERICHIA COLI //P05834
 10 F-MAMMA1001292//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT) //1.3e-73:208:69//HOMO SAPIENS (HUMAN) //Q14681
 F-MAMMA1001296//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.9e-22:41:80//HOMO SAPIENS (HUMAN) //P39193
 15 F-MAMMA1001298//HYPOTHETICAL PROTEIN HI0371 //0.99:29:37//HAEMOPHILUS INFLUENZAE //P44668
 F-MAMMA1001305//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP) //9.9e-62:222:54//HOMO SAPIENS (HUMAN) //Q07960
 F-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD) //2.1e-09:46:60//HOMO SAPIENS (HUMAN) //P20931
 20 F-MAMMA1001324//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)] //2.5e-43:128:50//FRIEND MURINE LEUKEMIA VIRUS (ISOLATE PVC-211) (F-MULV) //P26808
 F-MAMMA1001330//HEMOGLOBIN ZETA CHAIN (FRAGMENTS) //0.30:51:37//MACROPUS EUGENII (TAMMAR WALLABY) //P81044
 25 F-MAMMA1001341//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR- INDUCIBLE NUCLEAR PROTEIN NUP475) //0.024:89:39//HOMO SAPIENS (HUMAN) //P26651
 F-MAMMA1001343//PROBABLE E5 PROTEIN //0.60:64:29//HUMAN PAPILLOMAVIRUS TYPE 16 //P06927
 F-MAMMA1001346//PROTEINASE INHIBITOR IIB (FRAGMENTS) //0.97:33:45//SOLANUM TUBEROSUM (POTATO) //P01082
 30 F-MAMMA1001383//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-30:86:77//HOMO SAPIENS (HUMAN) //P39194
 F-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG) //9.2e-91:195:92//HOMO SAPIENS (HUMAN) //P02750
 35 F-MAMMA1001397//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.5e-19:55:69//HOMO SAPIENS (HUMAN) //P39188
 F-MAMMA1001408//SALIVARY GLUE PROTEIN SGS-7 PRECURSOR //0.60:45:35//DROSOPHILA MELANOGASTER (FRUIT FLY) //P02841
 F-MAMMA1001411//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) //5.8e-06:153:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P08640
 40 F-MAMMA1001419//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.3e-16:99:51//HOMO SAPIENS (HUMAN) //P39194
 F-MAMMA1001420//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//0.0018:23:65//HOMO SAPIENS (HUMAN) //P39190
 45 F-MAMMA1001435//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.7e-22:60:58//HOMO SAPIENS (HUMAN) //P39195
 F-MAMMA1001442
 F-MAMMA1001446//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-23:48:75//HOMO SAPIENS (HUMAN) //P39194
 50 F-MAMMA1001452//GENE 35 PROTEIN (GP35) //0.61:31:45//MYCOBACTERIOPHAGE L5 //Q05245
 F-MAMMA1001465//HYPOTHETICAL PROTEIN E-115 //0.0026:68:38//HUMAN ADENOVIRUS TYPE 2 //P03290
 F-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT) //3.7e-94:201:92//MUS MUSCULUS (MOUSE) //P52623
 55 F-MAMMA1001487//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //4.6e-16:89:41//NYCTICEBUS COUCANG (SLOW LORIS) //P08548
 F-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-

TRAL PROTEINASE) (CANP) (MU-TYPE).//6.2e-59:86:97//HOMO SAPIENS (HUMAN).//P07384
 F-MAMMA1001502//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.21:79:30//STREPTOMYCES FRADIAE//
 P26800
 F-MAMMA1001510
 5 F-MAMMA1001522//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.67:98:31//STREPTO-
 MYCES FRADIAE//P20186
 F-MAMMA1001547//PROBABLE MOLYBDENUM-PTERIN BINDING PROTEIN//0.97:35:42//HAEMOPHILUS
 INFLUENZAE//P45183
 F-MAMMA1001551//HYPOTHETICAL PROTEIN MJ0458.1.//0.038:31:41//METHANOCOCCUS JANNASCHII//
 10 P81308
 F-MAMMA1001575
 F-MAMMA1001576//TUBULIN GAMMA CHAIN.//1.6e-86:162:99//XENOPUS LAEVIS (AFRICAN CLAWED
 FROG).//P23330
 F-MAMMA1001590//!!!! ALU SUBFAMILY SX WARNING ENTRY.!!!!//0.0035:38:55//HOMO SAPIENS (HUMAN).//
 15 P39195
 F-MAMMA1001600//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.85:53:33//HOMO SAPIENS
 (HUMAN).//P29279
 F-MAMMA1001604//HYPOTHETICAL 11.1 KD PROTEIN C30D11.02C IN CHROMOSOME I.//0.14:82:29//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09902
 20 F-MAMMA1001606//HIGH MOBILITY GROUP PROTEIN HMG1-C.//8.2e-05:77:37//HOMO SAPIENS (HUMAN).//
 P52926
 F-MAMMA1001620//!!!! ALU SUBFAMILY SX WARNING ENTRY.!!!!//5.5e-05:24:66//HOMO SAPIENS (HU-
 MAN).//P39195
 F-MAMMA1001627//CUTICLE COLLAGEN 40.//0.82:131:31//CAENORHABDITIS ELEGANS//P34804
 25 F-MAMMA1001630//!!!! ALU SUBFAMILY SQ WARNING ENTRY.!!!!//8.6e-26:57:78//HOMO SAPIENS (HU-
 MAN).//P39194
 F-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.9e-38:160:55//HOMO SAPIENS (HUMAN).//P49910
 F-MAMMA1001635
 F-MAMMA1001649//SPERM PROTAMINE P1.//0.39:31:41//TACHYGLOSSUS ACULEATUS ACULEATUS (AUS-
 30 TRALIAN ECHIDNA).//P35311
 F-MAMMA1001654//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
 TEIN KINASE 1).//5.6e-06:99:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P18160
 F-MAMMA1001663//VERY HYPOTHETICAL XYLU PROTEIN.//0.99:27:37//ESCHERICHIA COLI//P05056
 F-MAMMA1001670//CUTICLE COLLAGEN 1.//0.033:97:37//CAENORHABDITIS ELEGANS//P08124
 35 F-MAMMA1001671
 F-MAMMA1001679//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.92:32:50//HOMO SAPIENS (HU-
 MAN).//P08572
 F-MAMMA1001683//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.00026:147:34//STREP-
 TOMYCES FRADIAE//P20186
 40 F-MAMMA1001686
 F-MAMMA1001692//SMALL HYDROPHOBIC PROTEIN (SMALL PROTEIN 1A).//1.0:34:26//BOVINE RESPIRA-
 TORY SYNCYTIAL VIRUS (STRAIN A51908) (BRS).//P24616
 F-MAMMA1001711//!!!! ALU SUBFAMILY SQ WARNING ENTRY.!!!!//1.1e-28:56:69//HOMO SAPIENS (HU-
 MAN).//P39194
 45 F-MAMMA1001715//!!!! ALU SUBFAMILY J WARNING ENTRY.!!!!//1.6e-08:39:71//HOMO SAPIENS (HUMAN).//
 P39188
 F-MAMMA1001730//METALLOTHIONEIN-B (MTB).//1.0:17:64//STRONGYLOCENTROTUS PURPURATUS
 (PURPLE SEA URCHIN).//Q27287
 F-MAMMA1001735//TUBULIN BETA-5 CHAIN (CLASS-V).//5.1e-121:213:97//GALLUS GALLUS (CHICKEN).//
 50 P09653
 F-MAMMA1001740
 F-MAMMA1001743//!!!! ALU SUBFAMILY SX WARNING ENTRY.!!!!//1.3e-09:100:42//HOMO SAPIENS (HU-
 MAN).//P39195
 F-MAMMA1001744//POU DOMAIN PROTEIN 2.//0.97:59:38//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA
 55 DANIO).//Q90270
 F-MAMMA1001745//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-43:199:42//HOMO SAPIENS (HU-
 MAN).//P08547
 F-MAMMA1001751//TWK-8 PROTEIN.//2.9e-15:77:36//CAENORHABDITIS ELEGANS//P34410

EP 1 074 617 A2

F-MAMMA1001754//MALE SPECIFIC SPERM PROTEIN MST84DD//0.019:20:45//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q001645
F-MAMMA1001757//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION//0.94:30:43//PSEUDOMONAS PUTIDA//P25753
5 F-MAMMA1001760//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/4.6e-34:103:59//HOMO SAPIENS (HUMAN)//P39191
F-MAMMA1001764
F-MAMMA1001768//HYPOTHETICAL PROTEIN UL61//0.042:167:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169)//P16818
10 F-MAMMA1001769//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-29:97:69//HOMO SAPIENS (HUMAN)//P39194
F-MAMMA1001771//TRANSMEMBRANE PROTEIN SEX PRECURSOR//3.3e-09:123:32//HOMO SAPIENS (HUMAN)//P51805
F-MAMMA1001783//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-09:55:61//HOMO SAPIENS (HUMAN)//P39188
15 F-MAMMA1001785//RAS-RELATED PROTEIN RABC//1.9e-06:120:25//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P34143
F-MAMMA1001788//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//9.3e-29:46:76//HOMO SAPIENS (HUMAN)//P08547
20 F-MAMMA1001790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.7e-24:69:69//HOMO SAPIENS (HUMAN)//P39188
F-MAMMA1001806//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REGION//0.95:58:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36042
F-MAMMA1001812//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.8e-12:53:69//HOMO SAPIENS (HUMAN)//P39195
25 F-MAMMA1001815//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.11:30:70//HOMO SAPIENS (HUMAN)//P08547
F-MAMMA1001817//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.9e-16:86:55//HOMO SAPIENS (HUMAN)//P39188
30 F-MAMMA1001818
F-MAMMA1001820//VITTELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23)//0.0030:63:42//DROSOPHILA MELANOGASTER (FRUIT FLY)//P13238
F-MAMMA1001824//APTOTOXIN VII (PARALYTIC PEPTIDE VII) (PP VII)//0.99:26:34//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER)//P49271
35 F-MAMMA1001836//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-35:77:88//HOMO SAPIENS (HUMAN)//P39195
F-MAMMA1001837//ZINC FINGER PROTEIN 191//1.3e-27:106:58//HOMO SAPIENS (HUMAN)//O14754
F-MAMMA1001848//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.0e-19:92:58//HOMO SAPIENS (HUMAN)//P39188
40 F-MAMMA1001851
F-MAMMA1001854
F-MAMMA1001858//ISOTOCIN-NEUROPHYSIN IT 1 PRECURSOR//0.93:42:38//CATOSTOMUS COMMERSONI (WHITE SUCKER)//P15210
F-MAMMA1001864//PROBABLE ABC TRANSPORTER PERMEASE PROTEIN MG189//0.77:161:27//MYCOPLASMA GENITALIUM//P47435
45 F-MAMMA1001868//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70)//0.00013:219:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38911
F-MAMMA1001874//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2)//0.0075:76:31//MUS MUSCULUS (MOUSE)//P07978
50 F-MAMMA1001878//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT)//0.020:10:80//LYCOPERSICON ESCULENTUM (TOMATO)//Q01157
F-MAMMA1001880
F-MAMMA1001890//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.1e-34:56:83//HOMO SAPIENS (HUMAN)//P39192
55 F-MAMMA1001907//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-12:44:68//HOMO SAPIENS (HUMAN)//P39194
F-MAMMA1001908//HYPOTHETICAL 16.2 KD PROTEIN IN PRP24-RRN9 INTERGENIC REGION//0.00013:77:

37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q003525
 F-MAMMA1001931//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III//0.41:106:29//
 CAENORHABDITIS ELEGANS//Q09564
 F-MAMMA1001956//OCTAPEPTIDE-REPEAT PROTEIN T2//0.00053:149:30//MUS MUSCULUS (MOUSE)//
 5 Q06666
 F-MAMMA1001963//HYPOTHETICAL PROTEIN IN NAC 5'REGION (ORF X) (FRAGMENT)//1.0:46:28//KLEB-
 SIELLA AEROGENES//Q08600
 F-MAMMA1001969//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.7e-34:97:68//HOMO SAPIENS (HU-
 MAN)//P08547
 10 F-MAMMA1001970//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.2e-07:67:37//HOMO SAPIENS (HU-
 MAN)//P08547
 F-MAMMA1001992//PROTEIN Q300//0.53:14:71//MUS MUSCULUS (MOUSE)//Q02722
 F-MAMMA1002009//PROBABLE E5 PROTEIN//0.17:56:32//HUMAN PAPILLOMAVIRUS TYPE 31//P17385
 F-MAMMA1002011//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (PROTEIN KINASE
 15 C SUBSTRATE, 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L PROTEIN)//1.0:100:31//HOMO SAPIENS
 (HUMAN)//P29966
 F-MAMMA1002032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.1e-21:86:65//HOMO SAPIENS (HUMAN)//
 P39188
 F-MAMMA1002033//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.5e-20:67:58//HOMO SAPIENS (HUMAN)//
 20 P39188
 F-MAMMA1002041//MALE SPECIFIC SPERM PROTEIN MST84DC//1.0:17:52//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01644
 F-MAMMA1002042//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.19:45:46//HOMO SAPIENS (HUMAN)//
 P39192
 25 F-MAMMA1002047//TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXOGLUTARATE AMI-
 NOTRANSFERASE) (TAT)//0.0017:50:46//RATTUS NORVEGICUS (RAT)//P04694
 F-MAMMA1002056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.2e-37:70:77//HOMO SAPIENS (HU-
 MAN)//P39194
 F-MAMMA1002058//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-08:26:76//HOMO SAPIENS (HUMAN)//
 30 P39188
 F-MAMMA1002068//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//2.0e-11:78:46//HOMO SAPIENS (HU-
 MAN)//P08547
 F-MAMMA1002078//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.96:26:46//COTURNIX COTURNIX
 JAPONICA (JAPANESE QUAIL)//P50682
 35 F-MAMMA1002082//SUPPRESSOR PROTEIN SRP40//0.23:95:32//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P32583
 F-MAMMA1002084//HYPOTHETICAL 7.5 KD PROTEIN//1.0:40:35//VACCINIA VIRUS (STRAIN COPENHA-
 GEN)//P20520
 F-MAMMA1002093
 40 F-MAMMA1002108//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.00079:143:33//STREP-
 TOMYCES FRADIAE//P20186
 F-MAMMA1002118//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:43:34//METRIDIDIUM SENILE
 (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE)//O47493
 F-MAMMA1002125//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.9e-14:60:68//HOMO SAPIENS (HU-
 45 MAN)//P39192
 F-MAMMA1002132
 F-MAMMA1002140//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.4e-24:69:65//HOMO SAPIENS (HUMAN)//
 P39188
 F-MAMMA1002143//SERUM PROTEIN MSE55//2.1e-16:166:43//HOMO SAPIENS (HUMAN)//Q00587
 50 F-MAMMA1002145//36.4 KD PROLINE-RICH PROTEIN//0.00014:84:29//LYCOPERSICON ESCULENTUM (TO-
 MATO)//Q00451
 F-MAMMA1002153
 F-MAMMA1002155
 F-MAMMA1002156//METALLOPROTEINASE INHIBITOR PRECURSOR//0.90:58:34//STREPTOMYCES NI-
 55 GRESCENS//P01077
 F-MAMMA1002158
 F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)//6.0e-66:157:70//HOMO SAPI-
 ENS (HUMAN)//P15880

EP 1 074 617 A2

F-MAMMA1002174//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.5e-25:56:64//HOMO SAPIENS (HUMAN)//
P39188

5 F-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE
1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR
B) (NKEF-B)//9.0e-09:28:100//HOMO SAPIENS (HUMAN)//P32119

F-MAMMA1002209//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)
(TAFII-130) (TAFII130)//0.0023:132:33//HOMO SAPIENS (HUMAN)//O00268

10 F-MAMMA1002215//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//0.00032:68:35//HOMO SAPIENS (HU-
MAN)//P02452

F-MAMMA1002219//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//0.0079:224:24//SACCHARO-
MYCES CEREVISIAE (BAKER'S YEAST)//P25386

F-MAMMA1002230

15 F-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EX-
CHANGE FACTOR)//1.4e-118:151:94//RATTUS NORVEGICUS (RAT)//P70541

F-MAMMA1002243//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)//0.028:112:33//MUS
MUSCULUS (MOUSE)//P70315

F-MAMMA1002250//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)//0.0012:80:32//ORYCTOLA-
GUS CUNICULUS (RABBIT)//P06333

20 F-MAMMA1002267//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.17:139:28//TRYPANOSOMA
BRUCEI BRUCEI//P24499

F-MAMMA1002268//60S RIBOSOMAL PROTEIN L22//0.00026:163:30//DROSOPHILA MELANOGASTER
(FRUIT FLY)//P50887

F-MAMMA1002269//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE//0.35:14:57//HELICOBACTER PY-
LORI (CAMPYLOBACTER PYLORI)//Q48251

25 F-MAMMA1002282//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-05:32:65//HOMO SAPIENS (HU-
MAN)//P39192

F-MAMMA1002292//TROPOMYOSIN 2//1.4e-05:100:30//SACCHAROMYCES CEREVISIAE (BAKER'S
YEAST)//P40414

30 F-MAMMA1002293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.8e-25:127:44//HOMO SAPIENS (HUMAN)//
P39188

F-MAMMA1002294//ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF)//0.00011:138:38//BOVINE HERPESVI-
RUS TYPE 1 (STRAIN P8-2)//P30020

F-MAMMA1002297//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.15:144:30//SACCHAROMY-
CES CEREVISIAE (BAKER'S YEAST)//P32323

35 F-MAMMA1002298//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.0e-05:40:50//MUS MUSCULUS
(MOUSE)//P05143

F-MAMMA1002299//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0.84:65:32//STRUTHIO
CAMELUS (OSTRICH)//O21405

40 F-MAMMA1002308//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-29:61:73//HOMO SAPIENS (HUMAN)//
P39188

F-MAMMA1002310//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.00016:70:38//MUS
MUSCULUS (MOUSE)//P15265

F-MAMMA1002311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.4e-09:84:54//HOMO SAPIENS (HU-
MAN)//P39189

45 F-MAMMA1002312//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION (URF Y)//0.48:
48:33//BACTERIOPHAGE T4//P33084

F-MAMMA1002317

F-MAMMA1002319//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE
(EC 2.7.7.49); ENDONUCLEASE]//0.011:128:27//MUS MUSCULUS (MOUSE)//P11369

50 F-MAMMA1002322//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.2e-20:92:57//HOMO SAPIENS (HU-
MAN)//P39195

F-MAMMA1002329//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.051:33:36//XENOPUS LAEVIS (AFRI-
CAN CLAWED FROG)//P03931

55 F-MAMMA1002332//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.5e-20:116:51//HOMO SAPIENS (HU-
MAN)//P08547

F-MAMMA1002333//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.0017:214:31//BOS TAURUS (BO-
VINE)//P02453

F-MAMMA1002339//COPPER-METALLOTHIONEIN (CU-MT)//0.59:42:38//HELIX POMATIA (ROMAN SNAIL)

(EDIBLE SNAIL).//P55947
 F-MAMMA1002347//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.43:26:61//HOMO SAPIENS (HUMAN).//
 P39188
 5 F-MAMMA1002351//HYPOTHETICAL PROTEIN MJ0304.//2.3e-07:139:25//METHANOCOCCUS JANNAS-
 CHII.//Q57752
 F-MAMMA1002352
 F-MAMMA1002353//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00028:31:80//HOMO SAPIENS (HUMAN).//
 P39188
 10 F-MAMMA1002355//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.2e-28:87:73//HOMO SAPIENS (HU-
 MAN).//P39193
 F-MAMMA1002356//RELAXIN.//0.95:31:35//SQUALUS ACANTHIAS (SPINY DOGFISH).//P11953
 F-MAMMA1002359//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.93:44:36//GUILLARDIA THETA
 (CRYPTOMONAS PHI).//O78487
 15 F-MAMMA1002360//LATE L2 MU CORE PROTEIN PRECURSOR (PROTEIN X).//0.94:30:43//BOVINE ADENO-
 VIRUS TYPE 2 (MASTADENOVIRUS BOS2).//Q96626
 F-MAMMA1002361//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.0e-08:45:68//HOMO SAPIENS (HUMAN).//
 P39188
 F-MAMMA1002362//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.58:23:26//LUMBRICUS TERRESTRIS
 (COMMON EARTHWORM).//Q34942
 20 F-MAMMA1002380//SALIVARY GLUE PROTEIN SGS-3, PRECURSOR.//0.23:100:27//DROSOPHILA SIMU-
 LANS (FRUIT FLY).//P13729
 F-MAMMA1002384
 F-MAMMA1002385//HYPOTHETICAL 40.9 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//3.8e-14:125:
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38241
 25 F-MAMMA1002392//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:17:58//BRANCHIOSTOMALANCEO-
 LATUM (COMMON LANCELET) (AMPHIOXUS).//O21003
 F-MAMMA1002411//30S RIBOSOMAL PROTEIN S17.//0.85:49:32//SYNECHOCYSTIS SP. (STRAIN PCC
 6803).//P73311
 30 F-MAMMA1002413//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//0.97:41:
 39//DROSOPHILA AFFINIS (FRUIT FLY).//P51926
 F-MAMMA1002417//RFBJ PROTEIN.//0.99:31:35//SHIGELLA FLEXNERI.//P37786
 F-MAMMA1002427//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.6e-33:135:59//HOMO SAPIENS (HU-
 MAN).//P39194
 35 F-MAMMA1002428//HYPOTHETICAL PROTEIN C18.//0.97:34:44//SWINEPOX VIRUS (STRAIN KASZA)
 (SPV).//P32217
 F-MAMMA1002434//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.1e-36:56:78//HOMO SAPIENS (HU-
 MAN).//P39189
 F-MAMMA1002446
 40 F-MAMMA1002454//EARLY NODULIN 20 PRECURSOR (N-20).//0.77:57:45//MEDICAGO TRUNCATULA (BAR-
 REL MEDIC).//P93329
 F-MAMMA1002461//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//1.3e-05:193:32//CANIS FA-
 MILIARIS (DOG).//P50551
 F-MAMMA1002470//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION.//1.0e-75:231:
 60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795
 45 F-MAMMA1002475//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4 (SNF2-BETA) (BRG-1 PRO-
 TEIN) (MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR) (BRAHMA PROTEIN HOMOLOG 1).//0.013:
 99:30//HOMO SAPIENS (HUMAN).//P51532
 F-MAMMA1002480//NONSTRUCTURAL PROTEIN 5B.//1.0:23:43//HUMAN CORONAVIRUS (STRAIN 229E).//
 P19741
 50 F-MAMMA1002485//STANNIOCALCIN PRECURSOR.//2.1e-23:88:46//HOMO SAPIENS (HUMAN).//P52823
 F-MAMMA1002494//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP
 CRAYFISH).//P55848
 F-MAMMA1002498//6.7 KD PROTEIN (ORF 5).//1.0:26:42//BARLEY YELLOW DWARF VIRUS (ISOLATE PAV)
 (BYDV).//P09517
 55 F-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//5.0e-26:222:
 35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43571
 F-MAMMA1002530//CYTOSOLIC PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE
 2-ACYLHYDROLASE) / LYSOPHOSPHOLIPASE (EC 3.1.1.5).//4.5e-12:88:44//HOMO SAPIENS (HUMAN).//

P47712
 F-MAMMA1002545//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-29:97:71//HOMO SAPIENS (HUMAN)//P39195
 5 F-MAMMA1002554//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT)//0.46:54:40//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414
 F-MAMMA1002556//METALLOTHIONEIN 20-I ISOFORMS A AND B (MT-20-IA AND MT-20-IB)//0.99:21:47//MYTILUS EDULIS (BLUE MUSSEL)//P80251
 F-MAMMA1002566//TRANSCRIPTION FACTOR P65 (NUCLEAR FACTOR NF-KAPPA-B P65 SUBUNIT)//0.70:130:30//MUS MUSCULUS (MOUSE)//Q04207
 10 F-MAMMA1002571//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (FRAGMENT)//0.54:45:51//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P35084
 F-MAMMA1002573//PARATHYMOSIN//1.5e-07:69:46//HOMO SAPIENS (HUMAN)//P20962
 F-MAMMA1002585//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT)//0.38:36:36//MUS MUSCULUS (MOUSE)//P09542
 15 F-MAMMA1002590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.99:22:77//HOMO SAPIENS (HUMAN)//P39195
 F-MAMMA1002597//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-18:44:70//HOMO SAPIENS (HUMAN)//P39194
 F-MAMMA1002598//60S RIBOSOMAL PROTEIN L7//1.8e-16:40:100//HOMO SAPIENS (HUMAN)//P18124
 20 F-MAMMA1002603
 F-MAMMA1002612//30S RIBOSOMAL PROTEIN S16 (FRAGMENT)//1.0:29:37//THERMUS AQUATICUS//O07348
 F-MAMMA1002617//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT)//0.00041:81:34//RATTUS NORVEGICUS (RAT)//P10164
 25 F-MAMMA1002618//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT)//0.11:18:50//PSYCHODA CINE-REA//Q02027
 F-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)//1.8e-13:110:40//CAENORHABDITIS ELEGANS//Q09931
 30 F-MAMMA1002622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.4e-05:53:58//HOMO SAPIENS (HUMAN)//P39188
 F-MAMMA1002623//PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (EC 1.14.17.3) (PAM)//2.6e-07:37:78//HOMO SAPIENS (HUMAN)//P19021
 F-MAMMA1002625
 35 F-MAMMA1002629//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-19:49:73//HOMO SAPIENS (HUMAN)//P39188
 F-MAMMA1002636//COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT)//1.7e-07:189:32//HOMO SAPIENS (HUMAN)//P12110
 F-MAMMA1002637//KINESIN LIGHT CHAIN (KLC)//7.7e-54:227:52//RATTUS NORVEGICUS (RAT)//P37285
 40 F-MAMMA1002646//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//0.034:199:25//MUS MUSCULUS (MOUSE)//P19246
 F-MAMMA1002650//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)//1.7e-07:104:32//MUS MUSCULUS (MOUSE)//P97303
 F-MAMMA1002655//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//1.0:25:44//HOMO SAPIENS (HUMAN)//P22532
 45 F-MAMMA1002662
 F-MAMMA1002665//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.3e-07:54:57//HOMO SAPIENS (HUMAN)//P39194
 F-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME)//1.4e-10:144:31//ESCHERICHIA COLI//P27550
 50 F-MAMMA1002673//BREVICAN CORE PROTEIN PRECURSOR//0.76:64:39//BOS TAURUS (BOVINE)//Q28062
 F-MAMMA1002684//HYPOTHETICAL 11.8 KD PROTEIN IN GP55-NRDG INTERGENIC REGION//0.094:77:27//BACTERIOPHAGE T4//P07079
 55 F-MAMMA1002685//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.0017:177:34//RATTUS NORVEGICUS (RAT)//P02454
 F-MAMMA1002698
 F-MAMMA1002699//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION//1.2e-28:127:

EP 1 074 617 A2

47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47160
F-MAMMA1002701//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.0:14:92//HOMO SAPIENS (HUMAN)//
P39188
5 F-MAMMA1002708//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.9e-27:52:65//HOMO SAPIENS (HU-
MAN)//P39193
F-MAMMA1002711//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.7e-24:54:75//HOMO SAPIENS (HUMAN)//
P39188
F-MAMMA1002721
10 F-MAMMA1002727//SOX-13 PROTEIN (FRAGMENT)//0.70:36:38//MUS MUSCULUS (MOUSE)//Q04891
F-MAMMA1002728//HYPOTHETICAL 6.0 KD PROTEIN//1.0:25:44//THERMOPROTEUS TENAX VIRUS 1
(STRAIN KRA1) (TTV1)//P19305
F-MAMMA1002744//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION//1.0:52:34//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38834
F-MAMMA1002746//HYPOTHETICAL 5.6 KD PROTEIN (ORF A-45)//1.0:22:40//SULFOLOBUS VIRUS-LIKE
15 PARTICLE SSV1//P20198
F-MAMMA1002748
F-MAMMA1002754//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.1e-21:56:64//HOMO SAPIENS (HUMAN)//
P39188
20 F-MAMMA1002758//MALE SPECIFIC SPERM PROTEIN MST84DD//0.37:14:64//DROSOPHILA MELA-
NOGASTER (FRUIT FLY)//Q01645
F-MAMMA1002764//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.7e-32:79:60//HOMO SAPIENS (HU-
MAN)//P39194
F-MAMMA1002765//PARATHYMOSIN//0.79:63:28//BOS TAURUS (BOVINE)//P08814
F-MAMMA1002769//GAR2 PROTEIN//0.00037:192:27//SCHIZOSACCHAROMYCES POMBE (FISSION
25 YEAST)//P41891
F-MAMMA1002775//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME I//5.4e-54:240:49//
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09704
F-MAMMA1002780
F-MAMMA1002782//MARGATOXIN (MGTX)//1.0:31:38//CENTRUROIDES MARGARITATUS (SCORPION)//
30 P40755
F-MAMMA1002796//ICE NUCLEATION PROTEIN//0.0018:100:41//PSEUDOMONAS FLUORESCENS//
P09815
F-MAMMA1002807//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.3e-23:100:59//HOMO SAPIENS (HUMAN)//
P39188
35 F-MAMMA1002820//NEUROTOXIN IV (LQX IV)//1.0:18:50//LEIURUS QUINQUESTRIATUS QUINQUESTRIA-
TUS (EGYPTIAN SCORPION)//P01489
F-MAMMA1002830//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.7e-24:55:74//HOMO SAPIENS (HU-
MAN)//P39195
F-MAMMA1002833//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.6e-31:95:73//HOMO SAPIENS (HU-
40 MAN)//P39189
F-MAMMA1002835//HYPOTHETICAL 42.1 KD PROTEIN F13G3.3 IN CHROMOSOME I//1.0:54:37//
CAENORHABDITIS ELEGANS//Q19417
F-MAMMA1002838//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.5e-27:99:70//HOMO SAPIENS (HU-
MAN)//P39193
45 F-MAMMA1002842//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.3e-13:65:63//HOMO SAPIENS (HU-
MAN)//P39195
F-MAMMA1002843//METALLOTHIONEIN-II (MT-II)//0.97:19:47//MUS MUSCULUS (MOUSE)//P02798
F-MAMMA1002844//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//4.9e-08:119:36//
AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41479
50 F-MAMMA1002858//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.98:37:37//PAN TROGLODYTES
(CHIMPANZEE)//Q35647
F-MAMMA1002868//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.8e-10:51:62//HOMO SAPIENS (HUMAN)//
P39188
F-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN)//1.8e-95:194:
55 78//HOMO SAPIENS (HUMAN)//P48059
F-MAMMA1002871//G-PROTEIN COUPLED RECEPTOR HOMOLOG R33//1.0:51:35//RAT CYTOMEGALOVIRUS
(STRAIN MAASTRICHT)//O12000
F-MAMMA1002880

EP 1 074 617 A2

F-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN)//3.3e-22:180:35//HOMO SAPIENS (HUMAN)//P48060
 F-MAMMA1002886//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)//0.00011:148:39//ACANTHAMOEBA CASTELLANII (AMOEBA)//P19706
 5 F-MAMMA1002887
 F-MAMMA1002890//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.030:142:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323
 F-MAMMA1002892
 F-MAMMA1002895//HYPOTHETICAL PROTEIN UL61//0.00099:143:35//HUMAN CYTOMEGALOVIRUS (STRAIN AD169)//P16818
 10 F-MAMMA1002908//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)//0.12:44:43//ORYCTOLAGUS CUNICULUS (RABBIT)//P06333
 F-MAMMA1002909//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00011:28:75//HOMO SAPIENS (HUMAN)//P39188
 15 F-MAMMA1002930//BOMBYXIN A-7 PRECURSOR (BBX-A7) (4K-PROTHORACICOTROPIC HORMONE) (4K-PTTH)//0.99:45:46//BOMBYX MORI (SILK MOTH)//P26730
 F-MAMMA1002937//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1)//6.5e-24:147:34//HOMO SAPIENS (HUMAN)//P28698
 F-MAMMA1002938//CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE)//4.7e-11:44:68//MUS MUSCULUS (MOUSE)//Q61147
 20 F-MAMMA1002941//PROTEIN Q300//0.0076:21:61//MUS MUSCULUS (MOUSE)//Q02722
 F-MAMMA1002947//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//1.9e-08:152:38//STREPTOMYCES FRADIAE//P20186
 F-MAMMA1002964
 25 F-MAMMA1002970//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.0057:55:43//HOMO SAPIENS (HUMAN)//P39189
 F-MAMMA1002972//BRAIN-SPECIFIC HOMEODOMAIN PROTEIN 3A (BRN-3A) (OCT-T1) (HOMEODOMAIN PROTEIN RDC-1)//0.84:53:41//HOMO SAPIENS (HUMAN)//Q01851
 F-MAMMA1002973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/4.6e-11:54:68//HOMO SAPIENS (HUMAN)//P39192
 30 F-MAMMA1002982
 F-MAMMA1002987//HYPOTHETICAL 11.9 KD PROTEIN IN RPC8-MFA2 INTERGENIC REGION//0.17:47:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53906
 F-MAMMA1003003//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.6e-09:30:73//HOMO SAPIENS (HUMAN)//P39195
 35 F-MAMMA1003004//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.0071:41:58//HOMO SAPIENS (HUMAN)//P39195
 F-MAMMA1003007//SPERM PROTAMINE P1//0.0076:51:37//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA)//P35311
 40 F-MAMMA1003011//HISTONE MACRO-H2A.1//1.8e-60:175:70//RATTUS NORVEGICUS (RAT)//Q02874
 F-MAMMA1003013//ACTIN BINDING PROTEIN//0.097:83:31//SACCHAROMYCES EXIGUUS (YEAST)//P38479
 F-MAMMA1003015
 F-MAMMA1003019//MYOTUBULARIN//0.022:56:37//HOMO SAPIENS (HUMAN)//Q13496
 45 F-MAMMA1003026//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//0.0014:208:27//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341
 F-MAMMA1003031//PROBABLE E4 PROTEIN (E1^E4)//0.14:49:32//HUMAN PAPILLOMAVIRUS TYPE 6B//P06459
 F-MAMMA1003035//HYPOTHETICAL 24.4 KD PROTEIN IN LPD 3'REGION (ORF4)//5.1e-12:112:34//ZYMOONAS MOBILIS//O66114
 50 F-MAMMA1003039//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.4e-07:68:54//HOMO SAPIENS (HUMAN)//P39188
 F-MAMMA1003040//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/2.8e-39:90:57//HOMO SAPIENS (HUMAN)//P39190
 55 F-MAMMA1003044
 F-MAMMA1003047//SPERM HISTONE P2 PRECURSOR (PROTAMINE 2)//0.18:25:44//BOS TAURUS (BOVINE)//P19782
 F-MAMMA1003049//PROBABLE E4 PROTEIN//0.50:67:29//HUMAN PAPILLOMAVIRUS TYPE 6C//P20969

F-MAMMA1003055//WEAK TOXIN CM-2//0.99:23:30//NAJA HAJE HAJE (EGYPTIAN COBRA)//P01415
 F-MAMMA1003056//EXPORTED PROTEIN 7 (FRAGMENT)//1.0:52:32//STREPTOCOCCUS PNEUMONIAE//
 P35597
 F-MAMMA1003057//MD6 PROTEIN//1.5e-85:168:95//MUS MUSCULUS (MOUSE)//Q60584
 5 F-MAMMA1003066//REGB PROTEIN//1.0:62:27//PSEUDOMONAS AERUGINOSA//Q03381
 F-MAMMA1003089//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/5.1e-15:44:77//HOMO SAPIENS (HU-
 MAN)//P39190
 F-MAMMA1003099//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAMIN) (FILAMIN
 1)//4.8e-20:80:62//HOMO SAPIENS (HUMAN)//P21333
 10 F-MAMMA1003104//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII//0.98:22:40//SYNECHOCOCCUS
 ELONGATUS NAEGELI//P25900
 F-MAMMA1003113//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS)//0.67:35:45//GALLUS
 GALLUS (CHICKEN)//P02467
 F-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA)//5.2e-34:141:56//MUS MUSCULUS (MOUSE)//P46735
 15 F-MAMMA1003135//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION//3.6e-05:91:
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47170
 F-MAMMA1003140
 F-MAMMA1003146//MALE SPECIFIC SPERM PROTEIN MST87F//1.0:33:36//DROSOPHILA MELANOGASTER
 (FRUIT FLY)//P08175
 20 F-MAMMA1003150//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II//4.4e-10:254:30//
 CAENORHABDITIS ELEGANS//Q09625
 F-MAMMA1003166//BRAIN PROTEIN H5//4.0e-42:182:48//HOMO SAPIENS (HUMAN)//O43236
 F-NT2RM1000001//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70)//0.15:
 38:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA)//P34779
 25 F-NT2RM1000018
 F-NT2RM1000032//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.51:17:41//CYPRINUS CARPIO (COM-
 MON CARP)//P24948
 F-NT2RM1000035//3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (EC 1.1.1.34) (HMG-COA
 REDUCTASE)//0.00011:114:27//BLATTELLA GERMANICA (GERMAN COCKROACH)//P54960
 30 F-NT2RM1000037//METALLOTHIONEIN-II (MT-II)//0.025:19:47//SCYLLA SERRATA (MUD CRAB)//P02806
 F-NT2RM1000039//VITELLINE MEMBRANE VM34CA PROTEIN PRECURSOR//0.00083:84:33//DROSOPHILA
 MELANOGASTER (FRUIT FLY)//Q06521
 F-NT2RM1000055//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR//1.1e-07:34:55//PLASMODIUM LOPHU-
 RAE//P04929
 35 F-NT2RM1000059//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PRO-
 TEIN 2) (XMEF2) (RSRFR2)//0.18:83:36//HOMO SAPIENS (HUMAN)//Q02080
 F-NT2RM1000062//PROLINE-RICH PEPTIDE P-B//0.54:34:44//HOMO SAPIENS (HUMAN)//P02814
 F-NT2RM1000080//HYPOTHETICAL 35.7 KD PROTEIN SLR1128//2.1e-20:119:40//SYNECHOCYSTIS SP.
 (STRAIN PCC 6803)//P72655
 40 F-NT2RM1000086//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-
 MENT)//0.20:56:35//HOMO SAPIENS (HUMAN)//P10162
 F-NT2RM1000092//COLLAGEN-LIKE PROTEIN//0.0017:44:45//HERPESVIRUS SAIMIRI (SUBGROUP C /
 STRAIN 488)//P22576
 F-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-
 CINEURIN REGULATORY SUBUNIT)//5.7e-07:109:28//NEUROSPORA CRASSA//P87072
 45 F-NT2RM1000119//TRANSCRIPTIONAL REGULATOR IE63 (VMW63) (ICP27)//0.0050:135:32//HERPES SIM-
 PLEX VIRUS (TYPE 2 / STRAIN HG52)//P28276
 F-NT2RM1000127//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.032:68:32//SORGHUM
 VULGARE (SORGHUM)//P24152
 50 F-NT2RM1000131//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF)//0.82:33:39//BOS
 TAURUS (BOVINE)//P37359
 F-NT2RM1000132//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3)
 (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A)//2.7e-59:124:91//HOMO SAPIENS (HUMAN)//O75380
 F-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5)//2.5e-08:148:29//HOMO SAPIENS
 55 (HUMAN)//P49902
 F-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-
 CINEURIN REGULATORY SUBUNIT)//1.9e-07:109:27//NEUROSPORA CRASSA//P87072
 F-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE

SPAC10F6.02C//1.0e-12:94:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O42643
 F-NT2RM1000199//CUTICLE COLLAGEN 12 PRECURSOR//0.46:130:33//CAENORHABDITIS ELEGANS//
 P20630
 F-NT2RM1000242//PUTATIVE ATP SYNTHASE J CHAIN, MITOCHONDRIAL (EC 3.6.1.34)//0.85:38:36//
 5 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O13931
 F-NT2RM1000244//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X//0.0055:98:36//
 CAENORHABDITIS ELEGANS//Q11102
 F-NT2RM1000252//TRICHOHYALIN//2.9e-06:88:36//OVIS ARIES (SHEEP)//P22793
 F-NT2RM1000256//GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING]
 10 (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6- PHOSPHATE AMIDOTRANS-
 FERASE) (GFAT)//2.9e-54:153:67//MUS MUSCULUS (MOUSE)//P47856
 F-NT2RM1000257//MAGO NASHI PROTEIN//5.9e-64:136:89//DROSOPHILA MELANOGASTER (FRUIT FLY)//
 P49028
 F-NT2RM1000260
 15 F-NT2RM1000271//GALACTOKINASE (EC 2.7.1.6)//0.99:41:39//BACILLUS SUBTILIS//P39574
 F-NT2RM1000272//HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME III//8.8e-25:131:45//
 CAENORHABDITIS ELEGANS//Q09357
 F-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V- AT-
 PASE 28 KD ACCESSORY PROTEIN)//2.5e-63:121:94//BOS TAURUS (BOVINE)//P39942
 20 F-NT2RM1000300//TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN)//0.51:145:26//HOMO
 SAPIENS (HUMAN)//Q13428
 F-NT2RM1000314
 F-NT2RM1000318//50S RIBOSOMAL PROTEIN L23//0.83:28:35//AQUIFEX AEOLICUS//O66433
 F-NT2RM1000341
 25 F-NT2RM1000354//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5'REGION (ORF55)//0.95:43:37//RHODO-
 BACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA)//P26159
 F-NT2RM1000355//SPERM-SPECIFIC PROTEIN PHI-1//0.0016:73:43//MYTILUS EDULIS (BLUE MUSSEL)//
 Q04621
 F-NT2RM1000365//HYPOTHETICAL PROTEIN KIAA0140//3.5e-10:83:49//HOMO SAPIENS (HUMAN)//
 30 Q14153
 F-NT2RM1000377//DUAL SPECIFICITY PROTEIN PHOSPHATASE 9 (EC 3.1.3.48) (EC 3.1.3.16) (MITOGEN-
 ACTIVATED PROTEIN KINASE PHOSPHATASE 4) (MAP KINASE PHOSPHATASE 4) (MKP-4)//4.9e-18:113:
 38//HOMO SAPIENS (HUMAN)//Q99956
 F-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION//0.00023:67:
 35 31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53915
 F-NT2RM1000394//HISTONE H3.3 (H3.B) (H3.3Q)//4.7e-52:71:91//HOMO SAPIENS (HUMAN), MUS MUSCU-
 LUS (MOUSE), RATTUS NORVEGICUS (RAT), ORYCTOLAGUS CUNICULUS (RABBIT), GALLUS GALLUS
 (CHICKEN), SPISULA SOLIDISSIMA (ATLANTIC SURF-CLAM), DROSOPHILA MELANOGASTER (FRUIT FLY),
 AND DROSOPHILA HYDEI (FRUIT FLY)//P06351
 40 F-NT2RM1000399//ENDOTHELIN-2 PRECURSOR (ET-2) (FRAGMENT)//0.92:24:45//CANIS FAMILIARIS
 (DOG)//P12064
 F-NT2RM1000421//CUTICLE COLLAGEN 2C (FRAGMENT)//0.12:93:33//HAEMONCHUS CONTORTUS//
 P16252
 F-NT2RM1000430//PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)//0.13:86:31//NICO-
 45 TIANA TABACUM (COMMON TOBACCO)//Q03211
 F-NT2RM1000499//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT)//2.9e-17:75:49//HOMO SAPIENS
 (HUMAN)//Q15057
 F-NT2RM1000539//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION//2.9e-16:82:
 51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40089
 50 F-NT2RM1000553//GLYCOLIPID TRANSFER PROTEIN (GLTP)//6.4e-06:103:33//SUS SCROFA (PIG)//
 P17403
 F-NT2RM1000555//UNR PROTEIN//8.7e-77:105:95//RATTUS NORVEGICUS (RAT)//P18395
 F-NT2RM1000563//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.15:20:50//HO-
 MO SAPIENS (HUMAN)//P30808
 55 F-NT2RM1000623//CLARA CELL PHOSPHOLIPID-BINDING PROTEIN PRECURSOR (CCPBP) (CLARA CELLS
 10 KD SECRETORY PROTEIN) (CC10)//0.17:70:34//HOMO SAPIENS (HUMAN)//P11684
 F-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-)//2.0e-22:133:42//SACCHAROMYCES CER-
 EVISIAE (BAKER'S YEAST)//P43636

F-NT2RM1000661//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB)//0.0060:24:33//HOMO SAPIENS (HUMAN)//P25713
 F-NT2RM1000666//COLD SHOCK PROTEIN SCOF//9.1e-07:67:41//STREPTOMYCES COELICOLOR//P48859
 5 F-NT2RM1000669//CHLOROPLAST 50S RIBOSOMAL PROTEIN L31//0.071:69:31//PORPHYRA PURPUREA//P51290
 F-NT2RM1000672//SIGNAL RECOGNITION PARTICLE SEC65 SUBUNIT (FRAGMENT)//0.27:42:42//KLUYVEROMYCES LACTIS (YEAST)//O13475
 F-NT2RM1000691//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2)//4.3e-42:241:42//HOMO SAPIENS (HUMAN)//P29375
 10 F-NT2RM1000699//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32)//0.94:48:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P15565
 F-NT2RM1000702//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1//0.0013:139:25//DROSOPHILA MELANOGASTER (FRUIT FLY)//P26308
 15 F-NT2RM1000725//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//1.0:15:60//HOMO SAPIENS (HUMAN)//P02811
 F-NT2RM1000741//STATHMIN (CLONE XO20) (FRAGMENT)//1.0:53:32//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q09005
 F-NT2RM1000742//HYPOTHETICAL 24.1 KD PROTEIN IN DHFR 3'REGION (ORF2)//1.0:54:42//HERPESVIRUS SAIMIRI (STRAIN 484-77)//P25049
 20 F-NT2RM1000746//HYPOTHETICAL 16.8 KD PROTEIN C29E6.04 IN CHROMOSOME I//0.11:87:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09858
 F-NT2RM1000770//DXS6673E PROTEIN//2.0e-38:190:48//HOMO SAPIENS (HUMAN)//Q14202
 F-NT2RM1000772//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//4.3e-12:141:30//PODOSPORA ANSERINA//Q00808
 25 F-NT2RM1000780//MALE SPECIFIC SPERM PROTEIN MST87F//0.98:34:38//DROSOPHILA MELANOGASTER (FRUIT FLY)//P08175
 F-NT2RM1000781
 F-NT2RM1000800//24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION//7.9e-11:135:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P28707
 30 F-NT2RM1000802//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES I)//0.43:62:35//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII)//P09921
 F-NT2RM1000811
 35 F-NT2RM1000826//UNR PROTEIN//1.1e-110:144:83//RATTUS NORVEGICUS (RAT)//P18395
 F-NT2RM1000829//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:38:34//DROSOPHILA SIMULANS (FRUIT FLY)//P50270
 F-NT2RM1000833//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//1.4e-62:145:841//CANIS FAMILIARIS (DOG)//P38377
 40 F-NT2RM1000850//TESTIS-SPECIFIC PROTEIN KINASE 1 (EC 2.7.1.-)//6.1e-08:136:33//RATTUS NORVEGICUS (RAT)//Q63572
 F-NT2RM1000852//ATP-DEPENDENT RNA HELICASE ROK1//1.6e-34:212:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P45818
 F-NT2RM1000857//HISTONE H1.M6.1//0.76:31:48//TRYPANOSOMA CRUZI//P40273
 45 F-NT2RM1000867//MICROSOMAL SIGNAL PEPTIDASE 10.8 KD SUBUNIT (EC 3.4.-.-)//0.0082:76:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P46965
 F-NT2RM1000874//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.38:12:58//HOMO SAPIENS (HUMAN)//P30808
 F-NT2RM1000882//CYTOCHROME B5//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40312
 50 F-NT2RM1000883//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.79:22:59//HOMO SAPIENS (HUMAN)//P30808
 F-NT2RM1000885//HYPOTHETICAL 5.8 KD PROTEIN//0.76:18:38//CLOVER YELLOW MOSAIC VIRUS (CYMV)//P16485
 55 F-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE I135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)//6.2e-70:153:88//RATTUS NORVEGICUS (RAT)//O54888
 F-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR)//4.3e-12:159:28//OXYTRICHA FAL-

LAX//P02583
 F-NT2RM1000905//GLUTATHIONE S-TRANSFERASE 1-1 (EC 2.5.1.18) (CLASS-THETA)//0.98:39:35//LUCILIA
 CUPRINA (GREENBOTTLE FLY) (AUSTRALIAN SHEEP BLOWFLY)//P42860
 F-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III//1.3e-11:169:28//
 5 CAENORHABDITIS ELEGANS//P46577
 F-NT2RM1000927//CUTICLE COLLAGEN 1//0.00048:141:31//CAENORHABDITIS ELEGANS//P08124
 F-NT2RM1000962//HYPOTHETICAL 35.8 KD PROTEIN C4F8.04 IN CHROMOSOME I//7.1e-13:169:31//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14180
 F-NT2RM1000978//HYPOTHETICAL 20.2 KD PROTEIN IN MNN4-PTK1 INTERGENIC REGION//0.61:82:34//
 10 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36045
 F-NT2RM1001003//ALPHA-2 CATENIN (ALPHA N-CATENIN) (NEURAL ALPHA-CATENIN)//1.6e-21:211:31//
 GALLUS GALLUS (CHICKEN)//P30997
 F-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I//3.2e-15:119:36//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09701
 15 F-NT2RM1001043//ENDOTHELIN-1 (ET-1) (FRAGMENT)//0.78:32:34//MACACA FASCICULARIS (CRAB EAT-
 ING MACAQUE) (CYNOMOLGUS MONKEY)//Q28469
 F-NT2RM1001044
 F-NT2RM1001059//LORICRIN//8.6e-08:108:39//HOMO SAPIENS (HUMAN)//P23490
 F-NT2RM1001066//METALLOTHIONEIN-LIKE PROTEIN TYPE 2//0.99:24:50//LYCOPERSICON ESCULEN-
 20 TUM (TOMATO)//Q43513
 F-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1
 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148)//4.7e-15:148:33//HOMO
 SAPIENS (HUMAN)//P19174
 F-NT2RM1001074//HYPOTHETICAL PROTEIN F-215//8.6e-05:126:30//HUMAN ADENOVIRUS TYPE 2//
 25 P03291
 F-NT2RM1001082//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/6.5e-19:75:54//HOMO SAPIENS (HUMAN)//
 P39195
 F-NT2RM1001085//MALE SPECIFIC SPERM PROTEIN MST84DB//0.49:29:41//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01643
 30 F-NT2RM1001092//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//2.8e-42:200:38//HOMO SA-
 PIENS (HUMAN)//P51522
 F-NT2RM1001102//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION//1.7e-18:161:
 36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53331
 F-NT2RM1001105//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//4.0e-05:157:35//STREP-
 35 TOMYCES FRADIAE//P20186
 F-NT2RM1001112//NONHISTONE CHROMOSOMAL PROTEIN HMG-17//0.18:20:55//BOS TAURUS (BO-
 VINE)//P02313
 F-NT2RM1001115
 F-NT2RM1001139//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8)//2.0e-
 40 25:156:46//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN)//P10496
 F-NT2RM2000006//MITOCHONDRIAL RIBOSOMAL PROTEIN S12//0.76:45:35//LEISHMANIA TARENTOLAE
 (SAUROLEISHMANIA TARENTOLAE)//Q34940
 F-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA
 POLYMERASE III SUBUNIT 2)//3.9e-87:238:65//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25167
 45 F-NT2RM2000030//TOXINS 1 AND 2//0.98:21:42//TRIMERESURUS WAGLERI (WAGLER'S PIT VIPER)
 (TROPIDOLAEMUS WAGLERI)//P24335
 F-NT2RM2000032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00059:53:49//HOMO SAPIENS (HUMAN)//
 P39188
 F-NT2RM2000042//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//1.0:68:26//HOMO SAPIENS
 50 (HUMAN)//P22532
 F-NT2RM2000092//HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC REGION//7.0e-11:80:
 40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38748
 F-NT2RM2000093//OVARY MATURATING PARSIN (OMP)//1.0:26:38//LOCUSTA MIGRATORIA (MIGRATORY
 LOCUST)//P80045
 55 F-NT2RM2000101//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X//3.3e-09:56:35//
 CAENORHABDITIS ELEGANS//Q11096
 F-NT2RM2000124//CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT (EC 2.7.1.37) (PKA
 C-ALPHA)//3.1e-35:77:96//MUS MUSCULUS (MOUSE)//P05132

F-NT2RM2000191//3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) //3.3e-05:181:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD) //Q23917
 F-NT2RM2000192//REPLICATION PROTEIN E1 (FRAGMENTS) //0.019:148:25//COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN WASHINGTON B) (CRPV) //P51894
 5 F-NT2RM2000239//PROLINE-RICH PROTEIN MP-3 (FRAGMENT) //0.00032:111:32//MUS MUSCULUS (MOUSE) //P05143
 F-NNNNNNNNNNNN/METALLOTHIONEIN-LIKE PROTEIN TYPE 2 //0.046:59:33//LYCOPERSICON ESCULENTUM (TOMATO) //Q43512
 F-NT2RM2000250//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) //0.054:46:34//RATTUS NORVEGICUS (RAT) //P08699
 10 F-NT2RM2000259//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (P135 PROTEIN) (IER 2.9/ER2.6) //0.27:112:33//BOVINE HERPES VIRUS TYPE 1 (STRAIN JURA) //P29128
 F-NT2RM2000260//PROLINE-RICH PROTEIN MP-3 (FRAGMENT) //4.7e-22:191:35//MUS MUSCULUS (MOUSE) //P05143
 15 F-NT2RM2000287//HYPOTHETICAL 11.8 KD PROTEIN C1B3.02C IN CHROMOSOME I //5.0e-19:83:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //O13868
 F-NT2RM2000322//DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) (DAP DECARBOXYLASE) //0.47:117:29//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI) //P56129
 20 F-NT2RM2000359//SPORE GERMINATION PROTEIN 270-11 //0.12:83:36//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD) //P22698
 F-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN //1.3e-16:203:30//HOMO SAPIENS (HUMAN) //P11274
 F-NT2RM2000368//DEK PROTEIN //0.00027:100:32//HOMO SAPIENS (HUMAN) //P35659
 25 F-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE PHOSPHORYLASE) (PNPASE) //6.8e-36:170:47//ESCHERICHIA COLI //P05055
 F-NT2RM2000374//NODAL PRECURSOR //1.1e-32:64:95//MUS MUSCULUS (MOUSE) //P43021
 F-NT2RM2000395//IMMEDIATE-EARLY PROTEIN IE180 //0.31:41:43//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV) //P11675
 30 F-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT) //1.2e-30:228:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P32802
 F-NT2RM2000407//TRANSMEMBRANE PROTEIN SEX PRECURSOR //0.032:105:30//HOMO SAPIENS (HUMAN) //P51805
 35 F-NT2RM2000420//METALLOTHIONEIN (MT) //0.88:42:38//PLEURONECTES PLATESSA (PLAICE) //P07216
 F-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73 //2.0e-117:237:87//RATTUS NORVEGICUS (RAT) //Q08469
 F-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION //1.1e-08:157:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P36113
 40 F-NT2RM2000469//70 KD ANTIGEN //0.050:207:23//SHIGELLA FLEXNERI //P18010
 F-NT2RM2000490//BASIC PROLINE-RICH PEPTIDE P-E (IB-9) //0.022:25:44//HOMO SAPIENS (HUMAN) //P02811
 F-NT2RM2000502//MALE SPECIFIC SPERM PROTEIN MST84DD //0.0037:17:58//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q01645
 45 F-NT2RM2000504//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17 //1.7e-22:195:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //O42908
 F-NT2RM2000522//RAS-RELATED PROTEIN RABA (FRAGMENT) //3.6e-05:67:29//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD) //P34141
 F-NT2RM2000540//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III //8.4e-33:214:38//CAENORHABDITIS ELEGANS //Q18262
 50 F-NT2RM2000556//HYPOTHETICAL PROTEIN KIAA0288 (HA6116) //1.7e-09:133:36//HOMO SAPIENS (HUMAN) //P56524
 F-NT2RM2000566//INTEGRIN ALPHA-6 PRECURSOR (VLA-6) (CD49F) //2.2e-60:244:51//HOMO SAPIENS (HUMAN) //P23229
 55 F-NT2RM2000567//PROLINE-RICH PROTEIN MP-3 (FRAGMENT) //2.3e-09:192:34//MUS MUSCULUS (MOUSE) //P05143
 F-NT2RM2000569//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! //9.0e-08:43:72//HOMO SAPIENS (HUMAN) //P39188

F-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS)//
 9.1e-54:225:45//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//P73505
 F-NT2RM2000581//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)//0.079:111:34//HOMO SA-
 PIENS (HUMAN)//Q15427
 5 F-NT2RM2000588//HYPOTHETICAL PROTEIN KIAA0288 (HA6116)//2.3e-09:193:32//HOMO SAPIENS (HU-
 MAN)//P56524
 F-NT2RM2000594//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.18:33:42//HOMO SAPIENS (HUMAN)//
 P02811
 10 F-NT2RM2000599//DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANS-
 FERASE) (DNA METASE) (MCMT) (M.MMUI)//1.5e-09:68:45//MUS MUSCULUS (MOUSE)//P13864
 F-NT2RM2000609//GRANULIN 2//0.83:42:35//CYPRIUS CARPIO (COMMON CARP)//P81014
 F-NT2RM2000612//ZINC FINGER PROTEIN GCS1//7.2e-05:155:29//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P35197
 15 F-NT2RM2000623//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//1.8e-09:196:33//SACCHAROMY-
 CES CEREVISIAE (BAKER'S YEAST)//P32323
 F-NT2RM2000624//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR//0.070:113:27//DROSOPHILA ERECTA
 (FRUIT FLY)//P13730
 F-NT2RM2000635//SPERM PROTAMINE P1//0.54:47:38//ANTECHINUS STUARTII//P42129
 F-NT2RM2000636//OUTER MEMBRANE PROTEIN H.8 PRECURSOR//0.096:62:35//NEISSERIA GONOR-
 RHOEA//P11910
 20 F-NT2RM2000639//HYPOTHETICAL PROTEIN MJ0243//0.99:32:34//METHANOCOCCUS JANNASCHII//
 Q57694
 F-NT2RM2000649//NEURONAL CALCIUM SENSOR 1 (NCS-1)//0.00049:70:35//RATTUS NORVEGICUS
 (RAT), AND GALLUS GALLUS (CHICKEN)//P36610
 25 F-NT2RM2000669//50S RIBOSOMAL PROTEIN L34//1.0:34:44//BACILLUS SUBTILIS//P05647
 F-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2)//7.0e-116:243:87//HOMO SAPIENS (HUMAN), AND
 BOS TAURUS (BOVINE)//P32391
 F-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-I)//3.8e-21:174:35//HO-
 MO SAPIENS (HUMAN)//Q15404
 30 F-NT2RM2000718//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I//0.0022:
 174:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q13695
 F-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//1.6e-102:246:74//HOMO SAPIENS
 (HUMAN)//P28160
 F-NT2RM2000740//HYPOTHETICAL 131.1 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION//8.5e-51:212:
 35 49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38144
 F-NT2RM2000795//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//9.0e-41:125:53//HOMO SAPIENS (HU-
 MAN)//P39189
 F-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)//1.1e-128:291:89//
 RATTUS NORVEGICUS (RAT)//P23514
 40 F-NT2RM2000837//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR
 P57) (P57KIP2)//3.9e-05:113:36//HOMO SAPIENS (HUMAN)//P49918
 F-NT2RM2000951//HYPOTHETICAL 60.3 KD PROTEIN R08D7.7 IN CHROMOSOME III//2.5e-49:273:39//
 CAENORHABDITIS ELEGANS//P30646
 F-NT2RM2000952//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)
 45 (FRAGMENT)//0.037:234:23//RATTUS NORVEGICUS (RAT)//P16884
 F-NT2RM2000984//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III//6.3e-44:216:43//
 CAENORHABDITIS ELEGANS//P41879
 F-NT2RM2001004//SYNAPSINS IA AND IB//0.15:178:32//RATTUS NORVEGICUS (RAT)//P09951
 F-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1)//1.4e-87:188:90//MUS MUSCULUS (MOUSE)//
 50 Q60809
 F-NT2RM2001065//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.53:122:31//TRYPANOSOMA BRU-
 CEI BRUCEI//P24499
 F-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III//3.4e-13:171:30//
 CAENORHABDITIS ELEGANS//P46577
 55 F-NT2RM2001105//SPORE COAT PROTEIN SP96//7.8e-06:141:34//DICTYOSTELIUM DISCOIDEUM (SLIME
 MOLD)//P14328
 F-NT2RM2001131//PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03//2.3e-18:249:31//SCHIZOSAC-
 CHAROMYCES POMBE (FISSION YEAST)//Q10475

F-NT2RM2001141//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III//0.050:134:26//
 CAENORHABDITIS ELEGANS //P34681
 F-NT2RM2001152
 F-NT2RM2001177//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN)//0.86:42:40//GALLUS GAL-
 LUS (CHICKEN)//P32018
 5 F-NT2RM2001194//SMOOTHELIN//4.7e-05:77:32//HOMO SAPIENS (HUMAN)//P53814
 F-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.7e-18:218:35//MUS MUSCULUS
 (MOUSE)//P05143
 F-NT2RM2001201//CYSTEINE STRING PROTEIN (CCCS1)//0.041:22:59//TORPEDO CALIFORNICA (PACIFIC
 10 ELECTRIC RAY)//P56101
 F-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)//1.3e-13:183:32//
 RATTUS NORVEGICUS (RAT)//P97924
 F-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-
 DOHYDROLASE)//6.5e-121:218:98//RATTUS NORVEGICUS (RAT)//P13264
 15 F-NT2RM2001243//HYPOTHETICAL 200.0 KD PROTEIN IN GZF3-IME2 INTERGENIC REGION//0.00019:177:
 27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P42945
 F-NT2RM2001247//LEGUMIN B (FRAGMENT)//0.22:54:35//PISUM SATIVUM (GARDEN PEA)//P14594
 F-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR)//1.8e-109:207:98//MUS MUS-
 CULUS (MOUSE)//P53995
 20 F-NT2RM2001291//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.016:22:40//HOMO SAPIENS
 (HUMAN)//P22531
 F-NT2RM2001306//REF(2)P PROTEIN//0.61:51:33//DROSOPHILA MELANOGASTER (FRUIT FLY)//P14199
 F-NT2RM2001312//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.2e-11:33:72//HOMO SAPIENS (HUMAN)//
 P39195
 25 F-NT2RM2001319
 F-NT2RM2001324//ZYXIN//5.1e-22:91:38//GALLUS GALLUS (CHICKEN)//Q04584
 F-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//7.4e-10:159:27//PODOSPORA AN-
 SERINA//Q00808
 F-NT2RM2001360//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B)//1.0:27:48//
 30 DROSOPHILA MELANOGASTER (FRUIT FLY)//P05623
 F-NT2RM2001370//NAPE PROTEIN//0.98:44:31//PARACOCCLUS DENITRIFICANS (SUBSP. THIOSPHAERA
 PANTOTROPHA)//Q56348
 F-NT2RM2001393//VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN
 LV-1C; LIPOVITELLIN LV-2]//0.0024:163:31//ICHTHYOMYZON UNICUSPUS (SILVER LAMPREY)//Q91062
 35 F-NT2RM2001420
 F-NT2RM2001424//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U)//2.4e-41:140:59//
 HOMO SAPIENS (HUMAN)//Q00839
 F-NT2RM2001499//HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+
 BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR)
 40 (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG)//3.7e-71:201:68//HOMO SAPIENS (HUMAN)//P30825
 F-NT2RM2001504//CUTICLE COLLAGEN 2//0.028:41:39//CAENORHABDITIS ELEGANS//P17656
 F-NT2RM2001524//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III//6.7e-47:190:42//
 CAENORHABDITIS ELEGANS//Q09316
 F-NT2RM2001544//TELOMERE-BINDING PROTEIN 51 KD SUBUNIT//0.0027:136:33//EUPLOTES
 45 CRASSUS//Q06184
 F-NT2RM2001547//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION//8.5e-18:91:50//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40564
 F-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//3.9e-
 35:212:41//HOMO SAPIENS (HUMAN)//P19474
 50 F-NT2RM2001582//RESA PROTEIN//0.0033:72:27//BACILLUS SUBTILIS//P35160
 F-NT2RM2001588//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//1.0e-06:115:32//ZEA MAYS
 (MAIZE)//P14918
 F-NT2RM2001592//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN)//0.033:156:23//HO-
 MO SAPIENS (HUMAN)//P26371
 55 F-NT2RM2001605//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2)//1.1e-116:249:82//HOMO SAPIENS
 (HUMAN)//P29375
 F-NT2RM2001613//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//1.2e-97:192:100//RATTUS
 NORVEGICUS (RAT)//P38378

F-NT2RM2001632//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.00068:145:28//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P32323
 F-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PRO-
 TEIN OF 121 KD) (P145)//1.1e-39:235:47//RATTUS NORVEGICUS (RAT)//P52591
 5 F-NT2RM2001637//HYPOTHETICAL BHLF1 PROTEIN//0.075:197:29//EPSTEIN-BARR VIRUS (STRAIN B95-8)
 (HUMAN HERPESVIRUS 4)//P03181
 F-NT2RM2001641//NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (B5R)//0.013:29:68//HOMO SAPIENS
 (HUMAN)//P00387
 F-NT2RM2001648//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//3.2e-65:132:100//CANIS FA-
 10 MILIARIS (DOG)//P38377
 F-NT2RM2001652//PROTEIN TRANSPORT PROTEIN SEC7//1.6e-32:261:32//SACCHAROMYCES CEREVI-
 SIAE (BAKER'S YEAST)//P11075
 F-NT2RM2001659//CARBOXYPEPTIDASE A INHIBITOR//0.83:30:46//ASCARIS SUUM (PIG ROUNDWORM)
 (ASCARIS LUMBRICOIDES)//P19399
 15 F-NT2RM2001664//IKI3 PROTEIN//1.3e-31:265:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 Q06706
 F-NT2RM2001668//TONB PROTEIN//0.32:39:41//XANTHOMONAS CAMPESTRIS (PV. CAMPESTRIS)//
 Q34261
 F-NT2RM2001670//ZINC FINGER PROTEIN 174//3.6e-21:172:39//HOMO SAPIENS (HUMAN)//Q15697
 20 F-NT2RM2001671//HYPOTHETICAL 118.6 KD PROTEIN C29E6.03C IN CHROMOSOME 1//1.6e-10:229:24//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09857
 F-NT2RM2001675//DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDS)//1.0:184:21//METHANO-
 COCCUS JANNASCHII//Q57695
 F-NT2RM2001681//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1)//0.0039:199:22//
 25 DROSOPHILA MELANOGASTER (FRUIT FLY)//P54399
 F-NT2RM2001688//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION//2.6e-21:162:
 33//BACILLUS SUBTILIS//P42966
 F-NT2RM2001695//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.9e-41:60:81//HOMO SAPIENS (HUMAN)//
 P39194
 30 F-NT2RM2001696//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//9.8e-16:126:38//
 AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41479
 F-NT2RM2001698//PENAEIDIN-3B PRECURSOR (P3-B)//0.36:52:34//PENAEUS VANNAMEI (PENOEID
 SHRIMP) (EUROPEAN WHITE SHRIMP)//P81059
 F-NT2RM2001699//TRANSCRIPTION INITIATION FACTOR TFIID 30 KD SUBUNIT (TAFII-30) (TAFII30)//
 35 0.0012:79:40//HOMO SAPIENS (HUMAN)//Q12962
 F-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD)
 (FRAGMENT)//1.0e-30:140:53//MUS MUSCULUS (MOUSE)//P50544
 F-NT2RM2001706//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.5e-33:95:75//HOMO SAPIENS (HUMAN)//
 P39195
 40 F-NT2RM2001716//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECUR-
 SOR//0.010:116:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47179
 F-NT2RM2001718//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB//0.00029:77:37//BACILLUS SUBTI-
 LIS//P39217
 F-NT2RM2001723//POSTERIOR PITUITARY PEPTIDE//0.94:26:53//BOS TAURUS (BOVINE)//P01154
 45 F-NT2RM2001727//E7 PROTEIN//0.91:46:34//HUMAN.PAPILLOMAVIRUS TYPE 23//P50781
 F-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-
 ZYME)//4.9e-07:139:29//CAENORHABDITIS ELEGANS//Q09931
 F-NT2RM2001743//PROENKEPHALIN A PRECURSOR//0.75:65:35//CAVIA PORCELLUS (GUINEA PIG)//
 50 P47969
 F-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210//1.5e-14:119:36//HOMO SAPIENS (HUMAN)//
 Q92609
 F-NT2RM2001760//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//8.3e-58:119:99//CANIS FA-
 MILIARIS (DOG)//P38377
 55 F-NT2RM2001768//HYPOTHETICAL PROTEIN UL25//0.45:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN
 AD169)//P16761
 F-NT2RM2001771//ZINC FINGER PROTEIN 135//4.6e-80:224:60//HOMO SAPIENS (HUMAN)//P52742
 F-NT2RM2001782//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-

- PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//7.0e-06:61:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940
 F-NT2RM2001784//HYPOTHETICAL PROTEIN UL61.//0.00070:145:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
- 5 F-NT2RM2001785//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//1.5e-08:127:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871
 F-NT2RM2001797//ZINC FINGER PROTEIN 135.//1.6e-73:267:49//HOMO SAPIENS (HUMAN).//P52742
 F-NT2RM2001800//HYPOTHETICAL HELICASE MG018/MG017/MG016 HOMOLOG.//3.9e-12:171:33//MYCOPLASMA PNEUMONIAE.//P75093
- 10 F-NT2RM2001803//IKI3 PROTEIN.//1.6e-38:283:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06706
 F-NT2RM2001805//COLD SHOCK-LIKE PROTEIN CSPH.//0.51:46:32//SALMONELLA TYPHIMURIUM.//Q33793
 F-NT2RM2001813//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//5.0e-05:82:32//CAENORHABDITIS ELEGANS.//Q17963
- 15 F-NT2RM2001823//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//3.6e-49:233:45//HOMO SAPIENS (HUMAN).//O14647
 F-NT2RM2001839//RETICULOCALBIN 1 PRECURSOR.//5.2e-65:222:56//HOMO SAPIENS (HUMAN).//Q15293
 F-NT2RM2001840//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.6e-33:102:68//HOMO SAPIENS (HUMAN).//P39194
- 20 F-NT2RM2001855//BASP1 PROTEIN.//0.054:120:30//HOMO SAPIENS (HUMAN).//P80723
 F-NT2RM2001867//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//4.1e-19:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
 F-NT2RM2001879//HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME I.//5.9e-15:76:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09800
- 25 F-NT2RM2001886//HYPOTHETICAL 126.9 KD PROTEIN C22G7.04 IN CHROMOSOME I.//1.4e-41:249:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09798
 F-NT2RM2001896//HYPOTHETICAL 83.2 KD PROTEIN IN KAR4-PBN1 INTERGENIC REGION.//2.1e-59:197:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25582
 F-NT2RM2001903//HYPOTHETICAL PROTEIN MJ0263.//0.070:132:31//METHANOCOCCUS JANNASCHII.//O06917
- 30 F-NT2RM2001930//THROMBOSPONDIN 2 PRECURSOR.//7.1e-05:53:47//MUS MUSCULUS (MOUSE).//Q03350
 F-NT2RM2001935//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.00046:116:35//CAENORHABDITIS ELEGANS.//Q21184
 F-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27:216:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320
- 35 F-NT2RM2001950//HIRUDIN HV1 (BUFRUDIN).//0.59:43:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH).//P81492
 F-NT2RM2001982//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-8 SUBUNIT (G GAMMA-C).//0.72:35:42//BOS TAURUS (BOVINE).//P50154
 F-NT2RM2001983//PROLINE-RICH PEPTIDE P-B.//0.00035:23:52//HOMO SAPIENS (HUMAN).//P02814
- 40 F-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//8.6e-24:197:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37838
 F-NT2RM2001997
 F-NT2RM2001998//IMMEDIATE-EARLY PROTEIN IE180.//0.076:92:27//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
- 45 F-NT2RM2002004//SLF1 PROTEIN.//3.5e-06:235:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12034
 F-NT2RM2002014//HYPOTHETICAL PROTEIN HI0568.//2.1e-17:235:29//HAEMOPHILUS INFLUENZAE.//P71353
 F-NT2RM2002030//GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT).//9.5e-105:271:76//MUS MUSCULUS (MOUSE).//P47856
- 50 F-NT2RM2002049//SMALL PROLINE-RICH PROTEIN 2-1.//0.099:41:41//HOMO SAPIENS (HUMAN).//P35326
 F-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.012:217:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q07878
 F-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//
- 55

1.1e-09:65:53//MUS MUSCULUS (MOUSE)//Q61990
 F-NT2RM2002091//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//0.072:74:
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214
 F-NT2RM2002100//ATP-DEPENDENT RNA HELICASE ROK1//4.5e-50:289:41//SACCHAROMYCES CEREVI-
 5 SIAE (BAKER'S YEAST)//P45818
 F-NT2RM2002109//NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KI-
 NASE) (GP145-TRKC) (TRK-C)//1.4e-14:203:32//RATTUS NORVEGICUS (RAT)//Q03351
 F-NT2RM2002128//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//0.0025:139:31//
 XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437
 10 F-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12//9.2e-20:42:73//BRACHYDANIO RERIO (ZE-
 BRAFISH) (ZEBRA DANIO)//P47805
 F-NT2RM2002145//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR//0.0085:200:26//
 TRITICUM AESTIVUM (WHEAT)//P08488
 F-NT2RM2002178//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//5.8e-05:56:39//BOS TAURUS (BO-
 15 VINE)//P25508
 F-NT2RM2002580//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B)//2.9e-14:96:37//PETROMYZON MARINUS (SEA
 LAMPREY)//P25210
 F-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA
 20 POLYMERASE III SUBUNIT 2)//8.6e-95:271:67//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25167
 F-NT2RM4000027//INTERFERON-ACTIVATABLE PROTEIN 202 (IFI-202)//0.99:72:31//MUS MUSCULUS
 (MOUSE)//P15091
 F-NT2RM4000030//LAS1 PROTEIN//1.4e-14:184:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P36146
 25 F-NT2RM4000046//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT)//0.99:120:28//RATTUS NORVEGICUS
 (RAT)//P13941
 F-NT2RM4000061
 F-NT2RM4000085//ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX
 PROTEIN 9) (MHEL-5)//8.5e-40:263:38//MUS MUSCULUS (MOUSE)//O70133
 30 F-NT2RM4000086//HYPOTHETICAL PROTEIN HI1497//1.0:27:37//HAEMOPHILUS INFLUENZAE//P44221
 F-NT2RM4000104//ZINC FINGER PROTEIN 134//1.0e-26:64:56//HOMO SAPIENS (HUMAN)//P52741
 F-NT2RM4000139//PREPROTEIN TRANSLOCASE SECE SUBUNIT//0.99:38:42//THERMOTOGA MARITIMA//
 P35874
 F-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA
 35 LIGASE) (THRRS)//6.3e-34:181:40//HOMO SAPIENS (HUMAN)//P26639
 F-NT2RM4000156//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//
 4.6e-12:142:33//NICOTIANA TABACUM (COMMON TOBACCO)//P13983
 F-NT2RM4000167//KINESIN-LIKE PROTEIN KIF4//3.4e-123:269:91//MUS MUSCULUS (MOUSE)//P33174
 F-NT2RM4000169//M PROTEIN, SEROTYPE 2.2 PRECURSOR//9.7e-10:229:26//STREPTOCOCCUS PYO-
 40 GENES//P50469
 F-NT2RM4000191//P68-LIKE PROTEIN//2.1e-11:104:40//SACCHAROMYCES CEREVISIAE (BAKER'S
 YEAST)//P24783
 F-NT2RM4000197//CUTICLE PROTEIN CP463 (CPCP463)//0.84:29:37//CANCER PAGURUS (ROCK CRAB)//
 P81587
 45 F-NT2RM4000199//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-
 MENT)//1.8e-06:187:34//HOMO SAPIENS (HUMAN)//P10162
 F-NT2RM4000200//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3'REGION (ORF3)//0.52:42:40//BACILLUS LI-
 CHENIFORMIS//P22754
 F-NT2RM4000202//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN)//0.00044:
 50 168:32//ORYCTOLAGUS CUNICULUS (RABBIT)//P14282
 F-NT2RM4000210//EXTENSIN PRECURSOR//0.27:129:27//DAUCUS CAROTA (CARROT)//P06599
 F-NT2RM4000215//MAK16 PROTEIN//2.0e-65:234:52//SACCHAROMYCES CEREVISIAE (BAKER'S
 YEAST)//P10962
 F-NT2RM4000229//GAR2 PROTEIN//0.13:217:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//
 55 P41891
 F-NT2RM4000233//TRANSMEMBRANE PROTEIN SEX PRECURSOR//0.047:108:30//HOMO SAPIENS (HU-
 MAN)//P51805
 F-NT2RM4000244//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.67:59:27//BALAENOPTERA

PHYSALUS (FINBACK WHALE) (COMMON RORQUAL)//P24947
 F-NT2RM4000251//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.0059:108:35//MUS MUSCULUS (MOUSE)//P05143
 F-NT2RM4000265//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.1e-38:70:70//HOMO SAPIENS (HUMAN)//P39188
 5 F-NT2RM4000290//TRANSDUCIN-LIKE ENHANCER PROTEIN 3 (ESG3)//1.6e-115:209:94//HOMO SAPIENS (HUMAN)//Q04726
 F-NT2RM4000324//PRESPORE PROTEIN DP87 PRECURSOR//0.14:136:30//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//Q04503
 10 F-NT2RM4000327//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION//0.91:73:28//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41703
 F-NT2RM4000344//YME1 PROTEIN HOMOLOG (EC 3.4.24.-)//9.4e-78:241:55//CAENORHABDITIS ELE-GANS//P54813
 F-NT2RM4000349//CYSTEINE STRING PROTEIN (CCCS1)//0.055:22:59//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY)//P56101
 15 F-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN)//4.6e-26:208:35//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24371
 F-NT2RM4000356//COAT PROTEIN//0.11:105:36//SATELLITE TOBACCO MOSAIC VIRUS (STMV)//P17574
 F-NT2RM4000366//IMMEDIATE-EARLY PROTEIN//1.2e-05:215:24//HERPES VIRUS SAIMIRI (STRAIN 11)//Q01042
 20 F-NT2RM4000368//HYPOTHETICAL 7.3 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION//0.54:46:36//BACTERIOPHAGE RB69//Q64300
 F-NT2RM4000386//RHSC PROTEIN PRECURSOR//0.0096:162:29//ESCHERICHIA COLI//P16918
 F-NT2RM4000395//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION//4.5e-66:256:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43616
 25 F-NT2RM4000414//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION//0.13:33:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53820
 F-NT2RM4000421//MRNA TRANSPORT REGULATOR MTR10//5.0e-13:171:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q99189
 30 F-NT2RM4000425//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.1e-25:46:80//HOMO SAPIENS (HUMAN)//P39193
 F-NT2RM4000433//CUTICLE COLLAGEN 3A3//2.5e-06:77:38//HAEMONCHUS CONTORTUS//P16253
 F-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME 1//4.3e-09:215:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10297
 35 F-NT2RM4000471//TRNA SPLICING PROTEIN SPL1//6.7e-73:163:65//CANDIDA ALBICANS (YEAST)//P87185
 F-NT2RM4000486//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR//0.0012:121:34//GALLUS GALLUS (CHICKEN)//P15988
 F-NT2RM4000496//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RNA POLYMERASE II SUBUNIT 1)//5.9e-09:175:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P36594
 40 F-NT2RM4000511//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR//0.020:122:31//DROSOPHILA SIMULANS (FRUIT FLY)//P13729
 F-NT2RM4000514//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.46:68:32//ARTEMIA SANFRANCISCANA (BRINE SHRIMP) (ARTEMIA FRANCISCANA)//Q37708
 45 F-NT2RM4000515//GAR2 PROTEIN//3.2e-05:198:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P41891
 F-NT2RM4000520//HYPOTHETICAL 7.5 KD PROTEIN (ORF 63)//0.011:55:38//SPINACIA OLERACEA (SPINACH)//P08974
 F-NT2RM4000531//ZINC FINGER PROTEIN 169 (FRAGMENT)//3.6e-44:244:42//HOMO SAPIENS (HUMAN)//Q14929
 50 F-NT2RM4000532//PUTATIVE MEMBRANE PROTEIN 53//1.0:47:34//HERPES VIRUS SAIMIRI (STRAIN 11)//Q01049
 F-NT2RM4000534//HYPOTHETICAL 5.9 KD PROTEIN IN WRBA-PUTA INTERGENIC REGION//0.75:26:46//ESCHERICHIA COLI//P56614
 55 F-NT2RM4000585//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16; CORE PROTEIN P26]//0.019:86:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLIS.Y) (HIV-2)//P12450
 F-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN)//5.0e-23:224:29//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

F-NT2RM4000595//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//3.8e-62:226:50//
CAENORHABDITIS ELEGANS //P34284
F-NT2RM4000603//SRC SUBSTRATE CORTACTIN (AMPLAXIN) (EMS1 ONCOGENE).//0.077:132:22//HOMO
SAPIENS (HUMAN)//Q14247
5 F-NT2RM4000611//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHRO-
MOSOME III.//1.9e-06:82:32//CAENORHABDITIS ELEGANS //Q17963
F-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-
TIVATING ENZYME).//5.3e-79:213:62//ESCHERICHIA COLI.//P27550
F-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.3e-11:147:32//SYNECHOCYSTIS SP. (STRAIN
10 PCC 6803).//P74168
F-NT2RM4000689
F-NT2RM4000698//CHORION CLASS HIGH-CYSTEINE HCA PROTEIN 12 PRECURSOR (HC-A.12).//0.26:45:
33//BOMBYX MORI (SILK MOTH).//P05687
F-NT2RM4000700//THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//0.95:165:25//BORRELIA BURG-
15 DORFERI (LYME DISEASE SPIROCHETE).//P53364
F-NT2RM4000712//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)
(UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-
ZYME).//2.2e-82:152:63//CAENORHABDITIS ELEGANS //P34547
F-NT2RM4000717//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.80:54:40//DROSOPHILA SIMULANS
20 (FRUIT FLY).//P13729
F-NT2RM4000733//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.5e-08:139:28//MUS MUSCULUS (MOUSE).//
Q06666
F-NT2RM4000734//GASTRULA ZINC FINGER PROTEIN XLGCF26.1 (FRAGMENT).//7.2e-20:205:28//XENO-
PUS LAEVIS (AFRICAN CLAWED FROG).//P18715
25 F-NT2RM4000741//SPERM PROTAMINE P1.//0.89:52:38//ISOODON MACROURUS (SHORT-NOSED BANDI-
COOT).//P42136
F-NT2RM4000751//ZINC FINGER PROTEIN 26 (ZFP-26) (MKR3 PROTEIN) (FRAGMENT).//5.2e-77:246:52//
MUS MUSCULUS (MOUSE).//P10076
F-NT2RM4000764//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.062:33:42//OVIS ARIES (SHEEP).//
30 Q02958
F-NT2RM4000778
F-NT2RM4000779//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.014:53:45//VOLVOX CARTERI.//
P21997
F-NT2RM4000787//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//0.00011:73:
35 39//MUS MUSCULUS (MOUSE).//P98063
F-NT2RM4000790//SPORE COAT PROTEIN SP96.//0.00083:157:29//DICTYOSTELIUM DISCOIDEUM (SLIME
MOLD).//P14328
F-NT2RM4000795//CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLHYDROLASE)
(CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE) (PSEUDOCOLINESTERASE).//7.4e-41:271:36//
40 HOMO SAPIENS (HUMAN).//P06276
F-NT2RM4000796//5-METHYLCYTOSINE-SPECIFIC RESTRICTION ENZYME B (EC 3.1.21.-).//0.28:82:30//ES-
CHERICHIA COLI.//P15005
F-NT2RM4000798//PROTEIN TRANSPORT PROTEIN SEC7.//4.7e-38:165:48//SACCHAROMYCES CEREVI-
SIAE (BAKER'S YEAST).//P11075
45 F-NT2RM4000813//METALLOTHIONEIN-IB.//0.0025:25:44//OVIS ARIES (SHEEP).//P09577
F-NT2RM4000820
F-NT2RM4000833//HYPOTHETICAL PROTEIN MJ1136.//6.5e-42:206:41//METHANOCOCCUS JANNASCHII.//
Q58536
F-NT2RM4000848//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (BRN-3.0).//0.00060:
50 159:33//MUS MUSCULUS (MOUSE).//P17208
F-NT2RM4000852//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.0076:13:69//HOMO SAPIENS (HU-
MAN).//P35325
F-NT2RM4000855//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.0060:68:44//HOMO SAPIENS (HUMAN).//
P39194
55 F-NT2RM4000887//RTS1 PROTEIN (SCS1 PROTEIN).//0.23:153:24//SACCHAROMYCES CEREVISIAE (BAK-
ER'S YEAST).//P38903
F-NT2RM4000895//HYPOTHETICAL 53.5 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION.//3.3e-09:80:
46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43123

F-NT2RM4000950//HYPOTHETICAL PROTEIN MJ0572//0.090:68:29//METHANOCOCCUS JANNASCHII//
 Q57992
 F-NT2RM4000971//KINESIN LIGHT CHAIN (KLC)//0.79:201:24//LOLIGO PEALEII (LONGFIN SQUID)//P46825
 F-NT2RM4000979//MYOSIN REGULATORY LIGHT CHAIN 2, NONSARCOMERIC (MYOSIN RLC)//1.2e-07:25:
 5 96//HOMO SAPIENS (HUMAN)//P19105
 F-NT2RM4000996//ZINC FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC ZINC FINGER PRO-
 TEIN)//1.4e-56:253:46//MUS MUSCULUS (MOUSE)//P17141
 F-NT2RM4001002
 F-NT2RM4001016//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12;
 10 CORE SHELL PROTEIN P30]//0.25:101:31//FBR MURINE OSTEOSARCOMA VIRUS//P29175
 F-NT2RM4001032//CUTICLE COLLAGEN 2//2.6e-07:130:39//CAENORHABDITIS ELEGANS//P17656
 F-NT2RM4001047//MO25 PROTEIN//5.6e-107:252:80//MUS MUSCULUS (MOUSE)//Q06138
 F-NT2RM4001054//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//9.0e-109:209:94//CANIS FA-
 MILIARIS (DOG)//P38377
 15 F-NT2RM4001084//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN UXUR-IADA INTERGENIC RE-
 GION//0.57:95:30//ESCHERICHIA COLI//P39376
 F-NT2RM4001092//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III//2.5e-47:231:47//
 CAENORHABDITIS ELEGANS//Q09531
 F-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II//1.3e-08:243:23//
 20 CAENORHABDITIS ELEGANS//Q09417
 F-NT2RM4001140//HOMEODOMAIN PROTEIN MSH-D//7.1e-13:103:38//BRACHYDANIO RERIO (ZEBRAFISH)
 (ZEBRA DANIO)//Q01704
 F-NT2RM4001151//SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1)//0.26:96:34//HOMO SAPIENS (HUMAN)//
 P17600
 25 F-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN//3.6e-103:201:91//BOS TAURUS (BOVINE)//
 Q27969
 F-NT2RM4001160//GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18) (CLASS-PHI) (FRAGMENTS)//1.0:33:36//
 BRASSICA OLERACEA (CAULIFLOWER)//P48438 F-NT2RM4001187//PREPROTEIN TRANSLOCASE SECA
 SUBUNIT//0.44:158:27//MYCOPLASMA GENITALIUM//P47318
 30 F-NT2RM4001191//LONG NEUROTOXIN 2 (TOXIN C)//0.99:44:43//ASTROTIA STOKESI (STOKES'S SEA
 SNAKE) (DISTEIRA STOKESI)//P01381
 F-NT2RM4001200//ZINC FINGER PROTEIN 135//2.2e-82:245:59//HOMO SAPIENS (HUMAN)//P52742
 F-NT2RM4001203//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//0.028:94:
 40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214
 35 F-NT2RM4001204//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//0.0096:182:34//HOMO
 SAPIENS (HUMAN)//Q15428
 F-NT2RM4001217//RING CANAL PROTEIN (KELCH PROTEIN)//2.1e-21:221:29//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q04652
 F-NT2RM4001256//CBP3 PROTEIN PRECURSOR//0.30:55:32//SACCHAROMYCES CEREVISIAE (BAKER'S
 40 YEAST)//P21560
 F-NT2RM4001258//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.00031:132:39//STREP-
 TOMYCES FRADIAE//P20186
 F-NT2RM4001309//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC
 PEPTIDE P-F] (FRAGMENT)//0.048:132:28//HOMO SAPIENS (HUMAN)//P02812
 45 F-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-
 3-KINASE) (PI3K)//2.6e-37:124:65//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P54676
 F-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3)
 (MCAD)//1.7e-10:185:30//RATTUS NORVEGICUS (RAT)//P08503
 F-NT2RM4001320//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
 CIOGENITAL DYSPLASIA PROTEIN HOMOLOG)//1.5e-08:197:26//MUS MUSCULUS (MOUSE)//P52734
 50 F-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN)//7.7e-14:82:36//SACCHAROMY-
 CES CEREVISIAE (BAKER'S YEAST)//P32626
 F-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION//3.3e-
 16:128:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53742
 55 F-NT2RM4001347//HYPOTHETICAL 76.9 KD PROTEIN IN RPM2-TUB1 INTERGENIC REGION//0.067:111:33//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04511
 F-NT2RM4001371
 F-NT2RM4001382//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR//1.0e-08:82:39//PLASMODIUM LOPHU-

RAE//P04929
F-NT2RM4001384
F-NT2RM4001410//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//2.1e-08:185:31//SACCHAROMY-
CES CEREVISIAE (BAKER'S YEAST).//P32323
5 F-NT2RM4001411//EARLY NODULIN 20 PRECURSOR (N-20).//5.3e-05:105:38//MEDICAGO TRUNCATULA
(BARREL MEDIC).//P93329
F-NT2RM4001412//GTPASE-ACTIVATING PROTEIN (GAP) (RAS P21 PROTEIN ACTIVATOR) (P120GAP)
(RASGAP).//6.2e-17:109:41//RATTUS NORVEGICUS (RAT).//P50904
F-NT2RM4001414//ZINC FINGER PROTEIN 177.//8.3e-06:54:50//HOMO SAPIENS (HUMAN).//Q13360
10 F-NT2RM4001437//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-24:87:65//HOMO SAPIENS (HUMAN).//
P39192
F-NT2RM4001444//PROBABLE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE)
(ILERS) (FRAGMENT).//2.6e-45:197:47//CIONA INTESTINALIS.//Q94425
F-NT2RM4001454//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//0.0060:95:29//HOMO SAPIENS (HU-
15 MAN).//Q15057
F-NT2RM4001455//PROBABLE E5B PROTEIN.//0.41:44:36//HUMAN PAPILLOMAVIRUS TYPE 6B.//P06461
F-NT2RM4001483//ZINC FINGER PROTEIN 136.//1.7e-28:85:64//HOMO SAPIENS (HUMAN).//P52737
F-NT2RM4001489//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.086:111:34//HOMO SAPIENS (HUMAN).//
P23246
20 F-NT2RM4001519//ACID UREASE ALPHA SUBUNIT (EC 3.5.1.5) (UREA AMIDOHYDROLASE).//0.82:51:47//
LACTOBACILLUS FERMENTUM.//P26929
F-NT2RM4001522//TROPOMYOSIN.//0.030:117:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//
Q02088
F-NT2RM4001557
25 F-NT2RM4001565//HYPOTHETICAL 44.3 KD PROTEIN C1F7.07C IN CHROMOSOME I.//0.99:42:40//
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09919
F-NT2RM4001566//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.054:190:23//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P08640
30 F-NT2RM4001569//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (ACTIVATED
PROTEIN KINASE C RECEPTOR HOMOLOG).//0.72:64:31//TRYPANOSOMA BRUCEI BRUCEI.//Q94775
F-NT2RM4001582
F-NT2RM4001592//DNA REPAIR PROTEIN RAD9.//0.00037:198:31//SACCHAROMYCES CEREVISIAE (BAK-
ER'S YEAST).//P14737
35 F-NT2RM4001594//IMMEDIATE-EARLY PROTEIN IE180.//1.9e-05:147:34//PSEUDORABIES VIRUS (STRAIN
KAPLAN) (PRV).//P33479
F-NT2RM4001597//THIOL:DISULFIDE INTERCHANGE PROTEIN TLPA (CYTOCHROME C BIOGENESIS PRO-
TEIN TLPA).//5.7e-06:122:29//BRADYRHIZOBIUM JAPONICUM.//P43221
F-NT2RM4001605//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NU-
40 CLEOPORIN) (P140).//1.7e-128:249:96//RATTUS NORVEGICUS (RAT).//P37199
F-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//1.5e-35:128:47//SACCHAROMY-
CES CEREVISIAE (BAKER'S YEAST).//P36024
F-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3).//
5.8e-42:254:37//HOMO SAPIENS (HUMAN).//Q13368
45 F-NT2RM4001650//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.62:19:57//GALLUS GALLUS (CHICKEN).//
P17277
F-NT2RM4001662//PROTEIN KINASE C, ALPHA TYPE (EC 2.7.1.-) (PKC-ALPHA).//0.29:90:32//HOMO SAPI-
ENS (HUMAN).//P17252
F-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//1.1e-31:137:
50 44//ESCHERICHIA COLI.//P37339
F-NT2RM4001682//PROBABLE 60S RIBOSOMAL PROTEIN L22.//0.98:55:29//CAENORHABDITIS ELEGANS.//
P52819
F-NT2RM4001710//HYPOTHETICAL PROTEIN KIAA0039 (FRAGMENT).//0.56:113:28//HOMO SAPIENS (HU-
MAN).//Q15054
55 F-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//1.4e-108:255:77//HOMO SAPIENS (HUMAN).//
Q14141
F-NT2RM4001715//HYPOTHETICAL PROTEIN C19G10.16 IN CHROMOSOME I (FRAGMENT).//2.1e-36:148:
38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10342

F-NT2RM4001731//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III//1.1e-05:90:33//
 CAENORHABDITIS ELEGANS//P34284
 F-NT2RM4001741//TALIN//1.1e-106:208:99//MUS MUSCULUS (MOUSE)//P26039
 F-NT2RM4001746//EBNA-1 NUCLEAR PROTEIN//1.6e-09:155:38//EPSTEIN-BARR VIRUS (STRAIN B95-8)
 5 (HUMAN HERPESVIRUS 4)//P03211
 F-NT2RM4001754//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR//0.93:158:33//HOMO SAPIENS (HUMAN)//
 P29400
 F-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-)//5.1e-113:277:79//
 HOMO SAPIENS (HUMAN)//P27448
 10 F-NT2RM4001776//MYOSIN I ALPHA (MMI-ALPHA)//2.2e-73:262:54//MUS MUSCULUS (MOUSE)//P46735
 F-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1) (FRAGMENT)//5.3e-26:169:39//MUS MUSCULUS
 (MOUSE)//P55200
 F-NT2RM4001810//MALE SPECIFIC SPERM PROTEIN MST84DB//2.3e-05:68:42//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01643
 15 F-NT2RM4001813//RHODOCETIN ALPHA SUBUNIT//2.3e-05:115:34//AGKISTRODON RHODOSTOMA (MA-
 LAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA)//P81397
 F-NT2RM4001819//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)
 (CELL SURFACE GLYCOPROTEIN F4/80)//1.7e-06:159:25//MUS MUSCULUS (MOUSE)//Q61549
 F-NT2RM4001823//ZINC FINGER PROTEIN ZIC1 (ZINC FINGER PROTEIN OF THE CEREBELLUM 1)//2.6e-
 20 18:114:40//MUS MUSCULUS (MOUSE)//P46684
 F-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//4.0e-81:253:59//HOMO SA-
 PIENS (HUMAN)//P51523
 F-NT2RM4001836//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//0.21:176:30//NEPHILA CLA-
 VIPES (ORB SPIDER)//P46804
 25 F-NT2RM4001841//PROLINE-RICH PEPTIDE P-B//0.046:27:40//HOMO SAPIENS (HUMAN)//P02814
 F-NT2RM4001842//HYPOTHETICAL 7.0 KD PROTEIN B03B8.1 IN CHROMOSOME III//0.98:35:42//
 CAENORHABDITIS ELEGANS//Q11104
 F-NT2RM4001856//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION//2.3e-37:242:
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39722
 30 F-NT2RM4001858//T-BOX PROTEIN VEGT (T-BOX PROTEIN BRAT) (T-BOX PROTEIN ANTIPODEAN)//1.8e-
 23:78:64//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P87377
 F-NT2RM4001865//NEURONAL CALCIUM SENSOR 2 (NCS-2)//0.012:83:28//CAENORHABDITIS ELEGANS//
 P36609
 F-NT2RM4001876//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECUR-
 35 SOR//3.8e-10:242:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47179
 F-NT2RM4001880//EC PROTEIN HOMOLOG//0.22:59:32//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//
 P93746
 F-NT2RM4001905//60S RIBOSOMAL PROTEIN L40 (CEP52)//0.57:20:60//HOMO SAPIENS (HUMAN), RAT-
 TUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN)//P14793
 40 F-NT2RM4001922
 F-NT2RM4001930//PUTATIVE GLUCOSYLTRANSFERASE C08B11.8 (EC 2.4.1.-)//5.5e-45:167:53//
 CAENORHABDITIS ELEGANS//Q09226
 F-NT2RM4001938//RTOA PROTEIN (RATIO-A)//0.0036:120:32//DICTYOSTELIUM DISCOIDEUM (SLIME
 MOLD)//P54681
 45 F-NT2RM4001940//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-1 (FRAGMENT)//0.32:31:48//HOMO
 SAPIENS (HUMAN)//P78415
 F-NT2RM4001953//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.2e-43:56:85//HOMO SAPIENS (HUMAN)//
 P39192
 F-NT2RM4001965//IG ALPHA-1 CHAIN C REGION//0.56:73:34//GORILLA GORILLA GORILLA (LOWLAND GO-
 50 RILLA)//P20758
 F-NT2RM4001969//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CON-
 TAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H]//0.0016:140:27//HOMO SAPIENS (HUMAN)//P04280
 F-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//3.9e-21:103:51//HOMO SA-
 PIENS (HUMAN)//P51523
 55 F-NT2RM4001984//HYPOTHETICAL PROTEIN LAMBDA-SP5//0.0034:50:40//MUS MUSCULUS (MOUSE)//
 P15974
 F-NT2RM4001987//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN)//6.9e-
 17:115:31//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q08180

- F-NT2RM4002013//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//0.0062:117:28//CAENORHABDITIS ELEGANS.//Q23256
- F-NT2RM4002018//SPORE COAT PROTEIN SP96.//4.3e-06:203:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328
- 5 F-NT2RM4002034//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//0.78:132:25//HOMO SAPIENS (HUMAN).//P98171
- F-NT2RM4002044//VITELLOGENIN I PRECURSOR (MINOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP42].//0.062:201:24//GALLUS GALLUS (CHICKEN).//P87498
- F-NT2RM4002054//DUPLICATE PROCYCLIN.//0.0079:44:52//TRYPANOSOMA BRUCEI BRUCEI.//P14044
- 10 F-NT2RM4002055//PUTATIVE Z PROTEIN.//0.82:39:30//OVIS ARIES (SHEEP).//P08105
- F-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//7.0e-37:80:52//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P36419
- F-NT2RM4002063//SARCOSINE OXIDASE (EC 1.5.3.1).//2.2e-25:216:31//BACILLUS SP. (STRAIN NS-129).//P23342
- 15 F-NT2RM4002066//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//1.1e-94:260:71//HOMO SAPIENS (HUMAN).//Q93074
- F-NT2RM4002067//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!1.5e-15:51:70//HOMO SAPIENS (HUMAN).//P39188
- F-NT2RM4002073//ELASTIN PRECURSOR (TROPOELASTIN).//4.9e-05:88:36//HOMO SAPIENS (HUMAN).//P15502
- 20 F-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//7.2e-43:220:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
- F-NT2RM4002093//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB-1).//1.8e-93:255:72//HOMO SAPIENS (HUMAN).//P26599
- 25 F-NT2RM4002109//KINESIN-LIKE PROTEIN KIF4.//3.7e-101:260:78//MUS MUSCULUS (MOUSE).//P33174
- F-NT2RM4002128//HYPOTHETICAL PROTEIN IN CYCB 3'REGION PRECURSOR (ORF2) (FRAGMENT).//0.91:49:32//PARACOCCLUS DENITRIFICANS.//P29969
- F-NT2RM4002140//GROUCHO PROTEIN (ENHANCER OF SPLIT M9/10).//0.36:104:22//DROSOPHILA MELANOGASTER (FRUIT FLY).//P16371
- 30 F-NT2RM4002145//SLIT PROTEIN PRECURSOR.//8.6e-13:127:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014
- F-NT2RM4002146//MAGO NASHI PROTEIN.//7.9e-69:143:91//DROSOPHILA MELANOGASTER (FRUIT FLY).//P49028
- 35 F-NT2RM4002161//DUAL SPECIFICITY PROTEIN PHOSPHATASE (EC 3.1.3.48) (EC 3.1.3.16).//0.0062:99:26//CHLAMYDOMONAS EUGAMETOS.//Q39491
- F-NT2RM4002174//MRP PROTEIN.//4.5e-50:183:55//ESCHERICHIA COLI.//P21590
- F-NT2RM4002189//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.6e-14:233:29//HOMO SAPIENS (HUMAN).//Q02817
- 40 F-NT2RM4002194//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.92:108:28//HOMO SAPIENS (HUMAN).//P51805
- F-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5.8e-39:122:72//RATTUS NORVEGICUS (RAT).//Q07803
- F-NT2RM4002213//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III.//9.9e-27:110:43//CAENORHABDITIS ELEGANS.//Q03565
- 45 F-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//1.3e-21:147:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P40809
- F-NT2RM4002251//PROTEIN EF-7 (FRAGMENT).//0.00082:45:42//MUS MUSCULUS (MOUSE).//P97805
- F-NT2RM4002256//COLD-REGULATED PROTEIN 1 (FRAGMENT).//0.00015:114:42//HORDEUM VULGARE (BARLEY).//P23251
- 50 F-NT2RM4002266//CUTICLE COLLAGEN 2.//0.00013:142:33//CAENORHABDITIS ELEGANS.//P17656
- F-NT2RM4002278//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.//1.0:40:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288
- F-NT2RM4002281
- 55 F-NT2RM4002287//GAR2 PROTEIN.//0.00055:225:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
- F-NT2RM4002294//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//1.1e-60:152:75//HOMO SAPIENS (HUMAN).//Q92556

F-NT2RM4002301//GENERAL STRESS PROTEIN CTC (FRAGMENT)//0.56:43:39//BACILLUS CALDOLYTI-
 CUS//P42832
 F-NT2RM4002323//NONHISTONE CHROMOSOMAL PROTEIN HMG-17//0.0080:73:35//BOS TAURUS (BO-
 VINE)//P02313
 5 F-NT2RM4002339//METALLOTHIONEIN 10-III (MT-10-III)//0.67:34:38//MYTILUS EDULIS (BLUE MUSSEL)//
 P80248
 F-NT2RM4002344//METALLOTHIONEIN-I (MT-I)//0.84:41:31//MUS MUSCULUS (MOUSE)//P02802
 F-NT2RM4002373//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DY10 PRECURSOR//0.0019:190:28//
 TRITICUM AESTIVUM (WHEAT)//P10387
 10 F-NT2RM4002374//5E5 ANTIGEN//0.0059:170:32//RATTUS NORVEGICUS (RAT)//Q63003
 F-NT2RM4002383//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.13:17:88//HOMO SAPIENS (HUMAN)//
 P39193
 F-NT2RM4002390
 F-NT2RM4002398//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN)//0.034:110:
 27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38074
 15 F-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-
 TIVATING ENZYME)//4.0e-20:179:31//METHANOTRIX SOEHNENII//P27095
 F-NT2RM4002438//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.7e-15:41:95//HOMO SAPIENS (HUMAN)//
 P39194
 20 F-NT2RM4002446//CRYPTDIN-RELATED PROTEIN 4C-1 PRECURSOR (CRS4C)//0.0058:24:50//MUS MUS-
 CULUS (MOUSE)//P17534
 F-NT2RM4002452//METALLOTHIONEIN 10-II (MT-10-II)//0.83:48:37//MYTILUS EDULIS (BLUE MUSSEL)//
 P80247
 F-NT2RM4002457//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/4.9e-07:52:63//HOMO SAPIENS (HUMAN)//
 25 P39192
 F-NT2RM4002460//C-HORDEIN (CLONE PC-919) (FRAGMENT)//0.92:43:30//HORDEUM VULGARE (BAR-
 LEY)//P17992
 F-NT2RM4002479//RNA HELICASE-LIKE PROTEIN DB10//1.7e-28:200:41//NICOTIANA SYLVESTRIS (WOOD
 TOBACCO)//P46942
 30 F-NT2RM4002482//HYPOTHETICAL 65.9 KD PROTEIN YPR065W//8.8e-26:123:49//SACCHAROMYCES CER-
 EVISIAE (BAKER'S YEAST)//Q12514 F-NT2RM4002493//LARVAL CUTICLE PROTEIN I PRECURSOR//0.17:
 126:27//DROSOPHILA MIRANDA (FRUIT FLY)//P91627
 F-NT2RM4002499//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.4e-34:92:80//HOMO SAPIENS (HUMAN)//
 P39194
 35 F-NT2RM4002504//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.4e-19:55:83//HOMO SAPIENS (HUMAN)//
 P39189
 F-NT2RM4002527//WD-40 REPEAT PROTEIN MSI2//3.0e-07:193:27//ARABIDOPSIS THALIANA (MOUSE-
 EAR CRESS)//Q22468
 F-NT2RM4002532//AEROLYSIN REGULATORY PROTEIN//0.97:19:47//AEROMONAS SOBRIA//P09165
 40 F-NT2RM4002534//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32 PRECURSOR (YML32)//0.76:86:22//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25348
 F-NT2RM4002558//LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP)//4.2e-55:204:50//MUS MUSCU-
 LUS (MOUSE)//Q60714
 F-NT2RM4002565//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5//1.0:16:62//ASCARIS SUUM (PIG
 45 ROUNDWORM) (ASCARIS LUMBRICOIDES)//P07852
 F-NT2RM4002567//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION//2.7e-10:184:
 29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40032
 F-NT2RM4002571//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-
 UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOS-
 50 AMINYLTRANSFERASE) (GALNAC-T1)//2.4e-25:124:47//HOMO SAPIENS (HUMAN)//Q10472
 F-NT2RM4002593//HYPOTHETICAL 9.1 KD PROTEIN IN TETB-EXOA INTERGENIC REGION//0.95:36:38//BA-
 CILLUS SUBTILIS//P37509
 F-NT2RM4002594//MSP1 PROTEIN HOMOLOG//9.0e-68:227:60//CAENORHABDITIS ELEGANS//P54815
 F-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS)//
 55 3.3e-54:243:47//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//P73851
 F-NT2RP1000018//SUPPRESSOR PROTEIN SRP40//0.0023:131:25//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P32583
 F-NT2RP1000035//RING CANAL PROTEIN (KELCH PROTEIN)//1.0e-06:63:34//DROSOPHILA MELA-

NOGASTER (FRUIT FLY)//Q04652
 F-NT2RP1000040//LETHAL NEUROTOXIN TX1//0.69:21:47//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPIDER)//P17727
 F-NT2RP1000063//HYPOTHETICAL 25.1 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION//3.8e-14:130:
 5 30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40359
 F-NT2RP1000086//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION//0.16:44:40//ES-
 CHERICHIA COLI//P22847
 F-NT2RP1000101//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION//1.9e-06:74:32//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P38344
 10 F-NT2RP1000111//COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1)//2.7e-19:135:36//ARABIDOPSIS
 THALIANA (MOUSE-EAR CRESS)//P43254
 F-NT2RP1000112//DUAL SPECIFICITY PROTEIN KINASE TTK (EC 2.7.1.-) (PYT)//1.2e-39:91:62//HOMO SA-
 PIENS (HUMAN)//P33981
 F-NT2RP1000124//ATP-DEPENDENT PROTEASE LA 2 (EC 3.4.21.53)//0.074:131:24//MYXOCOCCUS XAN-
 15 THUS//P36774
 F-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF)//1.5e-49:186:56//MUS MUSCULUS
 (MOUSE)//P51859
 F-NT2RP1000163//METALLOTHIONEIN (MT)//0.98:41:34//PLEURONECTES PLATESSA (PLAICE)//P07216
 F-NT2RP1000170//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-
 20 MENT)//0.85:64:35//HOMO SAPIENS (HUMAN)//P10162
 F-NT2RP1000174//IMMEDIATE-EARLY PROTEIN IE180//0.00056:89:37//PSEUDORABIES VIRUS (STRAIN
 KAPLAN) (PRV)//P33479
 F-NT2RP1000191//NIFU PROTEIN//0.53:78:35//FRANKIA ALNI//P46045
 F-NT2RP1000202//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT)//
 25 9.1e-21:148:39//HOMO SAPIENS (HUMAN)//Q01485
 F-NT2RP1000243//HYPOTHETICAL PROTEIN MJ1136//1.4e-37:219:36//METHANOCOCCUS JANNASCHII//
 Q58536
 F-NT2RP1000259//HYPOTHETICAL PROTEIN TP0318//0.18:25:44//TREPONEMA PALLIDUM//O83338
 F-NT2RP1000272//SPLICING FACTOR, ARGININE/SERINE-RICH 3 (PRE-MRNA SPLICING FACTOR SRP20)
 30 (X16 PROTEIN)//1.6e-18:133:36//HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE)//P23152
 F-NT2RP1000324
 F-NT2RP1000326//HYPOTHETICAL 29.8 KD PROTEIN ZC97.1 IN CHROMOSOME III//1.0e-23:129:36//
 CAENORHABDITIS ELEGANS//P34599
 F-NT2RP1000333//ANTI-SILENCING PROTEIN 1//2.5e-45:147:57//SACCHAROMYCES CEREVISIAE (BAK-
 35 ER'S YEAST)//P32447
 F-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161//4.8e-14:119:34//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P25343
 F-NT2RP1000357//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT)//1.0:43:32//
 TRYPANOSOMA CRUZI//Q26327
 40 F-NT2RP1000358//HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3'REGION//7.9e-28:244:35//SACCHA-
 ROMYCES CEREVISIAE (BAKER'S YEAST)//P39744
 F-NT2RP1000363//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//2.2e-07:178:30//
 XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437
 F-NT2RP1000376//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//1.5e-20:254:31//HOMO
 45 SAPIENS (HUMAN)//P16157
 F-NT2RP1000409//CYTOCHROME C3 (CYTOCHROME C7) (C551.5)//1.0:34:26//DESULFUROMONAS ACE-
 TOXIDANS (CHLOROPSEUDOMONAS ETHYLICA)//P00137
 F-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN)//3.7e-131:230:97//RAT-
 TUS NORVEGICUS (RAT)//P55161
 50 F-NT2RP1000416//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR//0.83:54:40//DROSOPHILA SIMULANS
 (FRUIT FLY)//P13729
 F-NT2RP1000418//HYPOTHETICAL 9.9 KD PROTEIN IN GCVT-SPOIIIAA INTERGENIC REGION//0.24:91:35//
 BACILLUS SUBTILIS//P49779
 F-NT2RP1000439//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I//0.13:172:22//
 55 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10429
 F-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-
 CRYSTALLIN)//1.9e-08:167:24//HOMO SAPIENS (HUMAN)//Q08257
 F-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC//1.0e-18:149:34//EMERICELLA NIDULANS (AS-

PERGILLUS NIDULANS) //P17624
 F-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III //1.3e-43:
 180:47//CAENORHABDITIS ELEGANS //P34580
 F-NT2RP1000478//TUBULIN BETA-6 CHAIN (CLASS-VI) //1.5e-45:85:63//GALLUS GALLUS (CHICKEN) //
 5 P09207
 F-NT2RP1000481//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5'REGION (ORF55) //0.083:21:47//RHODO-
 BACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA) //P26159
 F-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM
 GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB) //6.6e-11:139:31//CERCOPITHEC-
 10 US AETHIOPS (GREEN MONKEY) (GRIVET) //P33194
 F-NT2RP1000513//60S RIBOSOMAL PROTEIN L22 //0.017:92:30//DROSOPHILA MELANOGASTER (FRUIT
 FLY) //P50887
 F-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-
 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-
 15 ZYME 1) //0.0055:86:36//MUS MUSCULUS (MOUSE) //Q61068
 F-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT) //1.2e-
 09:69:36//CRICETULUS GRISEUS (CHINESE HAMSTER) //P49020
 F-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1) //6.0e-39:141:65//MUS MUS-
 CULUS (MOUSE) //P97367
 20 F-NT2RP1000577//PUTATIVE ATP-DEPENDENT RNA HELICASE YDL031W //0.00016:48:45//SACCHAROMY-
 CES CEREVISIAE (BAKER'S YEAST) //Q12389
 F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR //0.00017:61:50//HOMO SAPIENS (HUMAN) //
 P04275
 F-NT2RP1000609//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE) //4.4e-07:128:
 25 31//SYNECHOCYSTIS SP. (STRAIN PCC 6803) //Q08871
 F-NT2RP1000629//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN
 AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN
 ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN) //4.2e-70:167:86//MUS MUSCULUS (MOUSE) //P35585
 F-NT2RP1000630//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR //
 30 0.0011:238:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P47179
 F-NT2RP1000677//COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR //0.99:71:33//HOMO SAPIENS (HUMAN) //
 Q07092
 F-NT2RP1000688//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! //0.0024:19:94//HOMO SAPIENS (HUMAN) //
 P39193
 35 F-NT2RP1000695//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III //2.2e-30:185:37//
 CAENORHABDITIS ELEGANS //Q18262
 F-NT2RP1000701//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP) //3.2e-65:128:93//RATTUS NOR-
 VEGICUS (RAT) //P54319
 F-NT2RP1000721//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)
 40 (TAFII-130) (TAFII130) //2.3e-06:139:34//HOMO SAPIENS (HUMAN) //O00268
 F-NT2RP1000730//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAG-
 MENT) //0.89:40:40//MUS MUSCULUS (MOUSE) //P09542
 F-NT2RP1000733//METALLOTHIONEIN-LIKE PROTEIN CRS5 //0.024:24:45//SACCHAROMYCES CEREVI-
 SIAE (BAKER'S YEAST) //P41902
 45 F-NT2RP1000738//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-
 3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C] //0.040:82:36//HOMO
 SAPIENS (HUMAN) //P02810
 F-NT2RP1000746//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION //2.0e-30:170:37//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P33201
 50 F-NT2RP1000767//PSEUDOMONAS PEPSIN PRECURSOR (EC 3.4.23.37) (PEPSTATIN-INSENSITIVE CAR-
 BOXYL PROTEINASE) //0.99:75:34//PSEUDOMONAS SP. (STRAIN 101) //P42790
 F-NT2RP1000782//CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA AS-
 SOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) //
 2.3e-23:159:35//HOMO SAPIENS (HUMAN) //P41732
 55 F-NT2RP1000796//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUA-
 MOUS CELL MARKER) (SPRP) //0.00018:79:32//SUS SCROFA (PIG) //P35323
 F-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN AC-
 TIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP) //3.1e-37:89:64//HOMO SAPIENS (HU-

MAN)//Q07960
 F-NT2RP1000833//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.32:29:48//HOMO SAPIENS (HUMAN)//P22531
 F-NT2RP1000834//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-)//6.4e-67:202:68//RATTUS NORVEGICUS (RAT)//P70473
 5 F-NT2RP1000836//HYPOTHETICAL 7.3 KD PROTEIN IN 100.KD PROTEIN REGION//1.0:35:54//HUMAN ADENOVIRUS TYPE 41//P23691
 F-NT2RP1000846//SMALL PROLINE-RICH PROTEIN 2-1//0.013:35:48//HOMO SAPIENS (HUMAN)//P35326
 F-NT2RP1000851//PERIOD CLOCK PROTEIN (FRAGMENT)//0.082:28:57//DROSOPHILA SALTANS (FRUIT FLY)//Q04536
 10 F-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)//2.5e-26:190:30//MUS MUSCULUS (MOUSE)//O35566
 F-NT2RP1000860//POTENTIAL TRANSCRIPTIONAL ADAPTOR//0.13:86:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q02336
 15 F-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III//7.6e-11:200:35//CAENORHABDITIS ELEGANS//Q09531
 F-NT2RP1000915//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION//1.4e-06:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40010
 F-NT2RP1000916//SUPPRESSOR PROTEIN SRP40//0.40:90:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583
 20 F-NT2RP1000943//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)//0.099:75:34//HOMO SAPIENS (HUMAN)//Q02817
 F-NT2RP1000944//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//7.6e-06:65:41//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341
 25 F-NT2RP1000947//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2)//3.6e-12:27:77//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P51669
 F-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN)//2.8e-15:169:28//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652
 30 F-NT2RP1000958//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION//4.2e-16:162:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40010
 F-NT2RP1000959//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPRK)//0.0031:34:44//HOMO SAPIENS (HUMAN)//P35321
 35 F-NT2RP1000966//NUCLEOLIN (PROTEIN C23)//1.5e-52:110:95//HOMO SAPIENS (HUMAN)//P19338
 F-NT2RP1000980//LIGHT-HARVESTING PROTEIN B-1015, ALPHA CHAIN PRECURSOR (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN)//0.87:37:45//RHODOPSEUDOMONAS VIRIDIS//P04123
 F-NT2RP1000988
 F-NT2RP1001011//PROTEIN P19//0.96:30:50//BACTERIOPHAGE PRD1//P17638
 40 F-NT2RP1001013//DNA-BINDING PROTEIN 65 (PROTEIN GP65)//1.0:20:45//BACTERIOPHAGE T4//P16012
 F-NT2RP1001014
 F-NT2RP1001033//TUBULIN GAMMA CHAIN//2.5e-16:112:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P25295
 F-NT2RP1001073//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION//7.6e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40089
 45 F-NT2RP1001079//SARCOSINE OXIDASE (EC 1.5.3.1)//4.8e-15:95:40//ARTHROBACTER SP. (STRAIN TE1826)//P40873
 F-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9//2.4e-29:126:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q06218
 50 F-NT2RP1001113//SMALL PROLINE-RICH PROTEIN 2-1//0.49:38:39//HOMO SAPIENS (HUMAN)//P35326
 F-NT2RP1001173//RHOMBOTIN-1 (CYSTEINE RICH PROTEIN TTG-1) (T-CELL TRANSLOCATION PROTEIN 1) (LIM-ONLY PROTEIN 1)//0.99:54:37//HOMO SAPIENS (HUMAN)//P25800
 F-NT2RP1001177//HISTONE MACRO-H2A.1//1.6e-29:85:76//RATTUS NORVEGICUS (RAT)//Q02874
 F-NT2RP1001185
 55 F-NT2RP1001199//NEUROTOXIN I//1.0:23:47//CENTRUROIDES SCULPTURATUS (BARK SCORPION)//P01491
 F-NT2RP1001247//TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4) (ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR)//3.3e-08:28:89//HOMO SAPIENS (HUMAN)//O00292

F-NT2RP1001248//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.33:49:28//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804

F-NT2RP1001253//GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6-PHOSPHATE DEAMINASE) (GNPDA) (OSCILLIN) (KIAA0060).//3.8e-46:115:81//HOMO SAPIENS (HUMAN).//P46926

5 F-NT2RP1001286//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN).//0.16:48:37//MUS MUSCULUS (MOUSE).//P16110

F-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//6.1e-05:92:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

10 F-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.2e-05:92:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

F-NT2RP1001310//PROBABLE E4 PROTEIN.//0.99:109:26//HUMAN PAPILLOMAVIRUS TYPE 5.//P06924

F-NT2RP1001311//SODIUM/HYDROGEN EXCHANGER 5 (NA(+)/H(+) EXCHANGER 5) (NHE-5) (FRAGMENT).//0.99:94:31//HOMO SAPIENS (HUMAN).//Q14940

15 F-NT2RP1001313//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40312

F-NT2RP1001361//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).//1.2e-47:117:74//BOS TAURUS (BOVINE).//Q02827

F-NT2RP1001385//CELL DIVISION PROTEIN FTSN.//0.64:107:28//ESCHERICHIA COLI.//P29131

20 F-NT2RP1001395//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.25:35:45//GALLUS GALLUS (CHICKEN).//P02467

F-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//2.2e-41:129:67//CAENORHABDITIS ELEGANS.//P91917

F-NT2RP1001424//UREASE ACCESSORY PROTEIN UREF (FRAGMENT).//0.87:24:45//ESCHERICHIA COLI.//Q03286

25 F-NT2RP1001432//CYSTEINE PROTEINASE INHIBITOR B (CYSTATIN B) (SCB).//1.0:35:42//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//Q10993

F-NT2RP1001449//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.053:37:37//OVIS ARIES (SHEEP).//P26372

30 F-NT2RP1001457//HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN CPR4-SSK22 INTERGENIC REGION.//2.9e-16:159:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25382

F-NT2RP1001466//HYPOTHETICAL PROTEIN MJ0284.//5.3e-15:162:35//METHANOCOCCUS JANNASCHII.//Q57732

F-NT2RP1001475//HYPOTHETICAL 195.1 KD PROTEIN IN DNA43-UBI1 INTERGENIC REGION.//0.69:119:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40457

35 F-NT2RP1001482//PROTEASOME COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C9).//1.0:58:32//HOMO SAPIENS (HUMAN).//P25789

F-NT2RP1001494//MALE STERILITY PROTEIN 2.//2.4e-12:84:42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891

40 F-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//6.3e-37:94:52//SPIRODELA POLYRRHIZA.//P42803

F-NT2RP1001546//LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53).//9.3e-11:98:29//HOMO SAPIENS (HUMAN).//P19397

F-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//2.2e-64:159:84//MUS MUSCULUS (MOUSE).//P47758

45 F-NT2RP1001616//HYPOTHETICAL 13.5 KD PROTEIN C45G9.7 IN CHROMOSOME III.//9.2e-05:49:42//CAENORHABDITIS ELEGANS.//Q09506

F-NT2RP1001665//REGB PROTEIN.//0.99:29:37//PSEUDOMONAS AERUGINOSA.//Q03381

F-NT2RP2000001//SMALL PROLINE-RICH PROTEIN 2-1.//0.64:36:41//HOMO SAPIENS (HUMAN).//P35326

50 F-NT2RP2000006//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40).//1.7e-19:74:52//HOMO SAPIENS (HUMAN).//P25685

F-NT2RP2000007//TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TM36) (TME1) (TM1).//0.93:126:23//HOMO SAPIENS (HUMAN).//P06468

F-NT2RP2000008//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//4.2e-35:156:54//HOMO SAPIENS (HUMAN).//Q06730

55 F-NT2RP2000027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.95:41:39//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P50665

F-NT2RP2000032//BAX PROTEIN, CYTOPLASMIC ISOFORM GAMMA.//1.0:35:34//HOMO SAPIENS (HUMAN).//P50665

MAN)//Q07815
 F-NT2RP2000040//BASIC PROLINE-RICH PEPTIDE IB-1//0.0024:58:36//HOMO SAPIENS (HUMAN)//P04281
 F-NT2RP2000045//DNAJ PROTEIN//1.1e-12:42:66//THERMUS AQUATICUS (SUBSP. THERMOPHILUS)//
 Q56237
 5 F-NT2RP2000054//GONADOLIBERIN III PRECURSOR (GONADOTROPIN-RELEASING HORMONE III) (GN-
 RH-III) (LH-RH III) (LULIBERIN III)//0.20:46:36//ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALM-
 ON)//P30973
 F-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-
 SILON)//1.3e-18:45:100//MUS MUSCULUS (MOUSE)//P49446
 10 F-NT2RP2000067//HOMEBOX PROTEIN HOX-A5 (S12-B) (FRAGMENT)//0.71:44:40//SALMO SALAR (AT-
 LANTIC SALMON)//P09637
 F-NT2RP2000070//INSULIN//0.94:30:43//HYSTRIX CRISTATA (CRESTED PORCUPINE)//P01328
 F-NT2RP2000076//ETS-LIKE PROTEIN POINTED P1 (D-ETS-2)//0.0013:76:40//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//P51022
 15 F-NT2RP2000077//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (U1-C)//0.24:49:40//HOMO SAPIENS
 (HUMAN)//P09234
 F-NT2RP2000079//PLATELET FACTOR 4 (PF-4)//0.15:52:30//SUS SCROFA (PIG)//P30034
 F-NT2RP2000088//HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION//1.0:36:44//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53245
 20 F-NT2RP2000091//HYPOTHETICAL PROTEIN HI0149 PRECURSOR//0.22:38:47//HAEMOPHILUS INFLUEN-
 ZAE//P43953
 F-NT2RP2000097//VIRUS ATTACHMENT PROTEIN (O61R)//0.75:33:36//AFRICAN SWINE FEVER VIRUS
 (STRAIN BA71V) (ASFV)//P32510
 F-NT2RP2000098
 25 F-NT2RP2000108//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.4e-09:50:70//HOMO SAPIENS (HUMAN)//
 P39195
 F-NT2RP2000114//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP)//0.024:52:44//HOMO SAPIENS (HU-
 MAN)//P42768
 F-NT2RP2000120//5.8 KD PROTEIN IN HMC OPERON (ORF 4)//0.67:37:32//DESULFOVIBRIO VULGARIS
 (STRAIN HILDENBOROUGH)//P33391
 30 F-NT2RP2000126//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1)//1.5e-23:94:47//HOMO
 SAPIENS (HUMAN)//O14646
 F-NT2RP2000133//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)//5.6e-10:82:39//HOMO SA-
 PIENS (HUMAN)//Q15427
 35 F-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN
 AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN
 ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)//6.7e-89:96:98//MUS MUSCULUS (MOUSE)//P35585
 F-NT2RP2000153//PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISO-
 MERASE) (CYCLOPHILIN) (PPIASE)//1.7e-05:136:33//BRUGIA MALAYI//Q27450
 40 F-NT2RP2000157//MLO2 PROTEIN//2.7e-06:62:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//
 Q09329
 F-NT2RP2000161//DIS3 PROTEIN HOMOLOG//2.7e-33:173:45//CAENORHABDITIS ELEGANS//Q17632
 F-NT2RP2000173//HYPOTHETICAL 10.5 KD PROTEIN IN SODA-COMGA INTERGENIC REGION//0.99:62:25//
 BACILLUS SUBTILIS//P54499
 45 F-NT2RP2000175//MALE SPECIFIC SPERM PROTEIN MST84DB//0.19:41:43//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01643
 F-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN
 NSP60)//4.1e-19:114:44//BOS TAURUS (BOVINE)//O02675
 F-NT2RP2000195//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.99:30:33//MICROTUS PENNSYLVANI-
 CUS (MEADOW VOLE)//P24949
 50 F-NT2RP2000205//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR (PERI-
 PLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN)//0.098:88:25//SH-
 EWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS)//Q54463
 F-NT2RP2000208//MALE SPECIFIC SPERM PROTEIN MST84DD//0.020:19:57//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01645
 55 F-NT2RP2000224//PUTATIVE CUTICLE COLLAGEN C09G5.4//0.0058:159:32//CAENORHABDITIS ELE-
 GANS//Q09455
 F-NT2RP2000232//P55-C-FOS PROTO-ONCOGENE PROTEIN (FRAGMENT)//1.0:44:38//OVIS ARIES

(SHEEP)//O02761
 F-NT2RP2000233//GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR)//
 0.34:53:43//CANIS FAMILIARIS (DOG)//P30552
 F-NT2RP2000239//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT)//0.019:
 5 69:33//RATTUS NORVEGICUS (RAT)//P10164
 F-NT2RP2000248//OVOMUCOID (FRAGMENT)//0.88:18:55//POLYPLECTRON EMPHANUM (PALAWAN PEA-
 COCK-PHEASANT)//P52250
 F-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W//6.4e-09:83:37//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST)//P40556
 10 F-NT2RP2000258//MYOSIN II HEAVY CHAIN, NON MUSCLE//0.081:217:28//DICTYOSTELIUM DISCOIDEUM
 (SLIME MOLD)//P08799
 F-NT2RP2000270//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-17:80:57//HOMO SAPIENS (HUMAN)//
 P39188
 F-NT2RP2000274//HYPOTHETICAL 5.8 KD PROTEIN//0.082:22:45//CLOVER YELLOW MOSAIC VIRUS
 15 (CYMV)//P16485
 F-NT2RP2000283//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III//0.39:38:34//
 CAENORHABDITIS ELEGANS//P34535
 F-NT2RP2000288
 F-NT2RP2000289//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION//0.40:38:42//ES-
 20 CHERICHIA COLI//P22847
 F-NT2RP2000297//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1)//2.3e-62:206:47//HO-
 MO SAPIENS (HUMAN)//Q03923
 F-NT2RP2000298//CUTICLE COLLAGEN 12 PRECURSOR//0.55:81:40//CAENORHABDITIS ELEGANS//
 P20630
 25 F-NT2RP2000310//RUBREDOXIN (RD)//0.13:43:41//TREPONEMA PALLIDUM//O83956
 F-NT2RP2000327//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:46:30//GADUS MORHUA (ATLANTIC
 COD)//P15996
 F-NT2RP2000328//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION//2.0e-21:198:
 31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53313
 30 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3)//1.8e-91:155:
 92//BOS TAURUS (BOVINE)//P08760
 F-NT2RP2000337//PROTEIN A54//0.75:48:35//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS
 (STRAIN COPENHAGEN)//P21072
 F-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116//9.7e-13:114:42//
 35 MUS MUSCULUS (MOUSE)//P17564
 F-NT2RP2000369//CALTRIN (CALCIUM TRANSPORT INHIBITOR)//0.98:47:34//MUS MUSCULUS (MOUSE)//
 Q09098
 F-NT2RP2000412//SHORT NEUROTOXIN D PRECURSOR//0.66:57:36//AIPYSURUS LAEVIS (OLIVE SEA
 SNAKE)//P19960
 40 F-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F)//1.0e-27:96:67//HO-
 MO SAPIENS (HUMAN)//P52597
 F-NT2RP2000420//ZINC FINGER PROTEIN 191//0.16:47:38//HOMO SAPIENS (HUMAN)//O14754
 F-NT2RP2000422//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGLU-
 COSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE)//3.6e-19:148:36//
 45 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09687
 F-NT2RP2000438//TUBULIN GAMMA CHAIN//0.86:190:27//RETICULOMYXA FILOSA//P54405
 F-NT2RP2000448//OXYSTEROL-BINDING PROTEIN//3.7e-13:140:42//HOMO SAPIENS (HUMAN)//P22059
 F-NT2RP2000459//NEURONAL PROTEIN 3.1 (P311 PROTEIN)//1.0:45:35//HOMO SAPIENS (HUMAN)//
 Q16612
 50 F-NT2RP2000498//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.062:25:68//HOMO SAPIENS (HUMAN)//
 P39194
 F-NT2RP2000503
 F-NT2RP2000510//TOXIN IV-5//1.0:51:33//TITYUS BAHIENSIS (BRAZILIAN SCORPION)//P56608
 F-NT2RP2000516//SLYX PROTEIN//1.0:52:32//ESCHERICHIA COLI//P30857
 55 F-NT2RP2000523//PHORBOLIN I (FRAGMENTS)//1.4e-06:36:47//HOMO-SAPIENS (HUMAN)//P31941
 F-NT2RP2000603//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-III)//0.93:119:26//TRITICUM
 AESTIVUM (WHEAT)//P04723
 F-NT2RP2000617//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE)//0.056:16:62//OVIS ARIES

EP 1 074 617 A2

(SHEEP), AND CAPRA HIRCUS (GOAT)//P04102
F-NT2RP2000634//NEDD-4 PROTEIN (EC 6.3.2.-) (KIAA0093) (FRAGMENT)//1.8e-05:128:28//HOMO SAPIENS (HUMAN)//P46934
F-NT2RP2000644//HYPOTHETICAL PROTEIN HI1566 PRECURSOR//0.85:48:39//HAEMOPHILUS INFLUENZAE//P44257
5 F-NT2RP2000656//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (NERVE GROWTH FACTOR-INDUCED PROTEIN A) (NGFI-A)//1.0:111:24//RATTUS NORVEGICUS (RAT)//P08154
F-NT2RP2000658//URONATE ISOMERASE (EC 5.3.1.12) (GLUCURONATE ISOMERASE) (URONIC ISOMERASE)//0.49:79:31//ESCHERICHIA COLI//P42607
10 F-NT2RP2000668//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (45 KD MEROZOITE SURFACE ANTIGEN)//0.020:115:30//PLASMODIUM FALCIPARUM (ISOLATE 3D7)//P50498
F-NT2RP2000678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00085:38:68//HOMO SAPIENS (HUMAN)//P39188
F-NT2RP2000704//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-17:55:74//HOMO SAPIENS (HUMAN)//P39188
15 F-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS)//8.9e-47:106:59//TREPONEMA PALLIDUM//O83950
F-NT2RP2000715
F-NT2RP2000731//CONIDIATION-SPECIFIC PROTEIN 10//0.094:31:41//NEUROSPORA CRASSA//P10713
20 F-NT2RP2000758//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00027:31:74//HOMO SAPIENS (HUMAN)//P39188
F-NT2RP2000764//NIFS PROTEIN//2.7e-27:175:47//ANABAENA SP. (STRAIN PCC 7120)//P12623
F-NT2RP2000809//HYPOTHETICAL PROTEIN MG381 HOMOLOG//0.91:85:25//MYCOPLASMA PNEUMONIAE//P75219
25 F-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A)//2.8e-07:133:31//MUS MUSCULUS (MOUSE)//Q99104
F-NT2RP2000814//40S RIBOSOMAL PROTEIN S27A//0.93:44:38//LYCOPERSICON ESCULENTUM (TOMATO), AND SOLANUM TUBEROSUM (POTATO)//P27083
F-NT2RP2000816//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III//3.3e-21:123:39//CAENORHABDITIS ELEGANS//Q03565
30 F-NT2RP2000819//TROPOMYOSIN 5, CYTOSKELETAL TYPE//1.0:71:30//MUS MUSCULUS (MOUSE)//P21107
F-NT2RP2000841//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP)//0.0011:133:26//MUS MUSCULUS (MOUSE)//P27671
35 F-NT2RP2000842//LYSOPHOSPHATIDIC ACID RECEPTOR (EDG-2)//6.4e-13:22:95//HOMO SAPIENS (HUMAN)//Q92633
F-NT2RP2000845//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI)//0.92:24:41//MEDICAGO SCUTELLATA (SNAIL MEDIC)//P80321
F-NT2RP2000863//N-MYC PROTO-ONCOGENE PROTEIN//0.010:148:27//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P24793
40 F-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2//4.0e-100:199:94//HOMO SAPIENS (HUMAN)//O60841
F-NT2RP2000892//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN]//0.43:45:44//MUS MUSCULUS (MOUSE)//P28481
45 F-NT2RP2000931//MATRIN 3//2.8e-46:104:92//RATTUS NORVEGICUS (RAT)//P43244
F-NT2RP2000932//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT)//3.9e-07:113:31//MUS MUSCULUS (MOUSE)//Q05921
F-NT2RP2000938//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)//0.026:59:45//RATTUS NORVEGICUS (RAT)//Q01956
50 F-NT2RP2000943//HYPOTHETICAL PROTEIN KIAA0079 (HA3543)//5.9e-18:161:42//HOMO SAPIENS (HUMAN)//P53992
F-NT2RP2000965//INNER CENTROMERE PROTEIN (INCENP)//0.062:156:25//GALLUS GALLUS (CHICKEN)//P53352
F-NT2RP2000970//EC PROTEIN HOMOLOG//1.0:50:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P93746
55 F-NT2RP2000985//HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION//2.5e-06:53:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36159
F-NT2RP2000987//INSECT TOXIN 4 (INSECT TOXIN AAH IT4)//1.0:32:34//ANDROCTONUS AUSTRALIS HEC-

TOR (SAHARA SCORPION)//P21150
 F-NT2RP2001036//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.2e-33:65:81//HOMO SAPIENS (HUMAN)//
 P39193
 F-NT2RP2001044//HIRUSTASIN//0.97:15:66//HIRUDO MEDICINALIS (MEDICINAL LEECH)//P80302
 5 F-NT2RP2001056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.0e-24:85:65//HOMO SAPIENS (HUMAN)//
 P39194
 F-NT2RP2001065//BOWMAN-BIRK TYPE SEED TRYPSIN AND CHYMOTRYPSIN INHIBITOR (BTCI)//0.41:50:
 32//VIGNA UNGUICULATA (COWPEA)//P17734
 F-NT2RP2001070//PROBABLE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE)
 10 (FPRA PROTEIN)//6.2e-18:64:48//MYXOCOCCUS XANTHUS//P21159
 F-NT2RP2001081//SYNAPTOTAGMIN IV//7.8e-16:94:46//RATTUS NORVEGICUS (RAT)//P50232
 F-NT2RP2001094//METALLOTHIONEIN-I (MT-I)//1.0:24:33//RATTUS NORVEGICUS (RAT)//P02803
 F-NT2RP2001119//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.5e-11:61:63//HOMO SAPIENS (HUMAN)//
 P39195
 15 F-NT2RP2001127//XE169 PROTEIN (SMCX PROTEIN) (FRAGMENTS)//1.0e-47:155:58//MUS MUSCULUS
 (MOUSE)//P41230
 F-NT2RP2001137//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.10:68:39//BOS TAURUS (BOVINE)//
 P25508
 F-NT2RP2001149//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!/1.1e-13:81:59//HOMO SAPIENS (HUMAN)//
 20 P39188
 F-NT2RP2001168//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS)//0.0071:77:33//RATTUS
 NORVEGICUS (RAT)//P20468
 F-NT2RP2001173//CYTOSKELETON-ASSOCIATED PROTEIN CKAPI (TUBULIN FOLDING COFACTOR B)//
 1.0:36:41//HOMO SAPIENS (HUMAN)//Q99426
 25 F-NT2RP2001174//ZINC FINGER PROTEIN 137//7.2e-11:65:43//HOMO SAPIENS (HUMAN)//P52743
 F-NT2RP2001196//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3)//1.0:95:26//CAPRA HIR-
 CUS (GOAT)//Q36346
 F-NT2RP2001218//HYPOTHETICAL 59.2 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION//0.00024:80:
 23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40486
 30 F-NT2RP2001226//RABPHILIN-3A (FRAGMENT)//4.6e-05:121:39//MUS MUSCULUS (MOUSE)//P47708
 F-NT2RP2001233//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//3.2e-61:153:56//HOMO SAPIENS (HU-
 MAN)//P16415
 F-NT2RP2001245//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)//4.9e-05:230:21//HOMO SA-
 PIENS (HUMAN)//Q15431
 35 F-NT2RP2001268//HOMEBOX PROTEIN CEH-32//0.23:159:25//CAENORHABDITIS ELEGANS//Q23175
 F-NT2RP2001277
 F-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG)
 (BRAIN PROTEIN I47) (FRAGMENT)//1.0e-86:131:97//MUS MUSCULUS (MOUSE)//P28663
 F-NT2RP2001295
 40 F-NT2RP2001312//N-ACETYLGUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLU-
 COSAMINE-6-SULFATASE)//0.64:80:33//CAPRA HIRCUS (GOAT)//P50426
 F-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
 TEIN)//1.0e-36:118:65//HOMO SAPIENS (HUMAN)//Q13829
 F-NT2RP2001328//PROBABLE E5 PROTEIN//1.0:46:41//HUMAN PAPILLOMAVIRUS TYPE 33//P06426
 45 F-NT2RP2001347//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.5e-19:66:62//HOMO SAPIENS (HUMAN)//
 P39193
 F-NT2RP2001366//SPERM-SPECIFIC PROTEIN PHI-1//0.66:55:32//MYTILUS EDULIS (BLUE MUSSEL)//
 Q04621
 F-NT2RP2001378//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID) (FRAGMENT)//
 50 0.060:78:33//HOMO SAPIENS (HUMAN)//Q14003
 F-NT2RP2001381//26S PROTEASE REGULATORY SUBUNIT 8 (SUG1 HOMOLOG) (XSUG1)//1.0:167:26//
 XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P46470
 F-NT2RP2001392//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3//0.0080:82:32//OVIS ARIES (SHEEP)//
 P02441
 55 F-NT2RP2001394//POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN//0.024:39:53//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//P39769
 F-NT2RP2001397//G2/MITOTIC-SPECIFIC CYCLIN B2//1.4e-46:125:78//MESOCRICETUS AURATUS (GOLD-
 EN HAMSTER)//P37883

F-NT2RP2001420//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H]//0.00018:113:38//HOMO SAPIENS (HUMAN)//P04280
 F-NT2RP2001423//HYPOTHETICAL 9.4 KD PROTEIN IN GP31-CD INTERGENIC REGION (ORF A)//0.90:23:43//BACTERIOPHAGE T4//P17307
 5 F-NT2RP2001427//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.2e-11:38:68//HOMO SAPIENS (HUMAN)//P39188
 F-NT2RP2001436//DYNEIN LIGHT INTERMEDIATE CHAIN 2, CYTOSOLIC (LIC53/55) (LIC-2)//0.25:124:28//RATTUS NORVEGICUS (RAT)//Q62698
 F-NT2RP2001440//14-3-3 PROTEIN GAMMA (PROTEIN KINASE C INHIBITOR PROTEIN-1) (KCIP-1)//4.8e-62:145:90//RATTUS NORVEGICUS (RAT)//P35214
 10 F-NT2RP2001445
 F-NT2RP2001449//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)//9.5e-118:226:95//BOS TAURUS (BOVINE)//Q10568
 F-NT2RP2001450
 15 F-NT2RP2001467//SHORT NEUROTOXIN 1 (TOXIN V-II-1)//1.0:25:40//BUNGARUS FASCIATUS (BANDED KRAIT)//P10808
 F-NT2RP2001506
 F-NT2RP2001511//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III//0.49:124:29//CAENORHABDITIS ELEGANS//P34681
 20 F-NT2RP2001520//VITAMIN D-DEPENDENT CALCIUM-BINDING PROTEIN, INTESTINAL (CABP) (CALBINDIN D9K)//0.035:71:33//HOMO SAPIENS (HUMAN)//P29377
 F-NT2RP2001526
 F-NT2RP2001536//METALLOTHIONEIN-I (MT-1)//1.0:19:42//COLUMBA LIVIA (DOMESTIC PIGEON)//P15786
 F-NT2RP2001560//CUTICLE COLLAGEN 12 PRECURSOR//0.0018:144:35//CAENORHABDITIS ELEGANS//P20630
 25 F-NT2RP2001569//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.7e-31:102:67//HOMO SAPIENS (HUMAN)//P39194
 F-NT2RP2001576//SMP3 PROTEIN//0.00016:75:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04174
 30 F-NT2RP2001581//TRANSMEMBRANE PROTEIN SEX PRECURSOR//0.040:46:36//HOMO SAPIENS (HUMAN)//P51805
 F-NT2RP2001597//PROBABLE E4 PROTEIN//0.00042:113:34//HUMAN PAPILLOMAVIRUS TYPE 5//P06924
 F-NT2RP2001601
 F-NT2RP2001613//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT)//0.14:59:32//GALLUS GALLUS (CHICKEN)//P19601
 35 F-NT2RP2001628//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.056:140:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323
 F-NT2RP2001634//ALPHA-CATENIN//7.1e-12:152:35//DROSOPHILA MELANOGASTER (FRUIT FLY)//P35220
 40 F-NT2RP2001660//HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION//0.43:119:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40358
 F-NT2RP2001663//ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE)//1.2e-26:126:56//HOMO SAPIENS (HUMAN)//P06733
 45 F-NT2RP2001675//HYPOTHETICAL 107.7 KD PROTEIN IN RPSO 5' REGION (ORF1)//0.25:148:25//CAMPYLOBACTER JEJUNI//Q46089
 F-NT2RP2001677//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT)//0.010:101:31//RATTUS NORVEGICUS (RAT)//P10164
 50 F-NT2RP2001678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.6e-18:83:61//HOMO SAPIENS (HUMAN)//P39188
 F-NT2RP2001699//PROTEIN C14//0.98:51:31//VACCINIA VIRUS (STRAIN COPENHAGEN)//P21045
 F-NT2RP2001720//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 1)//0.16:145:30//PLASMODIUM FALCIPARUM (ISOLATE CAMP / MALAYSIA)//Q99317
 55 F-NT2RP2001721//MALE-SPECIFIC LETHAL-2 PROTEIN//0.00090:48:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//P50534
 F-NT2RP2001740//ANNEXIN VII (SYNEXIN) (FRAGMENT)//0.50:43:25//BOS TAURUS (BOVINE)//P20072
 F-NT2RP2001748//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-

MENT).//0.77:111:28//HOMO SAPIENS (HUMAN)//P10162
 F-NT2RP2001762
 F-NT2RP2001813//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I)//1.0:22:40//PICEA ABIES
 (NORWAY SPRUCE) (PICEA EXCELSA)//O47040
 5 F-NT2RP2001839//SCY1 PROTEIN//6.8e-17:204:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P53009
 F-NT2RP2001861//D15KZ1 PROTEIN (FRAGMENT)//0.31:56:39//MUS MUSCULUS (MOUSE)//O61466
 F-NT2RP2001869//CORNEODESMOSIN (S PROTEIN) (FRAGMENT)//0.97:78:30//SUS SCROFA (PIG)//
 O19084
 10 F-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER
 MOLECULE 1)//3.5e-36:106:66//HOMO SAPIENS (HUMAN)//P55008
 F-NT2RP2001883//CATHEPSIN L (EC 3.4.22.15)//0.95:29:41//OVIS ARIES (SHEEP)//Q10991
 F-NT2RP2001898//TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56)
 (5PTASE) (FRAGMENT)//1.6e-84:185:88//HOMO SAPIENS (HUMAN)//P32019
 15 F-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5//1.1e-17:180:34//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P53946
 F-NT2RP2001907//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2)//0.13:108:27//CANDIDA AL-
 BICANS (YEAST)//P46593
 F-NT2RP2001926//HYPOTHETICAL 7.6 KD PROTEIN YCF33//0.55:57:26//CYANOPHORA PARADOXA//
 20 P48273
 F-NT2RP2001936
 F-NT2RP2001943//HYPOTHETICAL 57.7 KD PROTEIN IN AIP1-CTF13 INTERGENIC REGION//1.8e-13:208:
 22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04305
 F-NT2RP2001946//HYPOTHETICAL 13.0 KD PROTEIN IN ALGR3 3'REGION//0.59:76:28//PSEUDOMONAS
 25 AERUGINOSA//P21485
 F-NT2RP2001947//ZINC FINGER PROTEIN DAN (N03)//0.53:68:29//RATTUS NORVEGICUS (RAT)//Q06880
 F-NT2RP2001969//CHLOROPLAST 30S RIBOSOMAL PROTEIN S18//0.0015:52:34//CHLORELLA VUL-
 GARIS//P56353
 F-NT2RP2001976//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A)//9.5e-07:201:22//MUS MUS-
 30 CULUS (MOUSE)//Q99104
 F-NT2RP2001985//PROLINE-RICH PROTEIN MP-2 PRECURSOR//0.016:90:32//MUS MUSCULUS (MOUSE)//
 P05142
 F-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73//8.0e-14:47:76//RATTUS
 NORVEGICUS (RAT)//Q08469
 35 F-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO)//
 2.9e-30:211:42//GALLUS GALLUS (CHICKEN)//P35331
 F-NT2RP2002032//FLOCCULANT-ACTIVE PROTEINS MO2.1 AND MO2.2//0.23:20:40//MORINGA OLEIFERA
 (HORSE RADISH TREE) (MORINGA PTERYGOSPERMA)//P24303
 F-NT2RP2002033//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.88:27:62//HOMO SAPIENS (HUMAN)//
 40 P39193
 F-NT2RP2002041
 F-NT2RP2002046//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE
 A INTERFERENCE PROTEIN)//1.0:85:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36027
 F-NT2RP2002047
 45 F-NT2RP2002058//DOM34 INTERACTING PROTEIN 2//9.4e-25:165:34//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//Q12220
 F-NT2RP2002066//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1)//5.7e-12:108:41//HOMO
 SAPIENS (HUMAN)//Q07157
 F-NT2RP2002070//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT)//0.88:28:50//AS-
 50 TERINA PECTINIFERA (STARFISH)//P11958
 F-NT2RP2002076//TRP-ASP REPEATS CONTAINING PROTEIN RBA-2//0.0031:124:27//CAENORHABDITIS
 ELEGANS//P90916
 F-NT2RP2002078//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR//0.82:30:40//OVIS ARIES (SHEEP)//
 Q02958
 55 F-NT2RP2002079//OUTER DENSE FIBER PROTEIN//0.34:41:39//HOMO SAPIENS (HUMAN)//Q14990
 F-NT2RP2002099//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U)//5.2e-08:81:48//HO-
 MO SAPIENS (HUMAN)//Q00839
 F-NT2RP2002105//COLLAGEN 1(X) CHAIN PRECURSOR//0.0012:100:34//BOS TAURUS (BOVINE)//P23206

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F-NT2RP2002124//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX24) (TRANSCRIPTION FACTOR ETR103) (ZINC FINGER PROTEIN 225) (AT225)//0.74:72:31//HOMO SAPIENS (HUMAN)//P18146
F-NT2RP2002137//NEUROTOXIN B-II//1.0:27:44//CEREBRATULUS LACTEUS (MILKY RIBBON WORM)//P01526
5 F-NT2RP2002154//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN)//0.0029:112:34//MUS MUSCULUS (MOUSE)//P16110
F-NT2RP2002172
F-NT2RP2002185//UBIQUITIN-LIKE PROTEIN DSK2//1.8e-07:87:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48510
10 F-NT2RP2002192
F-NT2RP2002193//CUTICLE COLLAGEN 40//0.0062:70:37//CAENORHABDITIS ELEGANS//P34804
F-NT2RP2002208//PEROXISOME ASSEMBLY PROTEIN PEX10 (PEROXIN-10)//0.00011:45:40//HOMO SAPIENS (HUMAN)//060683
15 F-NT2RP2002219
F-NT2RP2002231//V-TYPE SODIUM ATP SYNTHASE SUBUNIT E (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBUNIT E)//1.0:68:32//ENTEROCOCCUS HIRAE//P43436
F-NT2RP2002235//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5)//0.0022:66:45//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN CVG-2)//P37318
20 F-NT2RP2002252//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT)//0.071:110:31//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414
F-NT2RP2002256//CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE)//3.1e-31:75:84//MUS MUSCULUS (MOUSE)//O55127
F-NT2RP2002259//L-MYC-1 PROTO-ONCOGENE PROTEIN//1.9e-17:41:90//HOMO SAPIENS (HUMAN)//P12524
25 F-NT2RP2002270//HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION//2.1e-27:164:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53930
F-NT2RP2002292//IMMEDIATE-EARLY PROTEIN RSP40//0.018:107:23//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV)//P24827
30 F-NT2RP2002312//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE)//1.4e-52:174:55//HOMO SAPIENS (HUMAN)//Q92903
F-NT2RP2002316//HISTONE H1.C6/H1.C9//1.0:40:40//TRYPANOSOMA CRUZI//P40269
35 F-NT2RP2002325//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN 11A)//2.2e-06:145:26//CANDIDA BOIDINII (YEAST)//Q00316
F-NT2RP2002333//HYPOTHETICAL 39.1 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION (ORF 3)//0.30:86:32//ESCHERICHIA COLI//P23524
F-NT2RP2002373//SYNAPSINS IA AND IB//0.080:145:31//BOS TAURUS (BOVINE)//P17599
40 F-NT2RP2002385//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E; R PROTEIN]//0.021:66:28//MINK CELL FOCUS-FORMING MURINE LEUKEMIA VIRUS (ISOLATE CI-3)//P03388
F-NT2RP2002394
F-NT2RP2002408//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.00030:107:37//BOS TAURUS (BOVINE)//P02453
45 F-NT2RP2002426
F-NT2RP2002439//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)//0.00032:79:32//PLASMODIUM BERGHEI (STRAIN ANKA)//P23093
F-NT2RP2002442//HESA PROTEIN//6.0e-16:163:30//PLECTONEMA BORYANUM//P46037
50 F-NT2RP2002457
F-NT2RP2002464//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I//9.3e-18:165:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10264
F-NT2RP2002475//CYSTEINE-RICH HEART PROTEIN (HCRHP)//0.91:45:35//HOMO SAPIENS (HUMAN)//P50238
55 F-NT2RP2002479//ATP-BINDING CASSETTE TRANSPORTER 7 PRECURSOR (ABC TRANSPORTER 7 PROTEIN)//6.8e-96:186:94//HOMO SAPIENS (HUMAN)//O75027
F-NT2RP2002498//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC//0.65:37:45//PSEUDOMONAS AERUGINOSA//P04139

F-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744)//1.3e-31:124:59//HOMO SAPIENS (HUMAN)//Q02386
 F-NT2RP2002504//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140)//1.2e-123:240:92//RATTUS NORVEGICUS (RAT)//P37199
 5 F-NT2RP2002520//ACIDIC PROLINE-RICH PROTEIN HP43A PRECURSOR//0.94:83:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER)//P06680
 F-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X//4.0e-10:194:23//CAENORHABDITIS ELEGANS//Q11073
 F-NT2RP2002546
 10 F-NT2RP2002549//G2/MITOTIC-SPECIFIC CYCLIN C13-1 (A-LIKE CYCLIN) (FRAGMENT)//0.98:65:30//DAUCUS CAROTA (CARROT)//P25010
 F-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//2.6e-19:60:61//HOMO SAPIENS (HUMAN)//P51523
 F-NT2RP2002595//ANNEXIN VII (SYNEXIN)//1.2e-15:121:49//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q92125
 15 F-NT2RP2002606//PROTEIN TRANSPORT PROTEIN SEC2//0.00034:98:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P17065
 F-NT2RP2002609//HYPOTHETICAL 52.0 KD PROTEIN IN CLB6-SPT6 INTERGENIC REGION//0.00022:79:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53264
 20 F-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-)//6.2e-37:180:44//RATTUS NORVEGICUS (RAT)//Q63009
 F-NT2RP2002621//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT)//0.98:37:35//LEMUR CATTAL (RING-TAILED LEMUR)//Q34879
 F-NT2RP2002643//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5)//0.042:77:32//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10)//P37319
 25 F-NT2RP2002672//PROTEIN Q300//0.0018:41:43//MUS MUSCULUS (MOUSE)//Q02722
 F-NT2RP2002701//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I//3.6e-17:100:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09701
 F-NT2RP2002706//IMMEDIATE-EARLY PROTEIN IE180//0.00027:139:33//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV)//P33479
 30 F-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1//6.9e-09:96:40//MUS MUSCULUS (MOUSE)//P55194
 F-NT2RP2002727//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN)//3.6e-20:160:36//RATTUS NORVEGICUS (RAT)//P49816
 F-NT2RP2002736
 35 F-NT2RP2002740
 F-NT2RP2002741//RHO1 GDP-GTP EXCHANGE PROTEIN 2//2.0e-07:178:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P51862
 F-NT2RP2002750//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.6e-09:43:72//HOMO SAPIENS (HUMAN)//P39191
 40 F-NT2RP2002752//LOW CALCIUM RESPONSE LOCUS PROTEIN T//0.95:33:39//YERSINIA PSEUDOTUBERCULOSIS//Q00932
 F-NT2RP2002753//ENDOGLUCANASE EG-1 PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE)//0.71:78:33//TRICHODERMA LONGIBRACHIATUM//Q12714
 F-NT2RP2002769//50 KD SPICULE MATRIX PROTEIN PRECURSOR//0.44:76:32//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN)//P11994
 45 F-NT2RP2002778
 F-NT2RP2002800//CRAMBIN//0.99:20:50//CRAMBE ABYSSINICA (ABYSSINIAN CRAMBE)//P01542
 F-NT2RP2002839//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT)//0.010:87:31//HOMO SAPIENS (HUMAN)//P02812
 50 F-NT2RP2002857//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33)//0.00018:57:45//RATTUS NORVEGICUS (RAT)//P04474
 F-NT2RP2002862//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION//7.2e-27:140:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P33201
 F-NT2RP2002880//DNA REPAIR PROTEIN RAD32//0.83:67:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09683
 55 F-NT2RP2002891//HOMEBOX PROTEIN DLX-2 (DLX-5) (FRAGMENT)//0.99:70:24//RATTUS NORVEGICUS (RAT)//Q64204
 F-NT2RP2002925//ALPHA-1D ADRENERGIC RECEPTOR (ALPHA 1D-ADRENOCEPTOR) (ALPHA-1A

ADRENERGIC RECEPTOR)//0.31:48:43//HOMO SAPIENS (HUMAN)//P25100
 F-NT2RP2002928//CELL DIVISION CONTROL PROTEIN 40//2.8e-26:142:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40968
 F-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II//2.0e-31:186:35//CAENORHABDITIS ELEGANS//Q18964
 5 F-NT2RP2002939//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYL CYCLASE)//0.0022:98:39//CANIS FAMILIARIS (DOG)//P30803
 F-NT2RP2002954//U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A')//0.0019:107:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P43333
 10 F-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17-KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2)//2.8e-11:33:81//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P51669
 F-NT2RP2002979
 15 F-NT2RP2002980//30S RIBOSOMAL PROTEIN S10//1.1e-09:98:36//MYCOPLASMA CAPRICOLUM//P10129
 F-NT2RP2002986//RING CANAL PROTEIN (KELCH PROTEIN)//1.1e-19:141:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652
 F-NT2RP2002987//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.3e-07:78:47//HOMO SAPIENS (HUMAN)//P39192
 20 F-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)//8.0e-77:165:85//RATTUS NORVEGICUS (RAT)//O54888
 F-NT2RP2003000//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.8e-19:62:64//HOMO SAPIENS (HUMAN)//P39194
 25 F-NT2RP2003034//HYPOTHETICAL PROTEIN HI1458//1.0:42:35//HAEMOPHILUS INFLUENZAE//P44204
 F-NT2RP2003073//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//0.0051:16:87//HOMO SAPIENS (HUMAN)//P39189
 F-NT2RP2003099
 F-NT2RP2003108//BASIC PROLINE-RICH PEPTIDE IB-1//0.84:47:34//HOMO SAPIENS (HUMAN)//P04281
 30 F-NT2RP2003117
 F-NT2RP2003121//HYPOTHETICAL 96.7 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION//9.0e-08:99:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43572
 F-NT2RP2003125//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)//9.2e-08:134:28//MUS MUSCULUS (MOUSE)//P97303
 35 F-NT2RP2003129
 F-NT2RP2003137//UBIQUITIN//3.4e-06:70:30//NEUROSPORA CRASSA//P13117
 F-NT2RP2003157//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II//7.8e-13:84:40//CAENORHABDITIS ELEGANS//Q09217
 F-NT2RP2003158//26S PROTEASOME REGULATORY SUBUNIT S3 (PROTEASOME SUBUNIT P58)//3.1e-65:155:84//HOMO SAPIENS (HUMAN)//O43242
 40 F-NT2RP2003161//PROLINE-RICH PROTEIN MP-2 PRECURSOR//0.0011:59:42//MUS MUSCULUS (MOUSE)//P05142
 F-NT2RP2003164//ZYXIN//0.0037:85:36//MUS MUSCULUS (MOUSE)//Q62523
 F-NT2RP2003165//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.2e-24:77:64//HOMO SAPIENS (HUMAN)//P39194
 45 F-NT2RP2003177//MALE SPECIFIC SPERM PROTEIN MST84DB//0.55:38:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643
 F-NT2RP2003194//HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III//2.3e-14:87:37//CAENORHABDITIS ELEGANS//P30629
 50 F-NT2RP2003206//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3)//1.0:100:28//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM)//P41306
 F-NT2RP2003228//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21)//9.3e-82:211:81//HOMO SAPIENS (HUMAN)//P33991
 F-NT2RP2003230//SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSITOL/PHOSPHATIDYLCHOLINE TRANSFER PROTEIN) (PI/PC TP)//1.0:51:31//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA)//P53989
 55 F-NT2RP2003237//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//5.1e-44:66:84//HOMO SAPIENS (HUMAN)//P39194

F-NT2RP2003243//M PROTEIN, SEROTYPE 5 PRECURSOR//0.027:204:23//STREPTOCOCCUS PYO-
 GENES.//P02977
 F-NT2RP2003265//BP4A PROTEIN//0.95:35:34//BRASSICA NAPUS (RAPE)//P41505
 F-NT2RP2003272//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT)//5.5e-
 06:78:35//BRASSICA NAPUS (RAPE)//P40603
 5 F-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT
 SUPPRESSOR 1)//1.9e-19:145:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P30771
 F-NT2RP2003280
 F-NT2RP2003286//RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE)
 10 (RNA CYCLASE)//2.1e-32:137:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q08096
 F-NT2RP2003293//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//7.7e-12:175:33//HOMO SA-
 PIENS (HUMAN)//P51522
 F-NT2RP2003295//PTB-ASSOCIATED SPLICING FACTOR (PSF)//0.055:44:45//HOMO SAPIENS (HUMAN)//
 P23246
 15 F-NT2RP2003297
 F-NT2RP2003307//KINESIN LIGHT CHAIN (KLC)//2.0e-18:87:49//RATTUS NORVEGICUS (RAT)//P37285
 F-NT2RP2003308//CROOKED NECK PROTEIN//2.1e-91:244:67//DROSOPHILA MELANOGASTER (FRUIT
 FLY)//P17886
 F-NT2RP2003329//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III//5.8e-57:186:55//
 20 CAENORHABDITIS ELEGANS//P34284
 F-NT2RP2003339//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA)//0.98:11:72//DENDROASPIS POLYLEPIS
 POLYLEPIS (BLACK MAMBA)//P01416
 F-NT2RP2003347//60S RIBOSOMAL PROTEIN L38//0.83:42:33//OSTERTAGIA OSTERTAGI//O61570
 F-NT2RP2003367//SYNERGISTIC-TYPE VENOM PROTEIN C9S3, CHAIN 1//1.0:37:35//DENDROASPIS AN-
 25 GUSTICEPS (EASTERN GREEN MAMBA)//P01408
 F-NT2RP2003391//MRNA TRANSPORT REGULATOR MTR10//3.3e-11:229:24//SACCHAROMYCES CEREVI-
 SIAE (BAKER'S YEAST)//Q99189
 F-NT2RP2003393//PROTOCHLOROPHYLLIDE REDUCTASE CHLB SUBUNIT (EC 1.3.1.33) (NADPH- PROTO-
 CHLOROPHYLLIDE OXIDOREDUCTASE CHLB SUBUNIT) (FRAGMENT)//0.94:29:34//ARAUCARIA HETERO-
 30 PHYLLA//P37843
 F-NT2RP2003394
 F-NT2RP2003401//60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)//0.95:125:28//THERMUS
 AQUATICUS (SUBSP. THERMOPHILUS)//P45746
 F-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//9.8e-78:178:84//RATTUS
 35 NORVEGICUS (RAT)//P38378
 F-NT2RP2003445
 F-NT2RP2003446//HYPOTHETICAL PROTEIN E-115//0.00030:106:33//HUMAN ADENOVIRUS TYPE 2//
 P03290
 F-NT2RP2003456//PHOTOSYSTEM II REACTION CENTRE M PROTEIN//1.0:27:51//MARCHANTIA POLY-
 40 MORPHA (LIVERWORT)//P12168
 F-NT2RP2003466//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE)//6.7e-06:108:
 32//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//Q08871
 F-NT2RP2003480//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6)//7.2e-15:38:
 50//GALLUS GALLUS (CHICKEN)//Q98937
 45 F-NT2RP2003499//5E5 ANTIGEN//0.090:114:32//RATTUS NORVEGICUS (RAT)//Q63003
 F-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR)//2.0e-11:91:43//SUS
 SCROFA (PIG)//P04175
 F-NT2RP2003511//PARAMYOSIN, SHORT FORM (MIMIPARAMYOSIN)//0.0020:108:25//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//P35416
 50 F-NT2RP2003513//PTB-ASSOCIATED SPLICING FACTOR (PSF)//1.2e-05:96:36//HOMO SAPIENS (HU-
 MAN)//P23246
 F-NT2RP2003517//HYPOTHETICAL 12.9 KD PROTEIN CY49.27//0.0059:22:31//MYCOBACTERIUM TUBER-
 CULOSIS//Q10696
 F-NT2RP2003522//HYPOTHETICAL 10.0 KD PROTEIN//1.0:65:30//THERMOPROTEUS TENAX VIRUS 1
 55 (STRAIN KRA1) (TTV1)//P19283
 F-NT2RP2003533//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//8.7e-18:94:54//HOMO SAPIENS (HU-
 MAN)//P08547
 F-NT2RP2003543//SYNAPSINS IA AND IB//0.045:101:35//RATTUS NORVEGICUS (RAT)//P09951

EP 1 074 617 A2

F-NT2RP2003559//ITBA2 PROTEIN (DXS9879E)//0.98:37:37//HOMO SAPIENS (HUMAN)//Q14657
 F-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//6.4e-35:175:44//HOMO SAPIENS (HUMAN)//P19474
 F-NT2RP2003567//HYPOTHETICAL 11.2 KD PROTEIN T18D3.7 IN CHROMOSOME X//0.72:82:34//
 5 CAENORHABDITIS ELEGANS//Q22544
 F-NT2RP2003581//HOMEBOX PROTEIN OTX1//0.90:61:37//MUS MUSCULUS (MOUSE)//P80205
 F-NT2RP2003596//ELONGATION FACTOR P (EF-P)//0.83:61:32//MYCOPLASMA GENITALIUM//P47272
 F-NT2RP2003604//ALPHA-CATENIN//1.5e-11:152:33//DROSOPHILA MELANOGASTER (FRUIT FLY)//P35220
 10 F-NT2RP2003629//PHOSPHOLIPASE A2 ALPHA (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE)//0.97:85:27//CROTALUS ADAMANTEUS (EASTERN DIAMONDBACK RATTLESNAKE)//P00623
 F-NT2RP2003643//ACYLNEURAMINATE CYTIDYLYLTRANSFERASE (EC 2.7.7.43) (CMP-N- ACETYL-NEURAMINIC ACID SYNTHETASE) (CMP-NEUNAC SYNTHETASE) (CMP-SIALIC ACID SYNTHETASE)//3.9e-12:84:40//NEISSERIA MENINGITIDIS//Q57385
 15 F-NT2RP2003668//!!!! ALU-SUBFAMILY SX WARNING ENTRY !!!!!/5.0e-33:74:81//HOMO SAPIENS (HUMAN)//P39195
 F-NT2RP2003687//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.7e-05:40:67//HOMO SAPIENS (HUMAN)//P39188
 F-NT2RP2003691//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.5e-37:56:67//HOMO SAPIENS (HUMAN)//P39194
 20 F-NT2RP2003702//HYPOTHETICAL OXIDOREDUCTASE IN INLA 5'REGION (EC 1.-.-.-) (ORFA)//1.3e-07:98:37//LISTERIA MONOCYTOGENES//P25145
 F-NT2RP2003704//GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (EC 2.3.2.2) (GAMMA-GLUTAMYLTRANSFERASE 5) (GGT-REL)//0.66:23:52//HOMO SAPIENS (HUMAN)//P36269
 25 F-NT2RP2003706//GLUTAMYL AMINOPEPTIDASE (EC 3.4.11.7) (EAP) (AMINOPEPTIDASE A) (APA) (DIFFERENTIATION ANTIGEN GP160)//1.2e-22:187:35//HOMO SAPIENS (HUMAN)//Q07075
 F-NT2RP2003713//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 6 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 6) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 6) (DEUBIQUITINATING ENZYME 6) (PROTO-ONCOGENE TRE-2)//2.7e-06:119:34//HOMO SAPIENS (HUMAN)//P35125
 30 F-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//6.7e-27:68:75//HOMO SAPIENS (HUMAN)//Q05481
 F-NT2RP2003727//HYPOTHETICAL PROTEIN MG007 HOMOLOG//0.64:110:30//MYCOPLASMA PNEUMONIAE//P75105
 F-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2)//1.2e-72:147:90//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P51669
 35 F-NT2RP2003751//EXTRACELLULAR GLOBIN PRECURSOR//0.67:68:30//PSEUDOTERRANOVA DECIPIENS (COD WORM)//P26914
 F-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//1.0e-98:235:82//BOS TAURUS (BOVINE)//P53620
 40 F-NT2RP2003764//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//0.011:69:34//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341
 F-NT2RP2003769//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:33:36//EQUUS CABALLUS (HORSE)//P48663
 45 F-NT2RP2003770//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT)//0.029:35:42//PSEUDOMONAS AERUGINOSA//P23621
 F-NT2RP2003777//HYPOTHETICAL 82 KD AVIRULENCE PROTEIN IN AVRBS3 REGION//0.041:67:34//XANTHOMONAS CAMPESTRIS (PV. VESICATORIA)//P14728
 50 F-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II//4.7e-54:204:47//CAENORHABDITIS ELEGANS//Q09201
 F-NT2RP2003793//PSEUDO-HEVEIN (MINOR HEVEIN)//0.61:30:36//HEVEA BRASILIENSIS (PARA RUBBER TREE)//P80359
 F-NT2RP2003825//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT)//1.0:35:37//CANIS FAMILIARIS (DOG)//P13206
 55 F-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X//2.5e-05:80:38//CAENORHABDITIS ELEGANS//Q11076
 F-NT2RP2003857//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17)//0.54:28:50//ESCHERICHIA CO-

LI//P05834
 F-NT2RP2003859//DROSOCIN PRECURSOR//1.0:37:35//DROSOPHILA MELANOGASTER (FRUIT FLY)//
 P36193
 F-NT2RP2003871
 5 F-NT2RP2003885//CUTICLE PROTEIN 32 (LM-32) (LM-ACP 32) (FRAGMENT)//1.0:28:50//LOCUSTA MIGRA-
 TORIA (MIGRATORY LOCUST)//P11736
 F-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KI-
 NASE 1)//4.8e-110:268:80//MUS MUSCULUS (MOUSE)//P51954
 10 F-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMI-
 NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B)//0.00024:92:31//RATTUS NORVEGICUS (RAT)//
 O09175
 F-NT2RP2003968//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//9.2e-05:101:36//
 XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437
 F-NT2RP2003976//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.7e-21:62:62//HOMO SAPIENS (HUMAN)//
 15 P39188
 F-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8//2.7e-08:165:22//SAC-
 CHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39702
 F-NT2RP2003984//UNC-87 PROTEIN//0.75:71:28//CAENORHABDITIS ELEGANS//P37806
 F-NT2RP2003986//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.3e-19:47:70//HOMO SAPIENS (HUMAN)//
 20 P39193
 F-NT2RP2003988//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.2e-18:80:58//HOMO SAPIENS (HUMAN)//
 P39195
 F-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3)//
 1.0e-52:141:77//HOMO SAPIENS (HUMAN)//P20290
 25 F-NT2RP2004014//MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA (MIP2-ALPHA) (CINC-2-ALPHA)//
 0.99:45:26//RATTUS NORVEGICUS (RAT)//Q10746
 F-NT2RP2004041//SYNAPSINS IA AND IB//0.0022:51:37//BOS TAURUS (BOVINE)//P17599
 F-NT2RP2004042//CRUSTACEAN HYPERGLYCEMIC HORMONE PRECURSOR (CHH) (FRAGMENT)//1.0:49:
 28//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP)//Q26181
 30 F-NT2RP2004066//CALDESMON (CDM)//2.9e-05:175:21//GALLUS GALLUS (CHICKEN)//P12957
 F-NT2RP2004081//CADMIUM-METALLOTHIONEIN (CD-MT)//0.93:59:23//HELIIX POMATIA (ROMAN SNAIL)
 (EDIBLE SNAIL)//P33187
 F-NT2RP2004098//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//4.6e-09:121:30//HO-
 MO SAPIENS (HUMAN)//Q15404
 35 F-NT2RP2004124//NONHISTONE CHROMOSOMAL PROTEIN HMG-17//0.068:63:31//GALLUS GALLUS
 (CHICKEN)//P02314
 F-NT2RP2004142//HYPOTHETICAL 59.1 KD PROTEIN IN VPS15-YMC2 INTERGENIC REGION//7.9e-05:94:
 28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38262
 F-NT2RP2004152//LAMIN L(I)//0.25:167:19//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P09010
 40 F-NT2RP2004165//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//0.0014:124:
 31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214
 F-NT2RP2004170//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.012:125:30//MUS MUSCULUS
 (MOUSE)//P05143
 F-NT2RP2004172//HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC REGION//4.1e-26:214:
 45 35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36051
 F-NT2RP2004187//ZINC FINGER PROTEIN 174//3.7e-12:76:47//HOMO SAPIENS (HUMAN)//Q15697
 F-NT2RP2004194//HYPOTHETICAL 10.5 KD PROTEIN C31A2.13C IN CHROMOSOME I//0.0013:92:23//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09730
 F-NT2RP2004196//METALLOTHIONEIN 10-II (MT-10-II)//0.92:36:36//MYTILUS EDULIS (BLUE MUSSEL)//
 50 P80247
 F-NT2RP2004207//MALE ACCESSORY GLAND SECRETORY PROTEIN 355A PRECURSOR//0.92:62:35//
 DROSOPHILA SIMULANS (FRUIT FLY)//P33737
 F-NT2RP2004226//66 KD STRESS PROTEIN (P66)//0.030:113:26//PHYSARUM POLYCEPHALUM (SLIME
 MOLD)//P90587
 55 F-NT2RP2004232//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU)//2.0e-48:211:51//HOMO SAPIENS
 (HUMAN)//Q15139
 F-NT2RP2004239//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR//0.00038:111:
 36//TRITICUM AESTIVUM (WHEAT)//P08489

EP 1 074 617 A2

F-NT2RP2004240//METALLOTHIONEIN-II (MT-II) (METALLOTHIONEIN-LIKE PROTEIN) (MT-CE)//1.0:39:28//
 CAENORHABDITIS ELEGANS//P17512
 F-NT2RP2004242//RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN RGP1)//0.0036:
 64:28//ORYZA SATIVA (RICE)//P25766
 5 F-NT2RP2004245//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:21:42//PONGO PYGMAEUS PYG-
 MAEUS (BORNEAN ORANGUTAN)//P92896
 F-NT2RP2004270//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//0.00023:118:33//NEPHILA CLA-
 VIPES (ORB SPIDER)//P46804
 F-NT2RP2004300//PROBABLE E4 PROTEIN//0.18:77:40//HUMAN PAPILLOMAVIRUS TYPE 8//P06425
 10 F-NT2RP2004316
 F-NT2RP2004321//HYPOTHETICAL 10.8 KD PROTEIN SSR2439//1.0:50:28//SYNECHOCYSTIS SP. (STRAIN
 PCC 6803)//Q01904
 F-NT2RP2004339//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.0e-33:84:77//HOMO SAPIENS (HUMAN)//
 P39195
 15 F-NT2RP2004347//HYPOTHETICAL 40.9 KD PROTEIN F33H1.3 FROM CHROMOSOME II//0.78:96:30//
 CAENORHABDITIS ELEGANS//Q09556
 F-NT2RP2004364//MINOR OUTER CAPSID PROTEIN (NS26) (NONSTRUCTURAL PROTEIN VP9)//0.059:143:
 30//BOVINE ROTAVIRUS (STRAIN UK)//P04515
 F-NT2RP2004365//EAMZP30-47 PROTEIN (FRAGMENT)//0.27:38:39//EIMERIA ACERVULINA//P21959
 20 F-NT2RP2004366//GLYCOPROTEIN L PRECURSOR//0.64:71:28//MAREK'S DISEASE HERPESVIRUS
 (STRAIN GA) (MDHV)//P52510
 F-NT2RP2004373//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCO-
 PROTEIN) (HPRG) (FRAGMENT)//0.59:50:40//ORYCTOLAGUS CUNICULUS (RABBIT)//Q28640
 F-NT2RP2004389//HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III//4.0e-16:89:43//
 25 CAENORHABDITIS ELEGANS//P34388
 F-NT2RP2004392
 F-NT2RP2004396//SINGLE-STRANDED NUCLEIC ACID-BINDING PROTEIN//0.42:89:29//SACCHAROMY-
 CES CEREVISIAE (BAKER'S YEAST)//P10080
 F-NT2RP2004399//SOMATOTROPIN PRECURSOR (GROWTH HORMONE)//1.0:72:34//MESOCRICETUS AU-
 30 RATUS (GOLDEN HAMSTER)//P37886
 F-NT2RP2004400
 F-NT2RP2004412//SPERM PROTAMINE P1//0.24:38:31//NOTORYCTES TYPHLOPS (MARSUPIAL MOLE)//
 P42143
 F-NT2RP2004425//SUPPRESSOR PROTEIN SRP40//0.0087:197:22//SACCHAROMYCES CEREVISIAE (BAK-
 35 ER'S YEAST)//P32583
 F-NT2RP2004463//ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)//
 1.3e-05:121:37//MUS MUSCULUS (MOUSE)//Q01338
 F-NT2RP2004476//NICKEL-SENSITIVE T-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT (RBE-II)//0.20:68:
 36//RATTUS NORVEGICUS (RAT)//Q07652
 40 F-NT2RP2004490//FOS-RELATED ANTIGEN 1//0.94:59:33//HOMO SAPIENS (HUMAN)//P15407
 F-NT2RP2004512//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENTS)//1.0:37:
 32//PISASTER OCHRACEUS (SEA STAR)//P24998
 F-NT2RP2004523//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-15:57:71//HOMO SAPIENS (HUMAN)//
 P39194
 45 F-NT2RP2004538//KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES)//
 1.2e-48:121:60//HOMO SAPIENS (HUMAN)//Q12756
 F-NT2RP2004551//HYPOTHETICAL 7.6 KD PROTEIN (ORF 65)//1.0:20:50//EUGLENA GRACILIS//P32095
 F-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03//5.2e-07:150:30//SCHIZOSAC-
 CHAROMYCES POMBE (FISSION YEAST)//Q09903
 50 F-NT2RP2004580//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.7e-37:100:78//HOMO SAPIENS (HU-
 MAN)//P39192
 F-NT2RP2004587//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//8.2e-06:
 150:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214
 F-NT2RP2004594//HYPOTHETICAL 45.3 KD PROTEIN C09F5.7 IN CHROMOSOME II//0.84:105:24//
 55 CAENORHABDITIS ELEGANS//Q09458
 F-NT2RP2004600//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS)//0.17:127:29//RAT-
 TUS NORVEGICUS (RAT)//P30009
 F-NT2RP2004602//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-05:50:58//HOMO SAPIENS (HUMAN)//

P39188
 F-NT2RP2004614//HYPOTHETICAL 11.6 KD PROTEIN.//1.0:68:33//VACCINIA VIRUS (STRAIN COPENHA-
 GEN)//P20561
 F-NT2RP2004655//GLYCINE-RICH RNA-BINDING PROTEIN 7.//7.0e-05:70:42//ARABIDOPSIS THALIANA
 5 (MOUSE-EAR CRESS)//Q03250
 F-NT2RP2004664//HYPOTHETICAL 104.0 KD PROTEIN C32A11.03C IN CHROMOSOME I.//0.30:78:38//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10328
 F-NT2RP2004675
 F-NT2RP2004681
 10 F-NT2RP2004689//HYPOTHETICAL 78.3 KD PROTEIN IN RAM2-ATP7 INTERGENIC REGION.//0.021:179:24//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P34243
 F-NT2RP2004709//HYPOTHETICAL PROTEIN MJ0647.//0.90:39:43//METHANOCOCCUS JANNASCHII//
 Q58063
 F-NT2RP2004710//GAR2 PROTEIN.//0.085:60:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//
 15 P41891
 F-NT2RP2004736//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-15:97:49//HOMO SAPIENS (HUMAN)//
 P39188
 F-NT2RP2004743//MALE SPECIFIC SPERM PROTEIN MST87F.//0.43:24:41//DROSOPHILA MELANOGASTER
 (FRUIT FLY)//P08175
 20 F-NT2RP2004767//36.4 KD PROLINE-RICH PROTEIN.//0.0051:88:27//LYCOPERSICON ESCULENTUM (TO-
 MATO)//Q00451
 F-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1)//9.0e-29:
 166:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38692
 F-NT2RP2004775
 25 F-NT2RP2004791//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)
 (LEURS)//7.4e-60:226:53//CAENORHABDITIS ELEGANS//Q09996
 F-NT2RP2004799//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUC-
 CINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.2e-42:133:57//NEOCALLIMASTIX FRONTALIS (RU-
 MEN FUNGUS)//P53587
 30 F-NT2RP2004802//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//0.018:86:32//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST)//P38898
 F-NT2RP2004816//H<BETA>58 PROTEIN.//1.0e-68:145:93//MUS MUSCULUS (MOUSE)//P40336
 F-NT2RP2004841//DSRD PROTEIN.//0.83:33:39//ARCHAEOGLOBUS FULGIDUS//P70742
 F-NT2RP2004861//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3A.//0.0072:41:39//OVIS ARIES
 35 (SHEEP)//P02443
 F-NT2RP2004897//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:41:41//CASUARINA GLAUCA (SWAMP
 OAK)//Q39511
 F-NT2RP2004933//DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1)//8.4e-34:102:67//
 HOMO SAPIENS (HUMAN)//P53355
 40 F-NT2RP2004936//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2).//0.87:36:33//EC-
 TOTHIORHODOSPIRA VACUOLATA//P38524
 F-NT2RP2004959//STEM CELL FACTOR PRECURSOR (SCF) (MAST CELL GROWTH FACTOR) (MGF) (C-KIT
 LIGAND)//1.0:69:28//CANIS FAMILIARIS (DOG)//Q06220
 F-NT2RP2004961//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946)
 45 (FRAGMENT)//2.1e-21:73:58//HOMO SAPIENS (HUMAN)//Q06730
 F-NT2RP2004962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.17:28:57//HOMO SAPIENS (HUMAN)//
 P39189
 F-NT2RP2004967//HYPOTHETICAL 7.3 KD PROTEIN.//0.76:41:31//THERMOPROTEUS TENAX VIRUS 1
 (STRAIN KRA1) (TTV1)//P19301
 50 F-NT2RP2004978//SPERMATID-SPECIFIC PROTEIN T2 [CONTAINS: SPERM PROTAMINE SP2].//0.44:40:45//
 SEPIA OFFICINALIS (COMMON CUTTLEFISH)//P80002
 F-NT2RP2004982
 F-NT2RP2004985//HYPOTHETICAL PROTEIN KIAA0144.//1.2e-51:204:57//HOMO SAPIENS (HUMAN)//
 Q14157
 55 F-NT2RP2004999//LONG NEUROTOXIN 1 (ALPHA-BUNGAROTOXIN) (BGTX).//0.23:73:26//BUNGARUS MUL-
 TICINCTUS (MANY-BANDED KRAIT)//P01378
 F-NT2RP2005000//ATPASE STABILIZING FACTOR 15 KD PROTEIN.//0.12:37:32//SACCHAROMYCES CERE-
 VISIAE (BAKER'S YEAST)//P16965

F-NT2RP2005001//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.90:54:31//HOMO SAPIENS (HUMAN)//P22531
 F-NT2RP2005003//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR//1.6e-30:78:56//MUS MUSCULUS (MOUSE)//P15533
 5 F-NT2RP2005012//NPL1 PROTEIN (SEC63 PROTEIN)//0.00024:94:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P14906
 F-NT2RP2005018//GAG POLYPROTEIN (CORE POLYPROTEIN) [CONTAINS: CORE PROTEINS P19, P10] (FRAGMENT)//1.0:91:28//AVIAN ENDOGENOUS ROUS-ASSOCIATED VIRUS-0 (EV-2) (AVIAN RETROVIRUS RAV-0)//P06937
 10 F-NT2RP2005020
 F-NT2RP2005022//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//4.9e-11:106:35//PODOSPORA ANSERINA//Q00808
 F-NT2RP2005031
 15 F-NT2RP2005037//ANTI-SILENCING PROTEIN 1//2.2e-32:117:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32447
 F-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE)//9.3e-28:187:40//AMBYSTOMA MEXICANUM (AXOLOTL)//O57486
 F-NT2RP2005108//CUTICLE COLLAGEN 2//0.33:62:38//CAENORHABDITIS ELEGANS//P17656
 20 F-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA)//4.0e-54:161:63//CAENORHABDITIS ELEGANS//P34466
 F-NT2RP2005126//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT)//0.23:46:39//PLEUROCHRYYSIS HAPTONEMOFERA//P41552
 F-NT2RP2005139//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.016:43:37//BOS TAURUS (BOVINE)//P25508
 25 F-NT2RP2005140//HYPOTHETICAL 7.4 KD PROTEIN YCF33//0.96:51:39//GUILLARDIA THETA (CRYPTOMONAS PHI)//O78517
 F-NT2RP2005144//TUBBY PROTEIN//5.6e-08:66:45//MUS MUSCULUS (MOUSE)//P50586
 F-NT2RP2005147
 30 F-NT2RP2005159//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR//0.94:57:29//NICOTIANA TABACUM (COMMON TOBACCO), AND SPINACIA OLERACEA (SPINACH)//P12164
 F-NT2RP2005162//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//1.2e-33:139:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38821
 F-NT2RP2005168//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U)//2.8e-33:102:61//HOMO SAPIENS (HUMAN)//Q00839
 35 F-NT2RP2005204//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG)//3.9e-28:141:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q06624
 F-NT2RP2005227
 F-NT2RP2005239//TRNA SPLICING PROTEIN SPL1//2.0e-38:117:64//CANDIDA ALBICANS (YEAST)//P87185
 40 F-NT2RP2005254//OMEGA-AGATOXIN IB (OMEGA-AGA-IB) (FRAGMENT)//0.26:29:48//AGELENOPSIS APERTA (FUNNEL-WEB SPIDER)//P15970
 F-NT2RP2005270//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4)//0.037:82:34//GALLUS GALLUS (CHICKEN)//P17277
 F-NT2RP2005276//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4)//2.0e-59:174:61//RATTUS NORVEGICUS (RAT)//O35547
 45 F-NT2RP2005287//ZINC FINGER PROTEIN 26 (ZINC FINGER PROTEIN KOX20) (FRAGMENT)//1.5e-05:27:70//HOMO SAPIENS (HUMAN)//P17031
 F-NT2RP2005288//PROBABLE RUBREDOXIN HUPI//1.0:42:28//RHIZOBIUM LEGUMINOSARUM (BIOVAR VICIAE)//P28151
 50 F-NT2RP2005289//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.1e-21:75:70//HOMO SAPIENS (HUMAN)//P39193
 F-NT2RP2005293//TRANSLATION INITIATION FACTOR IF-2//0.58:170:24//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI)//P55972
 F-NT2RP2005315//CUTICLE COLLAGEN 7 (FRAGMENT)//0.091:65:38//CAENORHABDITIS ELEGANS//P18832
 55 F-NT2RP2005325//CHROMOGRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN I) (SP-I) [CONTAINS: PANCREASTATIN; WE-14]//9.5e-09:98:39//HOMO SAPIENS (HUMAN)//P10645
 F-NT2RP2005336//HYPOTHETICAL 68.7 KD PROTEIN IN STB1-MCK1 INTERGENIC REGION//0.00011:124:

- 28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P42846
 F-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 4 (EC 3.6.1.38)//4.7e-21:92:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q12675
 F-NT2RP2005354
 5 F-NT2RP2005358//MYOSIN IC HEAVY CHAIN//0.012:91:39//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569
 F-NT2RP2005360//ACROSIN PRECURSOR (EC 3.4.21.10)//0.0022:73:36//ORYCTOLAGUS CUNICULUS (RABBIT)//P48038
 F-NT2RP2005393//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II//0.00085:135:28//
 10 CAENORHABDITIS ELEGANS //Q09202
 F-NT2RP2005407//SQUALENE MONOOXYGENASE (EC 1.14.99.7) (SQUALENE EPOXIDASE) (SE)//0.96:109:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32476
 F-NT2RP2005436//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.0011:54:42//ZEA MAYS (MAIZE)//P14918
 15 F-NT2RP2005441//PROLINE-RICH PROTEIN MP-2 PRECURSOR//0.039:182:29//MUS MUSCULUS (MOUSE)//P05142
 F-NT2RP2005453
 F-NT2RP2005457//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B)//4.0e-10:124:37//BOS TAURUS (BOVINE)//Q02827
 20 F-NT2RP2005464//HYPOTHETICAL 9.5 KD PROTEIN//0.96:42:33//VACCINIA VIRUS (STRAIN COPENHAGEN)//P20553
 F-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2//4.6e-09:92:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38127
 F-NT2RP2005472//HYPOTHETICAL PROTEIN BB0129//0.76:80:32//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)//O51155
 25 F-NT2RP2005476//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0e-31:39:89//HOMO SAPIENS (HUMAN)//P39193
 F-NT2RP2005490//METALLOTHIONEIN-II (MT-II)//0.14:27:33//SCYLLA SERRATA (MUD CRAB)//P02806
 F-NT2RP2005491//DNA-DIRECTED RNA POLYMERASE SUBUNIT I (EC 2.7.7.6)//0.95:45:31//METHANOCOCCUS JANNASCHII//Q58785
 30 F-NT2RP2005495//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION//0.99:68:30//BACTERIOPHAGE T4//Q02407
 F-NT2RP2005496//ZINC FINGER PROTEIN 135//1.4e-54:120:59//HOMO SAPIENS (HUMAN)//P52742
 F-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55)//9.5e-76:146:86//RATTUS NORVEGICUS (RAT)//P36876
 35 F-NT2RP2005501//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP)//0.025:70:40//HOMO SAPIENS (HUMAN)//P17931
 40 F-NT2RP2005509//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//1.0:166:27//GALLUS GALLUS (CHICKEN)//P02457
 F-NT2RP2005520//CHROMOSOME ASSEMBLY PROTEIN XCAP-E//7.9e-45:118:79//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P50533
 45 F-NT2RP2005525//50S RIBOSOMAL PROTEIN L11//1.0:47:27//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)//O51354
 F-NT2RP2005531//PROTEIN-TYROSINE PHOSPHATASE MEG1 (EC 3.1.3.48) (PTPASE-MEG1) (MEG)//9.8e-13:84:45//HOMO SAPIENS (HUMAN)//P29074
 F-NT2RP2005539//RING CANAL PROTEIN (KELCH PROTEIN)//4.9e-10:90:33//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652
 50 F-NT2RP2005540//NUCLEOTIDE BINDING PROTEIN EXPZ//0.36:119:21//BACILLUS SUBTILIS//P39115
 F-NT2RP2005549//HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III//6.0e-39:179:46//CAENORHABDITIS ELEGANS//Q09253
 F-NT2RP2005555
 55 F-NT2RP2005557//HYPOTHETICAL 23.7 KD PROTEIN C13G6.14 IN CHROMOSOME I//4.9e-06:90:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09790
 F-NT2RP2005581
 F-NT2RP2005600//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.014:37:40//HOMO SAPIENS (HUMAN)//

P02811

F-NT2RP2005605//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I) (FRAGMENT)//0.64:26:42//MACACA MULATTA (RHESUS MACAQUE)//P55247

5 F-NT2RP2005620//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION//8.7e-31:138:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47160

F-NT2RP2005622//NEUROTOXIN-LIKE PROTEIN STR1 (ANATOXIN AAH STR1)//0.39:22:40//ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION)//P80950

10 F-NT2RP2005635//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION//5.8e-43:144:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38795

F-NT2RP2005637//VPU PROTEIN (U ORF PROTEIN)//0.91:33:45//CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIV(CPZ)) (CIV)//P17286

F-NT2RP2005640//METALLOTHIONEIN-LIKE PROTEIN LSC54//0.63:41:31//BRASSICA NAPUS (RAPE)//P43402

15 F-NT2RP2005645

F-NT2RP2005651//OCTAMER-BINDING TRANSCRIPTION FACTOR 3A (OCT-3A) (OCT-4)//0.0023:50:42//HOMO SAPIENS (HUMAN)//Q01860

F-NT2RP2005654//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION//6.1e-16:76:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40564

20 F-NT2RP2005669//METALLOTHIONEIN-II (MT-II)//0.76:16:50//SCYLLA SERRATA (MUD CRAB)//P02806

F-NT2RP2005675//PUTATIVE ORAL CANCER SUPPRESSOR (DELETED IN ORAL CANCER-1)//6.5e-26:116:54//MESOCRICETUS AURATUS (GOLDEN HAMSTER)//P49119

F-NT2RP2005683//HYPOTHETICAL PROTEIN HI0275//0.17:50:40//HAEMOPHILUS INFLUENZAE//P43975

25 F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE)//1.3e-16:75:30//PISUM SATIVUM (GARDEN PEA)//Q04708

F-NT2RP2005694//HYPOTHETICAL PROTEIN KIAA0032//9.6e-11:135:34//HOMO SAPIENS (HUMAN)//Q15034

F-NT2RP2005701//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.084:158:32//HOMO SAPIENS (HUMAN)//P10161

30 F-NT2RP2005712//METALLOTHIONEIN-II (MT-II)//0.19:14:50//STENELLA COERULEOALBA (STRIPED DOLPHIN)//P14425

F-NT2RP2005719//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT)//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT)//P02456

35 F-NT2RP2005722//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//7.8e-37:131:62//HOMO SAPIENS (HUMAN)//P16415

F-NT2RP2005723//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.98:23:60//HOMO SAPIENS (HUMAN)//P39192

F-NT2RP2005726//HYPOTHETICAL PROTEIN TP0375//0.98:30:43//TREPONEMA PALLIDUM//O83390

40 F-NT2RP2005732//PERIOD CLOCK PROTEIN (FRAGMENT)//0.41:20:55//DROSOPHILA ROBUSTA (FRUIT FLY)//Q03296

F-NT2RP2005741//SMR1 PROTEIN PRECURSOR (VCS-ALPHA 1)//0.38:58:36//RATTUS NORVEGICUS (RAT)//P13432

F-NT2RP2005748//ZINC FINGER PROTEIN KOX23 (FRAGMENT)//0.026:19:68//HOMO SAPIENS (HUMAN)//P17034

45 F-NT2RP2005752//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR//0.90:101:31//HOMO SAPIENS (HUMAN)//P02461

F-NT2RP2005753//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.50:22:59//HOMO SAPIENS (HUMAN)//P30808

50 F-NT2RP2005763//PUTATIVE ATP-DEPENDENT RNA HELICASE STE13//4.7e-14:108:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09181

F-NT2RP2005767//NONHISTONE CHROMOSOMAL PROTEIN 6B//4.1e-08:65:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P11633

F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE)//1.2e-14:65:61//HOMO SAPIENS (HUMAN)//P32322

55 F-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP)//1.3e-103:199:90//ORYCTOLAGUS CUNICULUS (RABBIT)//P42675

F-NT2RP2005781//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-

3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C]//0.090:73:36//HOMO SAPIENS (HUMAN)//P02810
 F-NT2RP2005784//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN)//3.5e-06:79:37//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)//P08393
 5 F-NT2RP2005804//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//1.8e-07:43:55//OWENIA FUSIFORMIS//P21260
 F-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION//6.3e-14:143:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40004
 10 F-NT2RP2005815//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE)//0.0017:123:37//MYCOBACTERIUM AVIUM//O07401
 F-NT2RP2005835//SHP1 PROTEIN//1.2e-08:135:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P34223
 15 F-NT2RP2005841//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//0.23:28:53//HOMO SAPIENS (HUMAN)//P22532
 F-NT2RP2005853//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION//0.99:33:48//BACTERIOPHAGE T4//P22917
 F-NT2RP2005857//CHROMOSOME ASSEMBLY PROTEIN XCAP-C//8.6e-84:235:66//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P50532
 20 F-NT2RP2005859//MALE SPECIFIC SPERM PROTEIN MST84DB//0.017:60:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643
 F-NT2RP2005868//ATP SYNTHASE B' CHAIN PRECURSOR (EC 3.6.1.34) (SUBUNIT II)//0.28:121:28//SPINACIA OLERACEA (SPINACH)//P31853
 F-NT2RP2005886//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]//0.80:130:28//TETRAHYMENA THERMOPHILA//P40631
 25 F-NT2RP2005890
 F-NT2RP2005901//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.35:18:44//DROSOPHILA YAKUBA (FRUIT FLY)//P03933
 30 F-NT2RP2005908//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.0e-28:61:65//HOMO SAPIENS (HUMAN)//P39194
 F-NT2RP2005933//PERIOD CLOCK PROTEIN (P230) (FRAGMENT)//1.7e-11:85:49//ACETABULARIA MEDITERRANEA (MERMAID'S WINE GLASS)//P12347
 F-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE)//7.2e-59:216:58//BOS TAURUS (BOVINE)//P25500
 35 F-NT2RP2005980//HYPOTHETICAL 11.5 KD PROTEIN IN RSP8A-AST1 INTERGENIC REGION//1.0:49:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38185
 F-NT2RP2006023//DNA REPAIR PROTEIN REC N (RECOMBINATION PROTEIN N) (FRAGMENT)//1.0:40:45//VIBRIO CHOLERAE//P52118
 40 F-NT2RP2006038//HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III//4.0e-11:90:34//CAENORHABDITIS ELEGANS//P34281
 F-NT2RP2006043//LAMININ BETA-1 CHAIN VARIANT (LAMININ BETA-1-2 CHAIN) (FRAGMENT)//0.00067:73:38//GALLUS GALLUS (CHICKEN)//Q01636
 F-NT2RP2006052//METALLOTHIONEIN-I (MT-I)//0.19:31:38//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET)//P02797
 45 F-NT2RP2006069//COLLAGEN ALPHA2(I) CHAIN (FRAGMENTS)//1.0:66:34//RATTUS NORVEGICUS (RAT)//P02466
 F-NT2RP2006071//RESTIN//0.40:156:29//GALLUS GALLUS (CHICKEN)//O42184
 F-NT2RP2006098//HYPOTHETICAL 21.7 KD PROTEIN IN TUP1-ABP1 INTERGENIC REGION//0.99:95:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25651
 50 F-NT2RP2006100//LONG NEUROTOXIN 4 (ALPHA-NEUROTOXIN)//0.94:43:34//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH)//P80156
 F-NT2RP2006103//50S RIBOSOMAL PROTEIN L32//0.40:36:38//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//P73014
 55 F-NT2RP2006106//CUTICLE COLLAGEN 1//0.28:85:29//CAENORHABDITIS ELEGANS//P08124
 F-NT2RP2006141//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I//1.9e-08:57:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09701
 F-NT2RP2006166

F-NT2RP2006184//HYPOTHETICAL 11.2 KD PROTEIN IN CSGC-MDOG INTERGENIC REGION PRECURSOR.//0.95:87:26//ESCHERICHIA COLI.//P75917
 F-NT2RP2006186//MICROTUBULE-ASSOCIATED PROTEIN 2.//0.088:124:33//MUS MUSCULUS (MOUSE).//P20357
 5 F-NT2RP2006196//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.0e-05:49:61//HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP2006200//PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR.//0.0013:205:32//HOMO SAPIENS (HUMAN).//P05997
 F-NT2RP2006219//GONADAL PROTEIN GDL.//3.5e-18:158:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//P22468
 10 F-NT2RP2006237//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEIN).//0.79:103:28//STREPTOCOCCUS PYOGENES.//P30141
 F-NT2RP2006238//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-07:127:39//MUS MUSCULUS (MOUSE).//P05143
 15 F-NT2RP2006258//PROBABLE E5 PROTEIN.//0.78:47:34//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1).//P24834
 F-NT2RP2006261//PENAEIDIN-3A PRECURSOR (P3-A).//0.61:35:40//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81058
 F-NT2RP2006275//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT).//1.2e-28:59:57//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401
 20 F-NT2RP2006312//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN).//1.6e-06:53:35//TETRAHYMENA PYRIFORMIS.//P40625
 F-NT2RP2006320//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.90:24:41//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612
 25 F-NT2RP2006321//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.0051:25:76//HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP2006323//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.84:33:39//HOMO SAPIENS (HUMAN).//P42768
 F-NT2RP2006333//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.56:37:40//CROTALUS DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333
 30 F-NT2RP2006334//SUCCINYL-COA LIGASE [GDP-FORMING], ALPHA-CHAIN 3 PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN 3).//0.00097:46:41//TRICHOMONAS VAGINALIS.//P53401
 F-NT2RP2006365//NONSPECIFIC LIPID-TRANSFER PROTEIN 4.3 PRECURSOR (LTP 4.3).//0.18:75:29//HORDEUM VULGARE (BARLEY).//Q42842
 35 F-NT2RP2006393//OMEGA-CONOTOXIN MVIIC PRECURSOR (FRAGMENT).//0.82:15:66//CONUS MAGUS (MAGUS CONE).//P37300
 F-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEO BOX).//1.4e-08:50:50//MUS MUSCULUS (MOUSE).//Q61658
 F-NT2RP2006441//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:22:54//MIMULUS GUTTATUS (SPOTTED MONKEY FLOWER) (YELLOW MONKEY FLOWER).//P20238
 40 F-NT2RP2006454//SPERM PROTAMINE P1.//0.60:47:36//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311
 F-NT2RP2006456
 F-NT2RP2006464//PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C).//0.91:79:30//SYNECHOCOCCUS SP. (STRAIN PCC 7002) (AGMENELLUM QUADRICLICATUM).//P31087
 45 F-NT2RP2006467//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.15:53:35//CAENORHABDITIS ELEGANS.//Q21184
 F-NT2RP2006472//HYPOTHETICAL 19 KD PROTEIN (ORF 167).//0.33:98:26//MARCHANTIA POLYMORPHA (LIVERWORT).//P12202
 50 F-NT2RP2006534
 F-NT2RP2006554//ANTI-SIGMA F FACTOR ANTAGONIST (STAGE II SPORULATION PROTEIN AA).//0.91:50:34//BACILLUS SPHAERICUS.//O32723
 F-NT2RP2006565//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1 (SCAMP 37).//6.0e-66:93:96//RATTUS NORVEGICUS (RAT).//P56603
 55 F-NT2RP2006571//CYTOCHROME P450 2B10 (EC 1.14.14.1) (CYP1B10) (TESTOSTERONE 16-ALPHA HYDROXYLASE) (P450-16-ALPHA) (CLONE PF3/46).//4.5e-40:138:57//MUS MUSCULUS (MOUSE).//P12791
 F-NT2RP2006573//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.53:46:39//BOS TAURUS (BO-

VINE)//P02318
 F-NT2RP2006598//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.3e-12:44:77//HOMO SAPIENS (HUMAN)//
 P39195
 F-NT2RP3000002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.4e-19:60:63//HOMO SAPIENS (HUMAN)//
 5 P39192
 F-NT2RP3000031//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV//2.1e-39:210:42//
 CAENORHABDITIS ELEGANS//Q20296
 F-NT2RP3000046//POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF//1.4e-25:149:44//
 PSEUDOMONAS PUTIDA//P25755
 10 F-NT2RP3000047//NPL4 PROTEIN//4.7e-48:275:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P33755
 F-NT2RP3000050//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//3.2e-72:232:59//HOMO SA-
 PIENS (HUMAN)//P51522
 F-NT2RP3000055//MALE SPECIFIC SPERM PROTEIN MST84DB//0.26:57:36//DROSOPHILA MELA-
 15 NOGASTER (FRUIT FLY)//Q01643
 F-NT2RP3000068//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION//0.0014:66:
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47170
 F-NT2RP3000072//HYPOTHETICAL 6.7 KD PROTEIN IN NOHA-CSPI INTERGENIC REGION//0.95:49:30//ES-
 CHERICHIA COLI//P77695
 20 F-NT2RP3000080//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.1e-17:64:68//HOMO SAPIENS (HUMAN)//
 P39188
 F-NT2RP3000085//BIOTIN CARBOXYLASE (EC 6.3.4.14) (A SUBUNIT OF ACETYL-COA CARBOXYLASE (EC
 6.4.1.2)) (ACC)//4.4e-43:169:51//BACILLUS SUBTILIS//P49787
 F-NT2RP3000092//CELL DIVISION CONTROL PROTEIN 1//0.00016:103:31//SACCHAROMYCES CEREVI-
 25 SIAE (BAKER'S YEAST)//P40986
 F-NT2RP3000109//ACYL CARRIER PROTEIN HOMOLOG (ACP)//0.76:83:28//MYCOPLASMA GENITALIUM//
 P47529
 F-NT2RP3000134
 F-NT2RP3000142//GAR2 PROTEIN//0.00098:241:20//SCHIZOSACCHAROMYCES POMBE (FISSION
 30 YEAST)//P41891
 F-NT2RP3000149//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.0014:33:36//PONGO PYGMAEUS ABE-
 LII (SUMATRAN ORANGUTAN)//P92694
 F-NT2RP3000186//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.3e-15:36:83//HOMO SAPIENS (HUMAN)//
 P39188
 35 F-NT2RP3000197//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION//0.91:21:52//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST)//P53820
 F-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//0.026:209:27//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//P08640
 40 F-NT2RP3000220//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//1.0:26:42//HOMO
 SAPIENS (HUMAN)//P30808
 F-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN)//2.1e-42:249:39//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q04652
 F-NT2RP3000235//HOMEBOX PROTEIN H40 (FRAGMENT)//0.55:45:40//APIS MELLIFERA (HONEYBEE)//
 45 P15858
 F-NT2RP3000247//HYPOTHETICAL PROTEIN KIAA0218//1.7e-82:123:69//HOMO SAPIENS (HUMAN)//
 Q93075
 F-NT2RP3000251//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN)//1.0:53:
 33//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q05319
 50 F-NT2RP3000252//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUS-
 TER 5'REGION//2.2e-06:96:32//HALOBACTERIUM CUTIRUBRUM//P17103
 F-NT2RP3000255//HISTONE H1.1 (FRAGMENT)//0.95:71:33//BOS TAURUS (BOVINE)//P02253
 F-NT2RP3000267//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182)//0.38:77:
 33//ESCHERICHIA COLI//P09160
 55 F-NT2RP3000299//MYOSIN IC HEAVY CHAIN//1.2e-11:147:34//ACANTHAMOEBA CASTELLANII (AMOEBE)//
 P10569
 F-NT2RP3000312//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//0.64:216:
 29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214

F-NT2RP3000320//TRANSLATION INITIATION FACTOR IF-2.//5.2e-05:184:22//AQUIFEX AEOLICUS//O67825
 F-NT2RP3000324//HYPOTHETICAL PROTEIN HI1036.//0.69:64:35//HAEMOPHILUS INFLUENZAE//P44097
 F-NT2RP3000333//WIR1A PROTEIN.//0.35:51:41//TRITICUM AESTIVUM (WHEAT)//Q01482
 F-NT2RP3000341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.1e-30:57:80//HOMO SAPIENS (HUMAN)//
 5 P39189
 F-NT2RP3000348
 F-NT2RP3000350//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUS-
 TER 5'REGION.//0.0011:77:35//HALOBACTERIUM CUTIRUBRUM//P17103
 F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3)//1.2e-97:222:
 10 84//BOS TAURUS (BOVINE)//P08760
 F-NT2RP3000361//PRE-MRNA SPLICING FACTOR PRP6.//2.2e-08:128:28//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//P19735
 F-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1e-107:206:99//MUS MUSCULUS (MOUSE)//P35293
 F-NT2RP3000393//HOMEBOX PROTEIN HOX-C4 (HOX-3E) (CP19)//0.0023:36:52//HOMO SAPIENS (HU-
 15 MAN)//P09017
 F-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//
 5.5e-27:116:44//MUS MUSCULUS (MOUSE)//O35286
 F-NT2RP3000403//PRE-MRNA PROCESSING PROTEIN PRP40.//0.00044:67:34//SACCHAROMYCES CERE-
 VISIAE (BAKER'S YEAST)//P33203
 20 F-NT2RP3000418//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE
 (EC 2.7.7.49); ENDONUCLEASE]//2.2e-16:228:34//MUS MUSCULUS (MOUSE)//P11369
 F-NT2RP3000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-17:79:55//HOMO SAPIENS (HUMAN)//
 P39188
 F-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//9.8e-10:201:
 25 26//ESCHERICHIA COLI//P37908
 F-NT2RP3000441//PROTEIN-EXPORT MEMBRANE PROTEIN SECG HOMOLOG.//0.91:48:35//MYCOBACTE-
 RIUM LEPRAE//P38388
 F-NT2RP3000449//HOMEBOX PROTEIN HOX-B8 (CHOX-2.4) (FRAGMENT)//1.0:42:33//GALLUS GALLUS
 (CHICKEN)//P23681
 30 F-NT2RP3000451
 F-NT2RP3000456//COLLAGEN ALPHA 1(I) CHAIN
 (FRAGMENTS)//0.00018:178:36//RATTUS NORVEGICUS (RAT)//P02454
 F-NT2RP3000484//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF)//0.098:40:27//BOS
 TAURUS (BOVINE)//P37359
 35 F-NT2RP3000487//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.00037:16:81//VOLVOX CART-
 ERI//P21997
 F-NT2RP3000512
 F-NT2RP3000526//HYPOTHETICAL NIN REGION PROTEIN ORF56.//0.51:37:43//BACTERIOPHAGE LAMB-
 DA//P03769
 40 F-NT2RP3000527//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//1.0e-16:234:30//HOMO SA-
 PIENS (HUMAN)//P51522
 F-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//3.4e-15:192:30//HOMO SA-
 PIENS (HUMAN)//P15151
 F-NT2RP3000542//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT).//0.60:51:39//AS-
 45 TERINA PECTINIFERA (STARFISH)//P11958
 F-NT2RP3000561//HYPOTHETICAL ATP-BINDING PROTEIN MJ0423.//0.79:53:32//METHANOCOCCUS JAN-
 NASCHII//Q57866
 F-NT2RP3000562//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B)//0.99:26:34//
 DROSOPHILA MAURITIANA (FRUIT FLY), AND DROSOPHILA SIMULANS (FRUIT FLY)//O18666
 50 F-NT2RP3000578//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION//1.5e-26:127:
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38755
 F-NT2RP3000582
 F-NT2RP3000584//METALLOTHIONEIN-II (MT-II).//0.28:27:29//MUS MUSCULUS (MOUSE)//P02798
 F-NT2RP3000590//UVS-2 PROTEIN.//4.8e-10:113:33//NEUROSPORA CRASSA//P33288
 55 F-NT2RP3000592//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)
 (TAFII-130) (TAFII130)//0.00087:178:31//HOMO SAPIENS (HUMAN)//O00268
 F-NT2RP3000596//YEMANUCLEIN-ALPHA.//1.8e-05:98:34//DROSOPHILA MELANOGASTER (FRUIT FLY)//
 P25992

F-NT2RP3000599//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//0.00095:90:37//HOMO
 SAPIENS (HUMAN)//Q15428
 F-NT2RP3000603//SE5 ANTIGEN//1.0e-09:181:34//RATTUS NORVEGICUS (RAT)//Q63003
 F-NT2RP3000605//STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULA-
 5 TORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1)//0.00098:76:34//HOMO SAPIENS (HUMAN)//
 P36956
 F-NT2RP3000622//HYPOTHETICAL PROTEIN MG096 HOMOLOG 5 (P02_ORF427)//0.15:52:36//MYCOPLAS-
 MA PNEUMONIAE//P75277
 F-NT2RP3000624//HYPOTHETICAL PROTEIN KIAA0256//5.4e-16:222:31//HOMO SAPIENS (HUMAN)//
 10 Q93073
 F-NT2RP3000628
 F-NT2RP3000632//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10)//2.0e-16:52:63//MUS
 MUSCULUS (MOUSE)//Q61967
 F-NT2RP3000644//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.7e-40:102:79//HOMO SAPIENS (HU-
 15 MAN)//P39194
 F-NT2RP3000661//HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II//6.0e-08:83:36//
 CAENORHABDITIS ELEGANS//Q09441
 F-NT2RP3000665//HOMEBOX PROTEIN PROPHET OF PIT-1 (PROP-1) (PITUITARY SPECIFIC HOMEODO-
 MAIN FACTOR)//0.13:48:35//HOMO SAPIENS (HUMAN)//O75360
 20 F-NT2RP3000685//HYPOTHETICAL 33.5 KD PROTEIN IN CAT1 5'REGION (ORFY)//0.26:202:23//CLOSTRID-
 IUM KLUYVERI//P38943
 F-NT2RP3000690//INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO- HYDRO-
 LASE) (PPASE)//0.99:131:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P00817
 F-NT2RP3000736//HYPOTHETICAL 28.7 KD PROTEIN IN RNR3-ARC15 INTERGENIC REGION//3.5e-27:211:
 25 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40516
 F-NT2RP3000739//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I//6.0e-23:114:42//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10149
 F-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC
 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III)//6.7e-12:85:36//RATTUS NORVEGICUS
 30 (RAT)//P10688
 F-NT2RP3000753//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER
 PROTEIN 1)//0.00011:208:28//CLOSTRIDIUM THERMOCELLUM//Q06852
 F-NT2RP3000759//ADP-RIBOSYLATION FACTOR 6//8.1e-28:141:38//GALLUS GALLUS (CHICKEN)//P26990
 F-NT2RP3000815//CYTOCHROME C-551 (C551) (CYTOCHROME C8)//0.24:45:37//PSEUDOMONAS DENI-
 35 TRIFICANS//P00103
 F-NT2RP3000825//ALPHA-LACTALBUMIN (LACTOSE SYNTHASE B PROTEIN (EC 2.4.1.22))//0.82:51:39//
 MACROPUS RUFOGRISEUS (RED-NECKED WALLABY)//P07458
 F-NT2RP3000826//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.025:79:37//BOS TAURUS (BOVINE)//
 P25508
 40 F-NT2RP3000836//HYPOTHETICAL PROTEIN IN KSGA 3'REGION (ORF L5) (FRAGMENT)//0.85:36:47//MYC-
 OPLASMA CAPRICOLUM//P43040
 F-NT2RP3000841//UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
 (UDPGT) (UGT1*7) (UGT1-07) (UGT1.7) (UGT1A7) (UGTP4) (FRAGMENT)//1.0:70:34//MUS MUSCULUS
 (MOUSE)//Q62452
 45 F-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-)//5.2e-72:247:61//HO-
 MO SAPIENS (HUMAN)//P27448
 F-NT2RP3000847//HYPOTHETICAL PROTEIN KIAA0161//0.037:55:30//HOMO SAPIENS (HUMAN)//P50876
 F-NT2RP3000850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.4e-31:90:75//HOMO SAPIENS (HUMAN)//
 P39194
 50 F-NT2RP3000852//HYDROPHOBIC SEED PROTEIN (HPS)//0.33:23:69//GLYCINE MAX (SOYBEAN)//P24337
 F-NT2RP3000859//IMMEDIATE-EARLY PROTEIN//3.6e-07:189:25//HERPESVIRUS SAIMIRI (STRAIN 11)//
 Q01042
 F-NT2RP3000865
 F-NT2RP3000868//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ISOFORM (FRAGMENT)//1.4e-09:232:28//
 55 GALLUS GALLUS (CHICKEN)//P29616
 F-NT2RP3000869//CUTICLE COLLAGEN 2//4.5e-08:58:46//CAENORHABDITIS ELEGANS//P17656
 F-NT2RP3000875//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2)//0.90:62:37//
 MUS MUSCULUS (MOUSE)//P43241

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F-NT2RP3000901//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.99:124:33//BOS TAURUS (BOVINE)//
 P02453
 F-NT2RP3000904
 F-NT2RP3000917//DHP1 PROTEIN//6.5e-60:229:55//SCHIZOSACCHAROMYCES POMBE (FISSION
 5 YEAST)//P40848
 F-NT2RP3000919//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I//2.4e-19:159:34//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10149
 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//3.7e-48:73:98//HOMO SAPIENS (HUMAN), AND RAT-
 TUS NORVEGICUS (RAT)//P39027
 10 F-NT2RP3000980//COPA/INCA PROTEIN (REPA3 PROTEIN)//0.24:19:47//ESCHERICHIA COLI//P13946
 F-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN//1.4e-10:78:48//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//P25159
 F-NT2RP3001004//HYPOTHETICAL 7.6 KD PROTEIN B0563.8 IN CHROMOSOME X//0.70:50:32//
 CAENORHABDITIS ELEGANS//Q11084
 15 F-NT2RP3001007
 F-NT2RP3001055//N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG//1.3e-05:
 138:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P36416
 F-NT2RP3001057//ZINC FINGER PROTEIN 45 (BRC1744)//4.0e-28:141:51//HOMO SAPIENS (HUMAN)//
 Q02386
 20 F-NT2RP3001081//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III//3.8e-08:144:29//
 CAENORHABDITIS ELEGANS//P34568
 F-NT2RP3001084//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//3.4e-06:217:32//NEPHILA CLA-
 VIPES (ORB SPIDER)//P46804
 F-NT2RP3001096//SYNAPTONEMAL COMPLEX PROTEIN SC65//1.1e-30:244:33//RATTUS NORVEGICUS
 25 (RAT)//Q64375
 F-NT2RP3001107//ARYLSULFATASE F (EC 3.1.6.-) (ASF) (FRAGMENT)//0.041:47:44//HOMO SAPIENS (HU-
 MAN)//P54793
 F-NT2RP3001109
 F-NT2RP3001111//MALE SPECIFIC SPERM PROTEIN MST84DC//0.17:28:39//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01644
 30 F-NT2RP3001113//INVOLUCRIN//0.00036:192:23//MUS MUSCULUS (MOUSE)//P48997
 F-NT2RP3001115
 F-NT2RP3001116//AMINOPEPTIDASE G (EC 3.4.11.-) (FRAGMENT)//0.99:29:51//STREPTOMYCES LIVI-
 DANS//Q54340
 35 F-NT2RP3001119//COLLAGEN ALPHA 4(IV) CHAIN (FRAGMENT)//0.0015:73:39//BOS TAURUS (BOVINE)//
 Q29442
 F-NT2RP3001120//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//1.3e-57:229:52//HOMO SAPIENS (HU-
 MAN)//P16415
 F-NT2RP3001126//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC REGION//2.8e-07:83:
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38888
 40 F-NT2RP3001133//CALCIUM BINDING PROTEIN//2.0e-08:171:32//DICTYOSTELIUM DISCOIDEUM (SLIME
 MOLD)//P35085
 F-NT2RP3001140//F-SPONDIN PRECURSOR//2.0e-147:244:97//RATTUS NORVEGICUS (RAT)//P35446
 F-NT2RP3001147//TROPOMYOSIN 2 (TMII)//0.11:159:23//SCHISTOSOMA MANSONI (BLOOD FLUKE)//
 45 P42638
 F-NT2RP3001150//OCTAPEPTIDE-REPEAT PROTEIN T2//6.2e-09:163:25//MUS MUSCULUS (MOUSE)//
 Q06666
 F-NT2RP3001155//DNA POLYMERASE ALPHA-BINDING PROTEIN (POB1/CTF4 PROTEIN) (CHROMOSOME
 REPLICATION PROTEIN CHL15)//4.1e-05:244:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 50 Q01454
 F-NT2RP3001176//LEUKOSIALIN PRECURSOR (LEUCOCYTE SIALOGLYCOPROTEIN) (SIALOPHORIN)
 (CD43) (LY 48) (B CELL DIFFERENTIATION ANTIGEN LP-3)//0.21:136:26//MUS MUSCULUS (MOUSE)//
 P15702
 F-NT2RP3001214//SAP1 PROTEIN//0.058:133:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 55 P39955
 F-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT)//2.1e-08:137:33//HOMO SA-
 PIENS (HUMAN)//P35663
 F-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-

BUTYROBETAINE HYDROXYLASE) //4.2e-05:131:26//PSEUDOMONAS SP. (STRAIN AK-1) //P80193
 F-NT2RP3001232//HYPOTHETICAL PROTEIN PRECURSOR IN CS5 3'REGION (FRAGMENT) //0.75:57:31//
 ESCHERICHIA COLI //P33792
 F-NT2RP3001236//TRANSFORMING PROTEIN MAF //0.017:136:30//AVIAN MUSCULOAPONEUROTIC FIB-
 5 ROSARCOMA VIRUS AS42 //P23091
 F-NT2RP3001239//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1 (FRAGMENT) //4.2e-55:221:49//
 TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY) //P14400
 F-NT2RP3001245
 F-NT2RP3001253//TROPOMYOSIN 2, MUSCLE THORACIC ISOFORM (TROPOMYOSIN I) //0.0042:142:24//
 10 DROSOPHILA MELANOGASTER (FRUIT FLY) //P09491
 F-NT2RP3001260//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR //0.0011:89:43//HOMO SAPIENS (HU-
 MAN) //P53420
 F-NT2RP3001268//ZINC FINGER PROTEIN 45 (BRC1744) //9.0e-29:194:44//HOMO SAPIENS (HUMAN) //
 Q02386
 15 F-NT2RP3001272//HYPOTHETICAL 75.2 KD PROTEIN C13F4.08C IN CHROMOSOME I //8.2e-17:183:26//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q10199
 F-NT2RP3001274//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOS-
 PHATASE T) (PPT) (FRAGMENT) //1.7e-09:78:39//MUS MUSCULUS (MOUSE) //Q60676
 F-NT2RP3001281//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! //7.7e-08:38:71//HOMO SAPIENS (HUMAN) //
 20 P39188
 F-NT2RP3001297//HYPOTHETICAL PROTEIN KIAA0281 (HA6725) //2.2e-57:159:70//HOMO SAPIENS (HU-
 MAN) //Q92556
 F-NT2RP3001307//SPERM PROTAMINE P1 //0.21:46:39//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLAT-
 YPUS) //P35307
 25 F-NT2RP3001318
 F-NT2RP3001325//ENHANCER OF RUDIMENTARY HOMOLOG //1.0:73:24//BRACHYDANIO RERIO (ZE-
 BRAFISH) (ZEBRA DANIO) //Q98874
 F-NT2RP3001338//ZINC FINGER PROTEIN 29 (ZINC FINGER PROTEIN KOX26) (FRAGMENT) //0.0021:56:
 35//HOMO SAPIENS (HUMAN) //P17037
 30 F-NT2RP3001339//CITRON PROTEIN //3.6e-06:90:33//MUS MUSCULUS (MOUSE) //P49025
 F-NT2RP3001340//HYPOTHETICAL PROTEIN UL61 //7.2e-11:202:34//HUMAN CYTOMEGALOVIRUS
 (STRAIN AD169) //P16818
 F-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PRO-
 TEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN) //7.7e-16:129:33//HOMO SAPIENS (HUMAN) //P53007
 35 F-NT2RP3001356//RAS-RELATED PROTEIN RABA (FRAGMENT) //0.00041:66:28//DICTYOSTELIUM DISCOI-
 DEUM (SLIME MOLD) //P34141
 F-NT2RP3001374
 F-NT2RP3001383//PTB-ASSOCIATED SPLICING FACTOR (PSF) //2.5e-06:190:32//HOMO SAPIENS (HU-
 MAN) //P23246
 40 F-NT2RP3001384//CHORION PROTEIN S15 //0.00079:94:37//DROSOPHILA VIRILIS (FRUIT FLY) //P13424
 F-NT2RP3001392//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN) //1.0:22:45//CAPRINE ARTHRITIS EN-
 CEPHALITIS VIRUS (CAEV) //P31834
 F-NT2RP3001396//HYPOTHETICAL 8.1 KD PROTEIN (ORF4) //1.0:37:32//STRAWBERRY MILD YELLOW
 EDGE-ASSOCIATED VIRUS (SMYEA) //Q00848
 45 F-NT2RP3001398//KRUEPPEL-RELATED ZINC FINGER PROTEIN 2 (HKR2 PROTEIN) (FRAGMENT) //1.9e-
 08:45:37//HOMO SAPIENS (HUMAN) //P10073
 F-NT2RP3001399//SSU72 PROTEIN //7.3e-18:84:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //
 P53538
 F-NT2RP3001407//SCY1 PROTEIN //1.5e-08:143:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //
 50 P53009
 F-NT2RP3001420//HYPOTHETICAL 7.9 KD PROTEIN //0.25:41:26//VACCINIA VIRUS (STRAIN COPENHA-
 GEN) //P20542
 F-NT2RP3001426//DNAJ PROTEIN //7.5e-15:78:43//HAEMOPHILUS INFLUENZAE //P43735
 F-NT2RP3001427//WERNER SYNDROME HELICASE //3.6e-13:159:33//HOMO SAPIENS (HUMAN) //Q14191
 55 F-NT2RP3001428//NUCLEOPROTEIN TPR //1.8e-53:117:99//HOMO SAPIENS (HUMAN) //P12270
 F-NT2RP3001432//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT) //0.96:52:
 21//TARSUS SYRICHTA (TARSIER) //Q36151
 F-NT2RP3001447//HYPOTHETICAL 5.5 KD PROTEIN IN REPLICATION ORIGIN REGION (ORF1) //0.96:45:35//

ESCHERICHIA COLI//P14505
 F-NT2RP3001449//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT)//0.0043:53:43//GALLUS GALLUS (CHICKEN)//P19601
 5 F-NT2RP3001453//MALE SPECIFIC SPERM PROTEIN MST84DB//0.0048:65:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643
 F-NT2RP3001457//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28//0.55:121:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q02767
 F-NT2RP3001459//MYOSIN IC HEAVY CHAIN//0.10:126:34//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569
 10 F-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A//3.0e-14:87:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P11632
 F-NT2RP3001490//METALLOTHIONEIN-LIKE PROTEIN LSC54//1.0:39:35//BRASSICA NAPUS (RAPE)//P43402
 F-NT2RP3001495//UBIQUITIN--PROTEIN LIGASE RSP5 (EC 6.3.2.-)//3.3e-14:148:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39940
 15 F-NT2RP3001497//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.13:44:38//BOS TAURUS (BOVINE)//P25508
 F-NT2RP3001527//SPERM PROTAMINE P1//0.35:29:37//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM)//P35305
 20 F-NT2RP3001529//HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION//3.3e-21:125:37//ESCHERICHIA COLI//P42641
 F-NT2RP3001538//HNF3/FH TRANSCRIPTION FACTOR GENESIS (WINGED HELIX PROTEIN CWH-3)//0.13:53:39//GALLUS GALLUS (CHICKEN)//P79772
 F-NT2RP3001554//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT)//2.3e-48:137:52//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY)//P14401
 25 F-NT2RP3001580//GERM CELL-LESS PROTEIN//8.2e-18:100:42//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01820
 F-NT2RP3001587//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2)//2.0e-47:188:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P52488
 30 F-NT2RP3001589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.4e-41:87:80//HOMO SAPIENS (HUMAN)//P39193
 F-NT2RP3001607//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:49:32//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS)//Q36362
 F-NT2RP3001608//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.0013:177:25//ZEA MAYS (MAIZE)//P14918
 35 F-NT2RP3001621//MALE SPECIFIC SPERM PROTEIN MST84DD//0.84:29:37//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01645
 F-NT2RP3001629//RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1) (FRAGMENTS)//0.91:57:24//CAVIA PORCELLUS (GUINEA PIG)//P80236
 40 F-NT2RP3001634//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.9e-11:73:54//HOMO SAPIENS (HUMAN)//P39189
 F-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210//1.1e-12:117:29//HOMO SAPIENS (HUMAN)//Q92609
 F-NT2RP3001646//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//0.0092:69:34//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341
 45 F-NT2RP3001671//RING CANAL PROTEIN (KELCH PROTEIN)//0.0042:55:41//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652
 F-NT2RP3001672
 F-NT2RP3001676//GTP-BINDING PROTEIN LEPA (FRAGMENT)//1.2e-15:56:62//PSEUDOMONAS FLUORESCENS//P26843
 50 F-NT2RP3001678//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//0.054:187:31//NEPHILA CLAVIPES (ORB SPIDER)//P46804
 F-NT2RP3001679//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III//1.5e-07:63:44//CAENORHABDITIS ELEGANS//P34679
 55 F-NT2RP3001688//GLUCOAMYLASE S1 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) (GAI)//1.0:83:28//SACCHAROMYCES DIASTATICUS (YEAST)//P04065
 F-NT2RP3001690//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM//0.021:247:24//HOMO SA-

PIENS (HUMAN)//P12883
 F-NT2RP3001698
 F-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR//7.7e-12:73:43//DROSOPHILA MEL-
 ANOGASTER (FRUIT FLY)//P54356
 5 F-NT2RP3001712//CEC-1 PROTEIN//1.9e-07:121:29//CAENORHABDITIS ELEGANS//P34618
 F-NT2RP3001716//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR//0.89:54:40//DROSOPHILA SIMULANS
 (FRUIT FLY)//P13729
 F-NT2RP3001724//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1)//7.5e-41:164:48//HO-
 MO SAPIENS (HUMAN)//O14646
 10 F-NT2RP3001727//HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III//1.5e-51:240:41//
 CAENORHABDITIS ELEGANS//P34669
 F-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT)//2.4e-122:267:86//HOMO SAPIENS (HUMAN)//
 Q14141
 F-NT2RP3001739//INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA+)/DICARBOXYLATE
 15 COTRANSPORTER//0.99:63:34//RATTUS NORVEGICUS (RAT)//P70545
 F-NT2RP3001752//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.0e-21:60:85//HOMO SAPIENS (HUMAN)//
 P39193
 F-NT2RP3001753//HYPOTHETICAL PROTEIN KIAA0127//7.9e-12:83:44//HOMO SAPIENS (HUMAN)//
 Q14140
 20 F-NT2RP3001764//DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-
 CIFICITY PROTEIN PHOSPHATASE PYST1)//7.7e-25:146:36//HOMO SAPIENS (HUMAN)//Q16828
 F-NT2RP3001777//SERINE/THREONINE-PROTEIN KINASE STE20 HOMOLOG (EC 2.7.1.-)//0.0096:204:25//
 CANDIDA ALBICANS (YEAST)//Q92212
 F-NT2RP3001782//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.91:34:44//PONGO PYGMAEUS ABELII
 25 (SUMATRAN ORANGUTAN)//P92694
 F-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M)//1.8e-33:159:53//
 HOMO SAPIENS (HUMAN)//P52272
 F-NT2RP3001799//LIGHT-HARVESTING PROTEIN B800/830/1020, ALPHA-2 CHAIN (EHS-ALPHA-2) (ANTEN-
 NA PIGMENT PROTEIN, ALPHA-2 CHAIN)//0.14:46:28//ECTOTHIORHODOSPIRA HALOCHLORIS//P80103
 30 F-NT2RP3001819//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR//0.00030:77:36//HOMO SAPIENS (HU-
 MAN)//P08123
 F-NT2RP3001844//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (FRAGMENT)//0.99:
 43:34//MACROPUS EUGENII (TAMMAR WALLABY)//Q28466
 F-NT2RP3001854//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEIN)//9.3e-10:213:
 35 24//STREPTOCOCCUS PYOGENES//P30141
 F-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1)//2.6e-61:220:60//HO-
 MO SAPIENS (HUMAN)//P55347
 F-NT2RP3001857//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1//1.0e-13:213:24//PODOSPORA AN-
 SERINA//Q00808
 40 F-NT2RP3001896//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//0.074:124:34//HOMO SA-
 PIENS (HUMAN)//Q15428
 F-NT2RP3001898//REGULATORY PROTEIN E2//0.36:131:29//CANINE ORAL PAPILLOMAVIRUS (COPV)//
 Q89420
 F-NT2RP3001915//CHITIN BIOSYNTHESIS PROTEIN CHS5 (CAL3 PROTEIN)//0.0021:237:23//SACCHARO-
 45 MYCES CEREVISIAE (BAKER'S YEAST)//Q12114
 F-NT2RP3001926//HYPOTHETICAL 14.0 KD PROTEIN IN RPL15B-GCR3 INTERGENIC REGION//1.0:63:34//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03880
 F-NT2RP3001929//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-14:35:60//HOMO SAPIENS (HUMAN)//
 P39195
 50 F-NT2RP3001931//HYPOTHETICAL 59.3 KD PROTEIN IN TAP42-ARP9 INTERGENIC REGION//0.86:162:24//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q05040
 F-NT2RP3001938//GLYCOPROTEIN GP50//0.0036:54:40//PSEUDORABIES VIRUS (STRAIN RICE) (PRV)//
 P07645
 F-NT2RP3001943//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X)//1.0:113:27//ES-
 55 CHERICHIA COLI//P23839
 F-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III//4.1e-56:208:47//
 CAENORHABDITIS ELEGANS//Q09251
 F-NT2RP3001969//PUFF II/9-2 PROTEIN PRECURSOR//0.0078:149:26//SCIARA COPROPHILA (FUNGUS

GNAT)//P22312
 F-NT2RP3001989//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE)//1.0:41:31//MUS MUSCULUS (MOUSE)//P02319
 F-NT2RP3002002//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.2e-44:69:79//HOMO SAPIENS (HUMAN)//
 5 P39195
 F-NT2RP3002004//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2)//0.00024:45:40//MUS MUSCULUS (MOUSE)//Q61345
 F-NT2RP3002007//TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C)//0.21:115:28//HOMO SAPIENS (HUMAN)//P24821
 10 F-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III//1.7e-25:139:48//CAENORHABDITIS ELEGANS//Q09232
 F-NT2RP3002033//ACTIVATOR OF APOPTOSIS HAKIRI (NEURONAL DEATH PROTEIN DP5)//0.14:65:41//HOMO SAPIENS (HUMAN)//O00198
 15 F-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT)//8.1e-108:192:98//MUS MUSCULUS (MOUSE)//P17427
 F-NT2RP3002054//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.046:176:31//STREPTOMYCES FRADIAE//P20186
 20 F-NT2RP3002056//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140)//1.4e-07:245:25//RATTUS NORVEGICUS (RAT)//P41777
 F-NT2RP3002057//SMALL HYDROPHOBIC PROTEIN//1.0:12:66//SIMIAN VIRUS 5 (STRAIN W3) (SV5)//P07577
 F-NT2RP3002062//PROTEASE A INHIBITOR 3 (PROTEINASE INHIBITOR I(A)3)//1.0:49:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P01094
 25 F-NT2RP3002063//ACYL CARRIER PROTEIN (ACP)//0.99:38:31//HAEMOPHILUS INFLUENZAE//P43709
 F-NT2RP3002081//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I//5.8e-35:253:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10429
 F-NT2RP3002097//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION//6.2e-06:99:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40164
 30 F-NT2RP3002102//HYPOTHETICAL 7.4 KD PROTEIN//0.68:34:47//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)//P19302
 F-NT2RP3002108//HYPOTHETICAL 105.5 KD PROTEIN R13F6.10 IN CHROMOSOME III//7.9e-19:179:34//CAENORHABDITIS ELEGANS//Q21986
 35 F-NT2RP3002142//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-17:37:75//HOMO SAPIENS (HUMAN)//P39188
 F-NT2RP3002146//CUTICLE COLLAGEN 40//0.00034:90:37//CAENORHABDITIS ELEGANS//P34804
 F-NT2RP3002147//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S)//0.011:166:28//HOMO SAPIENS (HUMAN)//P10163
 40 F-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS)//4.8e-11:60:53//HOMO SAPIENS (HUMAN)//P15170
 F-NT2RP3002163//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TARII130)//0.028:191:29//HOMO SAPIENS (HUMAN)//O00268
 F-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP//2.3e-131:223:91//MUS MUSCULUS (MOUSE)//Q02614
 45 F-NT2RP3002166//D-ALANYL CARRIER PROTEIN (DCP)//1.0:65:33//LACTOBACILLUS CASEI//P55153
 F-NT2RP3002173//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.4e-26:114:62//HOMO SAPIENS (HUMAN)//P39194
 F-NT2RP3002181//MALE SPECIFIC SPERM PROTEIN MST84DD//0.25:31:38//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01645
 50 F-NT2RP3002244//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE)//0.069:16:62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT)//P04102
 F-NT2RP3002248//MICROFIBRILLAR-ASSOCIATED PROTEIN 1 (ASSOCIATED MICROFIBRIL PROTEIN) (AMF)//0.0079:187:24//GALLUS GALLUS (CHICKEN)//P55080
 55 F-NT2RP3002255//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//4.6e-10:168:34//MUS MUSCULUS (MOUSE)//P05143
 F-NT2RP3002273//SCD6 PROTEIN//1.5e-11:160:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P45978

F-NT2RP3002276//PROBABLE E4 PROTEIN./0.91:54:29//HUMAN PAPILLOMAVIRUS TYPE 16//P06922
 F-NT2RP3002303//HYPOTHETICAL 30.2 KD PROTEIN C4D7.04C IN CHROMOSOME I./1.7e-42:191:43//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14171
 F-NT2RP3002304
 5 F-NT2RP3002330//NNP-1 PROTEIN./0.52:140:18//MUS MUSCULUS (MOUSE)//P56183
 F-NT2RP3002343//5E5 ANTIGEN./0.0056:189:30//RATTUS NORVEGICUS (RAT)//Q63003
 F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.15)
 / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) MITOCHONDRIAL PRECURSOR./0.
 1.0e-66:196:68//HOMO SAPIENS (HUMAN)//P13995
 10 F-NT2RP3002352//PRESYNAPTIC PROTEIN SAPI102 (SYNAPSE-ASSOCIATED PROTEIN 102) (NEUROEN-
 DOCRINE-DLG) (NE-DLG)/0.79:173:27//HOMO SAPIENS (HUMAN)//Q92796
 F-NT2RP3002377//PUTATIVE HELICASE YGR271W./1.0e-56:216:44//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//P53327
 F-NT2RP3002399//MINICHROMOSOME MAINTENANCE PROTEIN 6./1.4e-19:136:31//SACCHAROMYCES
 15 CEREVISIAE (BAKER'S YEAST).//P53091
 F-NT2RP3002402//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B)/0.74:107:36//EPSTEIN-BARR VIRUS
 (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204
 F-NT2RP3002455//DNAJ PROTEIN (FRAGMENT)/5.6e-06:57:42//AGROBACTERIUM TUMEFACIENS./0.
 P50018
 20 F-NT2RP3002484//HYPOTHETICAL 46.5 KD PROTEIN C12B10.04 IN CHROMOSOME I./0.00032:52:48//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10438
 F-NT2RP3002501//HYPOTHETICAL 34.9 KD PROTEIN IN FRE2-JEN1 INTERGENIC REGION./9.4e-42:209:
 42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36007
 F-NT2RP3002512//HYPOTHETICAL 37.4 KD PROTEIN IN GPM1-MCR1 INTERGENIC REGION./7.7e-32:162:
 25 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36059
 F-NT2RP3002529//PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C./2.1e-45:
 241:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09805
 F-NT2RP3002545
 F-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III./2.8e-41:161:52//
 30 CAENORHABDITIS ELEGANS//Q10010
 F-NT2RP3002566//IMMEDIATE-EARLY PROTEIN IE180./0.56:130:24//PSEUDORABIES VIRUS (STRAIN KA-
 PLAN) (PRV).//P33479
 F-NT2RP3002587
 F-NT2RP3002590
 35 F-NT2RP3002602//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (THIOREDOXIN-
 RELATED GLYCOPROTEIN 1)/0.00091:111:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17967
 F-NT2RP3002603//HYPOTHETICAL 14.2 KD PROTEIN IN BLAB 3'REGION./1.0:65:40//STREPTOMYCES CA-
 CAO1//P33654
 F-NT2RP3002628//DNAJ-LIKE PROTEIN SLR0093./2.4e-17:101:44//SYNECHOCYSTIS SP. (STRAIN PCC
 6803).//P50027
 40 F-NT2RP3002631//METALLOTHIONEIN-IB (MT-1B)/0.092:36:33//HOMO SAPIENS (HUMAN).//P07438
 F-NT2RP3002650//DUALIN./3.0e-21:184:37//GALLUS GALLUS (CHICKEN).//Q90830
 F-NT2RP3002659//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR/0.00016:223:33//HOMO SAPIENS (HU-
 MAN).//P08123
 45 F-NT2RP3002660//40S RIBOSOMAL PROTEIN S27A./0.16:72:31//CAENORHABDITIS ELEGANS//P37165
 F-NT2RP3002663//OXYSTEROL-BINDING PROTEIN./5.4e-23:168:41//HOMO SAPIENS (HUMAN).//P22059
 F-NT2RP3002671//HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC REGION./6.0e-38:
 203:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53893
 F-NT2RP3002682//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)/0.25:63:31//ARTEMIA
 50 SALINA (BRINE SHRIMP).//P19049
 F-NT2RP3002687//HYPOTHETICAL 30.4 KD PROTEIN IN LEF3-IAP2 INTERGENIC REGION./0.029:60:36//
 AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV).//P41469
 F-NT2RP3002688//KINESIN-LIKE PROTEIN KIF1B./5.3e-61:130:88//MUS MUSCULUS (MOUSE).//Q60575
 F-NT2RP3002701//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)/7.4e-05:109:33//MUS
 55 MUSCULUS (MOUSE).//P15265
 F-NT2RP3002713//PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAH BOX PROTEIN 10)/0.77:
 70:32//HOMO SAPIENS (HUMAN).//Q13206
 F-NT2RP3002763//HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I./6.7e-11:66:40//

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SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14056
 F-NT2RP3002770//COLLAGEN ALPHA 1(IX) CHAIN (FRAGMENT)//0.33:87:34//MUS MUSCULUS (MOUSE)//
 Q05722
 F-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN)//9.7e-36:187:39//DROSOPHILA
 5 MELANOGASTER (FRUIT FLY)//Q24371
 F-NT2RP3002799//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//5.6e-08:41:73//HOMO SAPIENS (HUMAN)//
 P39188
 F-NT2RP3002810//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.0034:35:65//HOMO SAPIENS (HUMAN)//
 P39193
 10 F-NT2RP3002818//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)//3.2e-
 17:148:37//MUS MUSCULUS (MOUSE)//P27790
 F-NT2RP3002861//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION//1.7e-05:95:
 31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P42951
 F-NT2RP3002869//TRYPSIN INHIBITOR II (BDTI-II)//0.97:23:39//BRYONIA DIOICA (RED BRYONY)//P11968
 15 F-NT2RP3002876//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33)//0.00017:140:31//RAT-
 TUS NORVEGICUS (RAT)//P04474
 F-NT2RP3002877//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.5e-06:55:60//HOMO SAPIENS (HUMAN)//
 P39194
 F-NT2RP3002909//P53-BINDING PROTEIN 53BP2 (BCL2-BINDING PROTEIN) (BBP)//4.6e-08:129:38//HOMO
 20 SAPIENS (HUMAN)//Q13625
 F-NT2RP3002911//HYPOTHETICAL PROTEIN C18//0.99:26:50//SWINEPOX VIRUS (STRAIN KASZA) (SPV)//
 P32217
 F-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN)//1.2e-23:113:47//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q04652
 25 F-NT2RP3002953//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN)//0.55:116:
 27//DROSOPHILA MELANOGASTER (FRUIT FLY)//P33450
 F-NT2RP3002955//HYPOTHETICAL 16.5 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION//0.87:67:37//
 BACILLUS SUBTILIS//P54445
 F-NT2RP3002969//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYN-
 30 THETASE 4) (LACS 4)//6.7e-56:189:59//HOMO SAPIENS (HUMAN)//O60488
 F-NT2RP3002972//HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION//0.0028:147:27//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48566
 F-NT2RP3002978//PROBABLE E5 PROTEIN//0.15:55:36//HUMAN PAPILLOMAVIRUS TYPE 51//P26553
 F-NT2RP3002985//METALLOTHIONEIN (MT)//0.0031:49:42//PLEURONECTES PLATESSA (PLAICE)//
 35 P07216
 F-NT2RP3002988//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PRO-
 TEIN)//1.0:111:29//MUS MUSCULUS (MOUSE)//Q01705
 F-NT2RP3003008//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III//0.96:112:25//
 CAENORHABDITIS ELEGANS//P41879
 40 F-NT2RP3003032
 F-NT2RP3003059//HYPOTHETICAL 52.3 KD PROTEIN C56F8.06C IN CHROMOSOME I PRECURSOR//9.7e-
 27:216:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10254
 F-NT2RP3003061//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//3.7e-25:167:34//HOMO
 SAPIENS (HUMAN)//P16157
 45 F-NT2RP3003068//SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE--TRNA LIGASE) (SERRS) (FRAG-
 MENT)//0.074:82:39//SULFOLOBUS SOLFATARICUS//O33780
 F-NT2RP3003071//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP)//0.0085:128:30//HOMO SAPI-
 ENS (HUMAN)//P50552
 F-NT2RP3003078//SPERM ACROSOMAL PROTEIN FSA-ACR.1 PRECURSOR (FRAGMENT)//0.028:165:31//
 50 VULPES VULPES (RED FOX)//P53353
 F-NT2RP3003101//TETRACYCLINE RESISTANCE PROTEIN, CLASS C (TETA(C))//1.0e-14:243:25//ES-
 CHERICHIA COLI//P02981
 F-NT2RP3003121//SUPPRESSOR PROTEIN SRP40//7.4e-05:143:27//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//P32583
 55 F-NT2RP3003133//65 KD YES-ASSOCIATED PROTEIN (YAP65)//0.024:61:42//GALLUS GALLUS (CHICK-
 EN)//P46936
 F-NT2RP3003138//KINESIN-LIKE PROTEIN KIF4//1.1e-118:151:93//MUS MUSCULUS (MOUSE)//P33174
 F-NT2RP3003139//ATP-BINDING CASSETTE TRANSPORTER ABC1//1.0:70:30//SCHIZOSACCHAROMYCES

POMBE (FISSION YEAST)//Q92337
 F-NT2RP3003145//MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (HMFG) (BREAST EPITHE-
 LIAL ANTIGEN BA46) (MFGM)//2.0e-12:121:37//HOMO SAPIENS (HUMAN)//Q08431
 F-NT2RP3003150
 5 F-NT2RP3003157//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//4.0e-79:260:54//HOMO SA-
 PIENS (HUMAN)//P51522
 F-NT2RP3003185//TROPOMYOSIN//0.077:122:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//
 Q02088
 F-NT2RP3003193//ZINC FINGER PROTEIN 135//7.2e-91:239:65//HOMO SAPIENS (HUMAN)//P52742
 10 F-NT2RP3003197//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION//1.3e-07:117:
 34//BACILLUS SUBTILIS//P42966
 F-NT2RP3003203//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I//9.9e-23:132:39//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10149
 F-NT2RP3003204//RAS-LIKE PROTEIN RASB//0.92:103:27//DICTYOSTELIUM DISCOIDEUM (SLIME
 15 MOLD)//P32252
 F-NT2RP3003210//VERY HYPOTHETICAL 13.2 KD PROTEIN IN PTC3-SAS3 INTERGENIC REGION//0.23:
 106:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38190
 F-NT2RP3003212//SUPPRESSOR PROTEIN SRP40//0.019:171:23//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P32583
 20 F-NT2RP3003230//CORONIN-LIKE PROTEIN P57//8.3e-74:183:73//BOS TAURUS (BOVINE)//Q92176
 F-NT2RP3003242//STANNIOCALCIN PRECURSOR//1.4e-21:127:37//HOMO SAPIENS (HUMAN)//P52823
 F-NT2RP3003251//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR//3.1e-51:198:52//MUS
 MUSCULUS (MOUSE)//P15533
 F-NT2RP3003264//E6 PROTEIN//1.0:31:41//HUMAN PAPILLOMAVIRUS TYPE 48//Q80920
 25 F-NT2RP3003278//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION//8.6e-07:80:33//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P38344
 F-NT2RP3003282//DYNAMIN 2 (DYNAMIN UDNM)//8.0e-108:226:88//MUS MUSCULUS (MOUSE)//P39054
 F-NT2RP3003290//BIOH PROTEIN//0.0055:107:30//ESCHERICHIA COLI//P13001
 F-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-)//1.3e-69:
 30 200:55//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//Q64948
 F-NT2RP3003302//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.4e-69:102:66//HOMO SAPIENS (HU-
 MAN)//P08547
 F-NT2RP3003311//MYOSIN II HEAVY CHAIN, NON MUSCLE//0.18:225:26//ACANTHAMOEBA CASTELLANII
 (AMOEBA)//P05659
 35 F-NT2RP3003313//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-
 MENT)//0.0014:142:33//HOMO SAPIENS (HUMAN)//P10162
 F-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
 (RO52)//8.8e-18:94:43//MUS MUSCULUS (MOUSE)//Q62191
 F-NT2RP3003330//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT)//1.3e-20:123:44//HOMO SAPIENS
 40 (HUMAN)//Q14681
 F-NT2RP3003344//HYPOTHETICAL 8.8 KD PROTEIN IN ICDC-MINE INTERGENIC REGION//1.0:28:42//ES-
 CHERICHIA COLI//P75991
 F-NT2RP3003346//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//6.9e-26:74:78//HOMO SAPIENS (HU-
 MAN)//P39191
 45 F-NT2RP3003353//HYPOTHETICAL 52.4 KD PROTEIN R08D7.2 IN CHROMOSOME III//3.7e-10:118:33//
 CAENORHABDITIS ELEGANS//P30641
 F-NT2RP3003377//PUTATIVE CUTICLE COLLAGEN F09G8.6//1.5e-05:102:37//CAENORHABDITIS ELE-
 GANS//P34391
 F-NT2RP3003384
 50 F-NT2RP3003385//SKD3 PROTEIN//5.1e-83:210:69//MUS MUSCULUS (MOUSE)//Q60649
 F-NT2RP3003403
 F-NT2RP3003409//SOX-22 PROTEIN//0.042:173:28//HOMO SAPIENS (HUMAN)//O15370
 F-NT2RP3003411//PROBABLE E3 PROTEIN//0.17:91:31//BOVINE PAPILLOMAVIRUS TYPE 2//P11300
 F-NT2RP3003427//HOLOTRICIN 3 PRECURSOR//0.012:36:41//HOLOTRICHIA DIOMPHALIA//Q25055
 55 F-NT2RP3003433
 F-NT2RP3003464//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//0.0042:110:
 40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214
 F-NT2RP3003490

F-NT2RP3003491//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK 10 KD PRO-
 TEIN)//0.99:49:34//LEPTOSPIRA INTERROGANS//P35472
 F-NT2RP3003500//SCY1 PROTEIN//6.8e-14:192:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P53009
 5 F-NT2RP3003543//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR//0.0026:175:30//HOMO SAPIENS (HU-
 MAN)//P29400
 F-NT2RP3003552//ANNEXIN VII (SYNEXIN) (FRAGMENT)//0.19:21:47//BOS TAURUS (BOVINE)//P20072
 F-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION//7.3e-27:159:
 43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40529
 10 F-NT2RP3003564//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48)//1.0:99:30//TURNIP YELLOW MOSAIC VI-
 RUS//P10358
 F-NT2RP3003572//PUTATIVE CUTICLE COLLAGEN F09G8.6//0.33:128:32//CAENORHABDITIS ELEGANS//
 P34391
 F-NT2RP3003576//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.1e-28:58:77//HOMO SAPIENS (HUMAN)//
 15 P39195
 F-NT2RP3003589//RAS-RELATED PROTEIN RAB-10//5.4e-54:114:94//CANIS FAMILIARIS (DOG)//P24409
 F-NT2RP3003621//COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF)//
 2.0e-15:89:40//HOMO SAPIENS (HUMAN)//P00748
 F-NT2RP3003625//MALE SPECIFIC SPERM PROTEIN MST84DD//0.99:22:50//DROSOPHILA MELA-
 20 NOGASTER (FRUIT FLY)//Q01645
 F-NT2RP3003656//HOMEODOMAIN PROTEIN OTX3 (ZOTX3)//0.30:111:25//BRACHYDANIO RERIO (ZE-
 BRAFISH) (ZEBRA DANIO)//Q90267
 F-NT2RP3003659//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION//1.1e-20:127:
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38755
 25 F-NT2RP3003665//PENAEIDIN-3C PRECURSOR (P3-C)//0.34:52:34//PENAEUS VANNAMEI (PENOEID
 SHRIMP) (EUROPEAN WHITE SHRIMP)//P81060
 F-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PRO-
 TEIN) (12E7)//8.7e-15:146:42//HOMO SAPIENS (HUMAN)//P14209
 F-NT2RP3003680//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION//4.3e-25:159:
 30 40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43601
 F-NT2RP3003686//NONHISTONE CHROMOSOMAL PROTEIN HMG-17//0.067:63:31//GALLUS GALLUS
 (CHICKEN)//P02314
 F-NT2RP3003701//F-SPONDIN PRECURSOR//1.8e-13:193:27//RATTUS NORVEGICUS (RAT)//P35446
 F-NT2RP3003716//SLIT PROTEIN PRECURSOR//1.3e-12:150:34//DROSOPHILA MELANOGASTER (FRUIT
 35 FLY)//P24014
 F-NT2RP3003726//INSERTION ELEMENT IS136 HYPOTHETICAL 16.9 KD PROTEIN//0.47:109:28//AGRO-
 BACTERIUM TUMEFACIENS//P05680
 F-NT2RP3003746//HYPOTHETICAL 7.7 KD PROTEIN IN FIXX 3'REGION (ORF1)//0.57:34:38//AZORHIZO-
 BIUM CAULINODANS//P26486
 40 F-NT2RP3003795//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-10:40:90//HOMO SAPIENS (HUMAN)//
 P39195
 F-NT2RP3003799//MATING-TYPE PHEROMONE BBP1(3) PRECURSOR//0.75:60:36//SCHIZOPHYLLUM
 COMMUNE (BRACKET FUNGUS)//P78744
 F-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC)//4.2e-
 45 51:72:95//GALLUS GALLUS (CHICKEN)//P00523
 F-NT2RP3003805//HYPOTHETICAL 32.1 KD PROTEIN IN DBP7-GCN3 INTERGENIC REGION//0.00069:160:
 25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36121
 F-NT2RP3003809//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS)//0.028:135:35//GALLUS GALLUS (CHICK-
 EN)//P12105
 50 F-NT2RP3003819//C-HORDEIN (PCP387) (FRAGMENT)//0.0026:90:33//HORDEUM VULGARE (BARLEY)//
 P06472
 F-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP)//5.6e-20:174:31//BOS TAURUS
 (BOVINE)//P02720
 F-NT2RP3003828//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-
 55 INHIBITABLE ADENYLYL CYCLASE)//0.0017:111:38//CANIS FAMILIARIS (DOG)//P30803
 F-NT2RP3003831//ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G)//1.1e-37:187:42//MUS MUSCU-
 LUS (MOUSE)//O08600
 F-NT2RP3003833//HYPOTHETICAL 6.4 KD PROTEIN IN INTE-PIN INTERGENIC REGION//1.0:38:39//ES-

CHERICHIA COLI//P75979
 F-NT2RP3003842
 F-NT2RP3003846//RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB)//
 0.61:54:35//DROSOPHILA MELANOGASTER (FRUIT FLY)//P43125
 5 F-NT2RP3003870//MALE SPECIFIC SPERM PROTEIN MST84DB//0.83:51:37//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01643
 F-NT2RP3003876//PROTEIN TRANSPORT PROTEIN SEC2//0.0017:151:27//SACCHAROMYCES CEREVI-
 SIAE (BAKER'S YEAST)//P17065
 F-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)
 10 (DUGT)//3.3e-23:76:64//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q09332
 F-NT2RP3003918//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPOBREVIN BINDING PROTEIN
 (VAP-33)//5.5e-45:127:69//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE)//Q16943
 F-NT2RP3003932
 F-NT2RP3003989//PREPROTEIN TRANSLOCASE SECE SUBUNIT//0.96:46:32//THERMOTOGA MARITIMA//
 15 P35874
 F-NT2RP3003992//NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67)//0.0011:170:26//SAC-
 CHAROMYCES CEREVISIAE (BAKER'S YEAST)//P27476
 F-NT2RP3004013//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAM-
 INASE) (RNA EDITING ENZYME 1)//3.6e-21:134:45//RATTUS NORVEGICUS (RAT)//P51400
 20 F-NT2RP3004016//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//0.00021:64:40//
 AUTOGRAPH CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41479
 F-NT2RP3004041//SPERM PROTAMINE P1//0.0028:43:46//ORNITHORHYNCHUS ANATINUS (DUCKBILL
 PLATYPUS)//P35307
 F-NT2RP3004051//MICROBIAL COLLAGENASE PRECURSOR (EC 3.4.24.3) (120 KD COLLAGENASE)//
 25 0.0079:194:24//CLOSTRIDIUM PERFRINGENS//P43153
 F-NT2RP3004070//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.4e-11:51:72//HOMO SAPIENS (HUMAN)//
 P39188
 F-NT2RP3004078//DNA BINDING PROTEIN RFX2//2.7e-114:243:87//MUS MUSCULUS (MOUSE)//P48379
 F-NT2RP3004093//HYPOTHETICAL 32.3 KD PROTEIN IN RHSE-NAHV INTERGENIC REGION (ORFB)//8.0e-
 13:111:41//ESCHERICHIA COLI//P37757
 30 F-NT2RP3004095//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-17:72:65//HOMO SAPIENS (HUMAN)//
 P39188
 F-NT2RP3004110//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-10:51:72//HOMO SAPIENS (HUMAN)//
 P39195
 35 F-NT2RP3004125//ZINC FINGER PROTEIN 75//1.1e-28:118:47//HOMO SAPIENS (HUMAN)//P51815
 F-NT2RP3004145//AEROLYSIN REGULATORY PROTEIN//0.012:45:33//AEROMONAS SOBRIA//P09165
 F-NT2RP3004148//METALLOTHIONEIN-I (MT-1)//0.055:18:50//COLUMBA LIVIA (DOMESTIC PIGEON)//
 P15786
 F-NT2RP3004155//UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG//1.7e-82:178:89//RATTUS
 40 NORVEGICUS (RAT)//Q63619
 F-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//1.7e-11:215:24//PODOSPORA AN-
 SERINA//Q00808
 F-NT2RP3004206//CROOKED NECK PROTEIN//3.8e-101:241:73//DROSOPHILA MELANOGASTER (FRUIT
 FLY)//P17886
 45 F-NT2RP3004207//CUTICLE COLLAGEN 12 PRECURSOR//0.13:130:33//CAENORHABDITIS ELEGANS//
 P20630
 F-NT2RP3004209//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-
 RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-
 TOUS NUCLEAR PROTEIN HOMOLOG)//6.5e-16:207:29//HOMO SAPIENS (HUMAN)//Q13107
 50 F-NT2RP3004215//PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT//1.0:69:31//SACCHAROMY-
 CES CEREVISIAE (BAKER'S YEAST)//P35179
 F-NT2RP3004242//HYPOTHETICAL 30.2 KD PROTEIN ZK632.i2 IN CHROMOSOME III//1.1e-64:191:63//
 CAENORHABDITIS ELEGANS//P34657
 F-NT2RP3004246//RING3 PROTEIN (KIAA9001)//0.060:101:28//HOMO SAPIENS (HUMAN)//P25440
 55 F-NT2RP3004253//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//1.1e-07:184:35//BOS TAURUS (BOVINE)//
 P02453
 F-NT2RP3004258//SUPPRESSOR PROTEIN SRP40//4.9e-08:98:39//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P32583

EP 1 074 617 A2

F-NT2RP3004262//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40)//1.6e-63:210:61//HOMO SAPIENS (HUMAN)//P25685
F-NT2RP3004282//HYPOTHETICAL PROTEIN F44G4.1 IN CHROMOSOME II (FRAGMENT)//1.6e-29:177:38//CAENORHABDITIS ELEGANS//P54073
5 F-NT2RP3004332//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT)//0.030:118:36//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414
F-NT2RP3004334
F-NT2RP3004341//ALPHA-INTERNEXIN (ALPHA-INX)//0.91:110:26//MUS MUSCULUS (MOUSE)//P46660
F-NT2RP3004348//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III//0.60:198:24//10 CAENORHABDITIS ELEGANS//P46012
F-NT2RP3004349//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0e-37:60:76//HOMO SAPIENS (HUMAN)//P39193
F-NT2RP3004378//HYPOTHETICAL 18.8 KD PROTEIN IN GNTR-GGT INTERGENIC REGION (O162)//0.0026:76:28//ESCHERICHIA COLI//P46854
15 F-NT2RP3004399//LEUCINE-RICH PRIMARY RESPONSE PROTEIN 1 (FOLLICLE-STIMULATING HORMONE PRIMARY RESPONSE PROTEIN)//4.4e-109:212:96//HOMO SAPIENS (HUMAN)//Q92674
F-NT2RP3004424//JTV-1 PROTEIN//4.5e-18:60:70//HOMO SAPIENS (HUMAN)//Q13155 F-NT2RP3004428//METALLOTHIONEIN-A (MTA)//0.0010:36:47//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN)//P04734
20 F-NT2RP3004451//MYOSIN IC HEAVY CHAIN//0.00072:113:34//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569
F-NT2RP3004454//VERPROLIN//3.3e-07:156:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P37370
F-NT2RP3004466//HYPOTHETICAL PROTEIN F-215//0.0013:125:32//HUMAN ADENOVIRUS TYPE 2//25 P03291
F-NT2RP3004470//HYPOTHETICAL 15.4 KD PROTEIN C16C10.11 IN CHROMOSOME III//1.0:33:51//CAENORHABDITIS ELEGANS//Q09254
F-NT2RP3004472//GERM CELL-LESS PROTEIN//7.3e-33:170:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01820
30 F-NT2RP3004475//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131)//8.4e-54:214:46//HOMO SAPIENS (HUMAN)//P98171
F-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35//3.9e-47:199:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P34110
F-NT2RP3004490//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//0.0013:121:33//35 XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437
F-NT2RP3004498//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSOR//0.066:87:35//BACILLUS SUBTILIS//P50840
F-NT2RP3004503//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-34:102:69//HOMO SAPIENS (HUMAN)//P39194
40 F-NT2RP3004504//SUPPRESSOR PROTEIN SRP40//0.64:93:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583
F-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1)//2.2e-16:90:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40484
F-NT2RP3004527
45 F-NT2RP3004534//S-PHASE ENTRY CYCLIN 6//0.38:148:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32943
F-NT2RP3004539//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IBP-1) (IGF-BINDING PROTEIN 1)//0.38:89:38//RATTUS NORVEGICUS (RAT)//P21743
F-NT2RP3004544//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 2 (CYTADHERENCE ACCESSORY PROTEIN 2)//0.0024:200:24//MYCOPLASMA PNEUMONIAE//P75471
50 F-NT2RP3004566//GASTRULA ZINC FINGER PROTEIN XLCGF17.1 (FRAGMENT)//4.6e-25:126:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P18713
F-NT2RP3004569//ANKYRIN//8.3e-07:150:28//MUS MUSCULUS (MOUSE)//Q02357
F-NT2RP3004572//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150)//1.6e-70:247:54//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24325
55 F-NT2RP3004578//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//1.5e-10:210:26//HOMO SAPIENS (HUMAN)//Q02224
F-NT2RP3004594//P54 PROTEIN PRECURSOR//0.0044:230:24//ENTEROCOCCUS FAECIUM (STREPTO-

COCCUS FAECIUM) //P13692
 F-NT2RP3004617//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR //1.5e-14:113:34//MUS
 MUSCULUS (MOUSE) //P15533
 F-NT2RP3004618//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III //4.5e-08:149:30//
 5 CAENORHABDITIS ELEGANS //P34681
 F-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN) //1.0e-24:75:48//
 DROSOPHILA MELANOGASTER (FRUIT FLY) //P54352
 F-NT2RP3004670//CUTICLE COLLAGEN 21/0.00090:159:29//CAENORHABDITIS ELEGANS //P17656
 F-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64 //4.0e-79:243:62//BOS TAURUS (BOVINE) //P35526
 10 F-NT2RP4000023
 F-NT2RP4000035//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-06:46:67//HOMO SAPIENS (HUMAN) //
 P39194
 F-NT2RP4000049//CALDESMON (CDM) //0.41:63:34//GALLUS GALLUS (CHICKEN) //P12957
 F-NT2RP4000051//DUALIN //2.3e-23:195:37//GALLUS GALLUS (CHICKEN) //Q90830
 15 F-NT2RP4000078//RING CANAL PROTEIN (KELCH PROTEIN) //1.2e-24:182:31//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY) //Q04652
 F-NT2RP4000102//XPAR7 PROTEIN //1.0:54:33//BACILLUS LICHENIFORMIS //Q99166
 F-NT2RP4000109//SLIT PROTEIN PRECURSOR //1.9e-60:230:46//DROSOPHILA MELANOGASTER (FRUIT
 FLY) //P24014
 20 F-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100
 KD SUBUNIT) //1.4e-91:157:100//BOS TAURUS (BOVINE) //Q10568
 F-NT2RP4000129//5E5 ANTIGEN //0.00072:124:37//RATTUS NORVEGICUS (RAT) //Q63003
 F-NT2RP4000147//ZINC FINGER PROTEIN GCS1 //1.5e-26:119:43//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST) //P35197
 25 F-NT2RP4000150
 F-NT2RP4000151//HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III //4.2e-31:180:47//
 CAENORHABDITIS ELEGANS //P32740
 F-NT2RP4000159//SPORE COAT PROTEIN SP96 //0.84:107:28//DICTYOSTELIUM DISCOIDEUM (SLIME
 MOLD) //P14328
 30 F-NT2RP4000167//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19:GCR2 INTERGENIC REGION //2.4e-08:133:
 32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40164
 F-NT2RP4000185//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN) //5.4e-05:143:
 32//HERBES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52) //P28284
 F-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN //1.8e-40:258:35//SACCHAROMYCES CEREVI-
 35 SIAE (BAKER'S YEAST) //P22579
 F-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA) //1.4e-20:104:40//APLYSIA
 CALIFORNICA (CALIFORNIA SEA HARE) //P15287
 F-NT2RP4000214//FERREDOXIN //1.0:19:42//MOORELLA THERMOACETICA (CLOSTRIDIUM THERMOACE-
 TICUM) //P00203
 40 F-NT2RP4000218//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-15:48:60//HOMO SAPIENS (HUMAN) //
 P39188
 F-NT2RP4000243//DUALIN //5.8e-78:192:70//GALLUS GALLUS (CHICKEN) //Q90830
 F-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1) //3.1e-83:207:76//MUS MUSCULUS
 (MOUSE) //Q03173
 45 F-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9) //5.5e-29:153:43//HELIANTHUS ANNUUS
 (COMMON SUNFLOWER) //Q23968
 F-NT2RP4000263//ANNEXIN VII (SYNEXIN) (FRAGMENT) //0.98:42:40//BOS TAURUS (BOVINE) //P20072
 F-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I //3.5e-71:209:66//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //P87115
 50 F-NT2RP4000312//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1) //8.9e-22:166:37//HO-
 MO SAPIENS (HUMAN) //Q15404
 F-NT2RP4000321//VERPROLIN //0.00018:260:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //
 P37370
 F-NT2RP4000323//ANTHOPLEURIN B (TOXIN AP-B) //0.42:15:46//ANTHOPLEURA XANTHOGRAMMICA (GI-
 55 ANT GREEN SEA ANEMONE) //P01531
 F-NT2RP4000355//HYPOTHETICAL 90.9 KD PROTEIN IN GCN20-CMK1 INTERGENIC REGION //0.75:125:29//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P43596
 F-NT2RP4000360//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT) //0.27:92:

33//RATTUS NORVEGICUS (RAT)//P10164
 F-NT2RP4000367//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0.99:52:32//HUMAN AD-
 ENOVIRUS TYPE 41//P23691
 5 F-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1)//4.1e-40:
 163:52//HOMO SAPIENS (HUMAN)//O75570
 F-NT2RP4000376//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP)//4.2e-59:125:80//RATTUS NOR-
 VEGICUS (RAT)//P54319
 F-NT2RP4000381//NEUROFILAMENT TRIPLET H PROTEIN (200-KD NEUROFILAMENT PROTEIN) (NF-H)//
 0.00058:194:30//MUS MUSCULUS (MOUSE)//P19246
 10 F-NT2RP4000398//ZINC FINGER PROTEIN 184 (FRAGMENT)//1.2e-45:153:39//HOMO SAPIENS (HUMAN)//
 Q99676
 F-NT2RP4000415//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR//
 0.00066:201:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47179
 F-NT2RP4000417//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B)//
 15 1.8e-25:196:40//MUS MUSCULUS (MOUSE)//P39098
 F-NT2RP4000424//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.0e-15:72:61//HOMO SAPIENS (HUMAN)//
 P39195
 F-NT2RP4000448//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/7.0e-23:63:82//HOMO SAPIENS (HUMAN)//
 P39192
 20 F-NT2RP4000449//REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2)//1.3e-41:102:45//
 KLUYVEROMYCES LACTIS (YEAST)//P33294
 F-NT2RP4000455//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT)//0.00014:92:30//GALLUS GALLUS
 (CHICKEN)//P19601
 F-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-
 25 RASE 7) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 7) (DEUBIQUITINATING ENZYME 7) (HERPESVI-
 RUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE)//1.0e-29:218:38//HOMO SAPIENS (HUMAN)//Q93009
 F-NT2RP4000480//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN
 ALGR3)//0.049:117:29//PSEUDOMONAS AERUGINOSA//P15276
 F-NT2RP4000481//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III//2.3e-05:152:23//
 30 CAENORHABDITIS ELEGANS//Q09475
 F-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1)//2.3e-48:172:52//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//P40484
 F-NT2RP4000500//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III//1.3e-23:165:35//
 CAENORHABDITIS ELEGANS//P34535
 35 F-NT2RP4000515//PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE PHOS-
 PHODIESTERASE) (FRAGMENT)//1.0:48:37//BOS TAURUS (BOVINE)//P15396
 F-NT2RP4000517//METALLOTHIONEIN-LIKE PROTEIN TYPE 2//1.0:41:36//VICIA FABA (BROAD BEAN)//
 Q41657
 F-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1//1.1e-11:93:36//SACCHAROMYCES CEREVI-
 40 SIAE (BAKER'S YEAST)//P45818
 F-NT2RP4000519//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.68:55:40//BOS TAURUS (BOVINE)//
 P25508
 F-NT2RP4000524//IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B ANTIGEN)//0.37:187:24//STREP-
 TOCOCCUS AGALACTIAE//P27951
 45 F-NT2RP4000528//NPL4 PROTEIN//2.1e-45:305:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P33755
 F-NT2RP4000541//HOMEBOX PROTEIN CHOX-1 (FRAGMENT)//0.23:28:50//GALLUS GALLUS (CHICK-
 EN)//P13544
 F-NT2RP4000556//HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME III//4.3e-14:174:34//
 50 CAENORHABDITIS ELEGANS//Q03574
 F-NT2RP4000560//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III//2.1e-19:155:36//
 CAENORHABDITIS ELEGANS//P34679
 F-NT2RP4000588//HYPOTHETICAL PROTEIN E-115//0.014:64:35//HUMAN ADENOVIRUS TYPE 2//P03290
 F-NT2RP4000614//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35)
 55 (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)//2.7e-27:188:44//GALLUS GALLUS (CHICKEN)//P30352
 F-NT2RP4000638//EARLY NODULIN 55-1 PRECURSOR (N-55-1) (FRAGMENT)//0.55:40:40//GLYCINE MAX
 (SOYBEAN)//Q05544
 F-NT2RP4000648//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.4e-06:31:74//HOMO SAPIENS (HUMAN)//

- P39188
F-NT2RP46000657//HYPOTHETICAL PROTEIN MJ1065//2.5e-40:237:40//METHANOCOCCUS JANNAS-CHII//Q58465
F-NT2RP4000704
- 5 F-NT2RP4000713//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//4.0e-07:134:40//STREPTOMYCES FRADIAE//P20186
F-NT2RP4000724//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//1.1e-62:109:88//HOMO SAPIENS (HUMAN)//P10266
F-NT2RP4000728//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.0033:190:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323
- 10 F-NT2RP4000737//PTB-ASSOCIATED SPLICING FACTOR (PSF)//1.0e-05:114:34//HOMO SAPIENS (HUMAN)//P23246
F-NT2RP4000739//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:20:50//ANAS PLATYRHYNCHOS (DOMESTIC DUCK)//P50655
- 15 F-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION//0.0013:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53915
F-NT2RP4000787//POLLEN SPECIFIC PROTEIN SF3//1.3e-13:79:39//HELIANTHUS ANNUUS (COMMON SUNFLOWER)//P29675
F-NT2RP4000817//SUPPRESSOR PROTEIN SRP40//1.3e-05:255:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583
- 20 F-NT2RP4000833
F-NT2RP4000837//MALE SPECIFIC SPERM PROTEIN MST54DB//0.18:38:44//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643
F-NT2RP4000839//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90)//0.026:38:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38129
- 25 F-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B)//2.8e-64:229:53//RATTUS NORVEGICUS (RAT)//O09175
F-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//3.6e-84:174:54//HOMO SAPIENS (HUMAN)//P16415
- 30 F-NT2RP4000878//MYELOID UPREGULATED PROTEIN//8.2e-88:227:74//MUS MUSCULUS (MOUSE)//O35682
F-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN)//9.1e-55:268:43//HOMO SAPIENS (HUMAN)//P22314
- 35 F-NT2RP4000907//BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB TYROSINE KINASE) (GP145-TRKB) (TRK-B)//5.4e-10:220:25//HOMO SAPIENS (HUMAN)//Q16620
F-NT2RP4000915//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT)//0.46:23:60//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P51407
F-NT2RP4000918//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB//0.00010:148:32//BACILLUS SUBTILIS//P39217
- 40 F-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN)//3.5e-27:220:36//HOMO SAPIENS (HUMAN)//Q06828
F-NT2RP4000927//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6)//0.64:75:37//BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA)//P29128
- 45 F-NT2RP4000928//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE)//3.1e-104:263:66//HOMO SAPIENS (HUMAN)//Q92903
F-NT2RP4000929//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION//0.93:107:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53288
- 50 F-NT2RP4000955//PUTATIVE CUTICLE COLLAGEN F09G8.6//2.0e-05:102:37//CAENORHABDITIS ELE-GANS//P34391
F-NT2RP4000973//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION//2.3e-17:78:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40564
- 55 F-NT2RP4000975//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.0041:142:33//HOMO SAPIENS (HUMAN)//P10162
F-NT2RP4000979//HYPOTHETICAL 14.5 KD PROTEIN//0.77:106:33//VACCINIA VIRUS (STRAIN COPENHAGEN)//P20517

F-NT2RP4000984//HYPOTHETICAL 124.8 KD PROTEIN C29E4.4 IN CHROMOSOME III.//0.90:94:25//
 CAENORHABDITIS ELEGANS.//P34343
 F-NT2RP4000989//ANTHOPLEURIN B (TOXIN AP-B).//0.76:41:41//ANTHOPLEURA XANTHOGRAMMICA (GI-
 ANT GREEN SEA ANEMONE).//P01531
 5 F-NT2RP4000996//PROTEIN Q300.//0.00024:41:53//MUS MUSCULUS (MOUSE).//Q02722
 F-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMER-
 ASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.7e-115:261:82//RATTUS NORVEGI-
 CUS (RAT).//O54888
 F-NT2RP4001004//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.50:61:34//ARABIDOPSIS THALIANA
 10 (MOUSE-EAR CRESS).//Q42377
 F-NT2RP4001006//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECUR-
 SOR.//0.010:152:29//BACILLUS SUBTILIS.//P50840
 F-NT2RP4001010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.9e-05:247:25//SACCHAROMYCES CEREVISIAE
 15 (BAKER'S YEAST).//P08640
 F-NT2RP4001029//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIV-
 ITY) (TRANSCRIPTION FACTOR NTF-1).//1.1e-14:175:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//
 P13002
 F-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)
 20 (LEURS).//1.5e-74:272:55//CAENORHABDITIS ELEGANS.//Q09996
 F-NT2RP4001057//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//0.0064:76:38//
 CAENORHABDITIS ELEGANS.//P34664
 F-NT2RP4001064//DUALIN.//2.5e-24:199:38//GALLUS GALLUS (CHICKEN).//Q90830
 F-NT2RP4001078//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)
 25 (TAFII-130) (TAFII130).//0.11:139:38//HOMO SAPIENS (HUMAN).//O00268
 F-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.5e-22:242:
 31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P13586
 F-NT2RP4001080//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RI-
 BONUCLEOPROTEIN I) (HNRNP I).//1.7e-82:178:69//SUS SCROFA (PIG).//Q29099
 30 F-NT2RP4001086//LEUCINE-RICH ACIDIC NUCLEAR PROTEIN.//0.00039:141:26//RATTUS NORVEGICUS
 (RAT).//P49911
 F-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAM-
 INASE) (RNA EDITING ENZYME 1).//9.9e-07:79:43//HOMO SAPIENS (HUMAN).//P78563
 F-NT2RP4001100//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.4e-16:207:
 35 35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
 F-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.1e-115:224:99//RATTUS
 NORVEGICUS (RAT).//P38378
 F-NT2RP4001122//TIPD PROTEIN.//7.5e-11:129:31//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//O15736
 F-NT2RP4001126//TRICHOHYALIN.//1.4e-19:257:28//OVIS ARIES (SHEEP).//P22793
 40 F-NT2RP4001138//PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-.-).//0.00010:204:25//METH-
 ANOCOCCUS JANNASCHII.//Q58896
 F-NT2RP4001143//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//4.5e-34:
 168:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616
 F-NT2RP4001148//SOF1 PROTEIN.//2.4e-41:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
 45 P33750
 F-NT2RP4001149//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//1.3e-08:106:41//VOLVOX CART-
 ERI.//P21997
 F-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//
 3.6e-24:194:32//GALLUS GALLUS (CHICKEN).//P35331
 50 F-NT2RP4001159//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0056:117:25//PLASMODI-
 UM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643
 F-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//
 5.9e-24:184:34//BRASSICA OLERACEA (CAULIFLOWER).//P52178
 F-NT2RP4001206//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0029:117:26//PLASMODI-
 UM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643
 55 F-NT2RP4001207//CHROMOSOME SEGREGATION PROTEIN CSE1.//1.0e-07:144:28//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//P33307
 F-NT2RP4001210//DERMORPHIN 1 PRECURSOR (CONTAINS: DELTORPHIN (DERMENKEPHALIN); DER-

MORPHIN]//0.019:130:30//PHYLLOMEDUSA SAUVAGEI (SAUVAGE'S LEAF FROG)//P05422
 F-NT2RP4001213//ZINC FINGER PROTEIN 177//3.2e-28:176:39//HOMO SAPIENS (HUMAN)//Q13360
 F-NT2RP4001219//DISULFIDE ISOMERASE MPD1 PRECURSOR (EC 5.3.4.1)//2.4e-13:108:37//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//Q12404
 5 F-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN)//2.7e-56:242:40//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q04652
 F-NT2RP4001235//REGULATORY PROTEIN E2//0.0080:100:38//HUMAN PAPILLOMAVIRUS TYPE 25//
 P36787
 F-NT2RP4001256//CUTICLE COLLAGEN 1//0.014:104:31//CAENORHABDITIS ELEGANS//P08124
 10 F-NT2RP4001260//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17)//0.00077:16:68//ESCHERICHIA
 COLI//P05834
 F-NT2RP4001274//HISTONE H1.M6.1//0.98:65:35//TRYPANOSOMA CRUZI//P40273
 F-NT2RP4001276//ELAV PROTEIN//0.00054:134:33//DROSOPHILA VIRILIS (FRUIT FLY)//P23241
 F-NT2RP4001313//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//
 15 0.014:71:35//NICOTIANA TABACUM (COMMON TOBACCO)//P13983
 F-NT2RP4001315//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9//2.3e-12:190:27//SAC-
 CHAROMYCES CEREVISIAE (BAKER'S YEAST)//P54787
 F-NT2RP4001336//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1//0.0037:108:31//PODOSPORA AN-
 SERINA//Q00808
 20 F-NT2RP4001339//HYPOTHETICAL PROTEIN MJ0810//1.2e-09:150:34//METHANOCOCCUS JANNASCHII//
 Q58220
 F-NT2RP4001343//HYPOTHETICAL 85.2 KD PROTEIN F52C9.3 IN CHROMOSOME III//1.4e-18:244:27//
 CAENORHABDITIS ELEGANS//Q10123
 F-NT2RP4001345//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
 25 (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE)
 (FRAGMENT)//4.0e-49:212:50//GALLUS GALLUS (CHICKEN)//P53760
 F-NT2RP4001351//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//5.7e-11:229:26//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P25386
 F-NT2RP4001353//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//0.00088:84:28//HO-
 MO SAPIENS (HUMAN)//Q15404
 30 F-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN)//1.0e-
 22:222:30//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q08180
 F-NT2RP4001373//OV-17 ANTIGEN PRECURSOR (IMMUNODOMINANT HYPODERMAL ANTIGEN)//0.51:92:
 26//ONCHOCERCA VOLVULUS//P36991
 35 F-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
 TEIN KINASE 1)//3.5e-13:146:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P18160
 F-NT2RP4001379//HYPOTHETICAL 64.2 KD PROTEIN IN SLT2-PUT2 INTERGENIC REGION//1.2e-14:207:
 28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38767
 F-NT2RP4001389//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAG-
 40 MENT)//0.073:112:33//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414
 F-NT2RP4001407//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//0.0019:233:24//HOMO SAPIENS (HU-
 MAN)//Q02224
 F-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT)//6.2e-89:195:81//HOMO SAPIENS (HUMAN)//Q14141
 F-NT2RP4001433//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//1.5e-85:216:56//HOMO SAPIENS (HU-
 45 MAN)//P28160
 F-NT2RP4001442//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (VERSION 1)//
 0.012:107:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P18616
 F-NT2RP4001447//60S ACIDIC RIBOSOMAL PROTEIN P2 (EL12)//0.0046:69:33//ARTEMIA SALINA (BRINE
 SHRIMP)//P02399
 50 F-NT2RP4001474//CBP3 PROTEIN PRECURSOR//0.0011:111:29//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P21560
 F-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (AL-
 PHA-KETOGLUTARATE DEHYDROGENASE)//6.2e-60:146:61//HOMO SAPIENS (HUMAN)//Q02218
 F-NT2RP4001498//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I//2.3e-24:137:37//
 55 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09701
 F-NT2RP4001502//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC REGION//6.0e-22:
 148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40206
 F-NT2RP4001507//CUTICLE COLLAGEN 40//0.00029:166:31//CAENORHABDITIS ELEGANS//P34804

F-NT2RP4001524//LACTOCOCCIN A IMMUNITY PROTEIN//0.74:96:30//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS), AND LACTOCOCCUS LACTIS (SUBSP. CREMORIS) (STREPTOCOCCUS CREMORIS)//Q00561

5 F-NT2RP4001529//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)//2.8e-06:79:41//DROSOPHILA MELANOGASTER (FRUIT FLY)//P13002

F-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION//5.4e-34:88:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25656

10 F-NT2RP4001551//CELL DIVISION CONTROL PROTEIN 68//1.5e-18:243:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32558

F-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-)//0.00030:158:24//MYCOBACTERIUM TUBERCULOSIS//P96902

F-NT2RP4001567//IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT)//0.00013:147:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P52170

15 F-NT2RP4001568//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT)//8.0e-22:119:42//HOMO SAPIENS (HUMAN)//Q15057

F-NT2RP4001571//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57)//0.012:167:28//BOS TAURUS (BOVINE)//P06836

F-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//6.8e-115:208:98//BOS TAURUS (BOVINE)//P53620

20 F-NT2RP4001575//M-RELATED PROTEIN PRECURSOR//0.22:184:25//STREPTOCOCCUS PYOGENES//P16946

F-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS)//7.4e-45:229:39//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//P73505

25 F-NT2RP4001610//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII)//0.41:74:28//SUS SCROFA (PIG)//P27917

F-NT2RP4001614//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//1.0:29:37//HOMO SAPIENS (HUMAN)//P02811

F-NT2RP4001634//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE (FRAGMENT)//0.16:233:23//RATTUS NORVEGICUS (RAT)//P04462

30 F-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/34MS19//4.2e-21:249:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40469

F-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK)//4.5e-18:111:44//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P25323

35 F-NT2RP4001656//HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II//3.4e-13:175:32//CAENORHABDITIS ELEGANS//Q09600

F-NT2RP4001677//HYPOTHETICAL 73.6 KD PROTEIN CY49.21//0.065:66:43//MYCOBACTERIUM TUBERCULOSIS//Q10690

F-NT2RP4001679//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-36:103:72//HOMO SAPIENS (HUMAN)//P39194

40 F-NT2RP4001696//PHOTOSYSTEM II REACTION CENTRE J PROTEIN//0.93:37:37//CHLORELLA VULGARIS//P56338

F-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT//4.3e-11:128:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10282

45 F-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT)//4.1e-22:201:27//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q09332

F-NT2RP4001739//HOMEBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL)//1.0:67:34//HOMO SAPIENS (HUMAN)//P31260

50 F-NT2RP4001753//ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KOX1) (FRAGMENT)//1.2e-19:72:62//HOMO SAPIENS (HUMAN)//P21506

F-NT2RP4001760//BREAKPOINT CLUSTER REGION PROTEIN//1.8e-13:179:28//HOMO SAPIENS (HUMAN)//P11274

F-NT2RP4001790//ZINC FINGER PROTEIN 38 (ZFP-38) (CTF1N51) (TRANSCRIPTION FACTOR RU49)//7.9e-38:147:49//MUS MUSCULUS (MOUSE)//Q007231

55 F-NT2RP4001803//CUTICLE COLLAGEN 12 PRECURSOR//0.40:48:39//CAENORHABDITIS ELEGANS//P20630

F-NT2RP4001822//NOVEL ANTIGEN 2 (NAG-2)//2.7e-27:173:36//HOMO SAPIENS (HUMAN)//O14817

F-NT2RP4001823//PUTATIVE CUTICLE COLLAGEN F09G8.6//3.3e-16:152:42//CAENORHABDITIS ELE-

GANS.//P34391
 F-NT2RP4001828//HOLIN.//0.99:33:36//BACTERIOPHAGE HP1.//P51727
 F-NT2RP4001838//METASTASIS-ASSOCIATED PROTEIN MTA1.//1.2e-07:95:31//HOMO SAPIENS (HUMAN).//
 Q13330
 5 F-NT2RP4001841//INTESTINAL MUCIN-LIKE PROTEIN (MLP) (FRAGMENT).//0.94:141:22//RATTUS NOR-
 VEGICUS (RAT).//P98089
 F-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//5.6e-52:276:45//MUS MUSCULUS (MOUSE).//P55194
 F-NT2RP4001861//HYPOTHETICAL 10.6 KD PROTEIN IN GALE-PEPT INTERGENIC REGION.//0.92:39:51//
 BACILLUS SUBTILIS.//P55185
 10 F-NT2RP4001889//HYPOTHETICAL BHLF1 PROTEIN.//0.32:97:31//EPSTEIN-BARR VIRUS (STRAIN B95-8)
 (HUMAN HERPESVIRUS 4).//P03181
 F-NT2RP4001893//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE
 L) (RIBONUCLEASE 4) (FRAGMENT).//3.6e-07:124:29//MUS MUSCULUS (MOUSE).//Q05921
 F-NT2RP4001896//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1
 15 INTERGENIC REGION.//3.9e-10:210:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42935
 F-NT2RP4001901//ACROSIN PRECURSOR (EC 3.4.21.10).//2.4e-07:53:45//ORYCTOLAGUS CUNICULUS
 (RABBIT).//P48038
 F-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//3.1e-19:170:32//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//Q12024
 20 F-NT2RP4001938//ZINC FINGER PROTEIN MOK-2.//1.3e-28:72:50//MUS MUSCULUS (MOUSE).//P24399
 F-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-
 ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-
 ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//4.8e-14:183:30//TRITICUM AESTIVUM
 (WHEAT).//Q43209
 25 F-NT2RP4001950//HYPOTHETICAL PROTEIN ORF-1137.//3.7e-07:115:29//MUS MUSCULUS (MOUSE).//
 P11260
 F-NT2RP4001953
 F-NT2RP4001966//WALL-ASSOCIATED PROTEIN PRECURSOR.//0.13:151:27//BACILLUS SUBTILIS.//
 Q07833
 30 F-NT2RP4001975//FIBRIL-FORMING COLLAGEN ALPHA CHAIN.//0.00031:190:31//RIFTIA PACHYPTILA
 (TUBE WORM).//P30754
 F-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:185:29//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY).//Q04652
 F-NT2RP4002047//GTP-BINDING PROTEIN GUF1 (GTPASE GUF1).//4.0e-49:158:65//SACCHAROMYCES
 35 CEREVISIAE (BAKER'S YEAST).//P46943
 F-NT2RP4002052//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I.//0.0047:148:27//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844
 F-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE F56D2.6.//
 0.057:66:30//CAENORHABDITIS ELEGANS.//Q20875
 40 F-NT2RP4002071//VERY HYPOTHETICAL 13.2 KD PROTEIN CY251.09.//0.94:45:46//MYCOBACTERIUM TU-
 BERCULOSIS.//Q10888
 F-NT2RP4002075//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.44:36:38//HUMAN IMMU-
 NODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804
 F-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.6e-19:46:76//HO-
 45 MO SAPIENS (HUMAN).//Q05481
 F-NT2RP4002081//MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).//
 2.8e-05:196:31//HOMO SAPIENS (HUMAN).//P22670
 F-NT2RP4002083//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.0064:29:55//OWENIA FUSI-
 FORMIS.//P21260
 50 F-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.1e-37:159:53//SCHIZOSACCHAROMYCES
 POMBE (FISSION YEAST).//P38938
 F-NT2RP4002791//30S RIBOSOMAL PROTEIN S20.//1.0:73:26//HELICOBACTER PYLORI (CAMPYLO-
 BACTER PYLORI).//P56027
 F-NT2RP4002888//HYPOTHETICAL PROTEIN TP0352.//0.98:52:26//TREPONEMA PALLIDUM.//O83371
 55 F-NT2RP4002905//G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) (FRAGMENT).//5.9e-05:138:27//
 GLYCINE MAX (SOYBEAN).//P25012
 F-NT2RP5003459//HOMEBOX PROTEIN HOX-A3 (HOX-1.5) (MO-10).//0.027:40:40//MUS MUSCULUS
 (MOUSE).//P02831

F-NT2RP5003461//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT)//1.1e-12:142:
 35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09779
 F-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//5.3e-13:215:28//PODOSPORA AN-
 SERINA//Q00808
 5 F-NT2RP5003492//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//0.0055:144:27//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//P08640
 F-NT2RP5003500//PROLINE-RICH PROTEIN MP-2 PRECURSOR//9.0e-05:103:38//MUS MUSCULUS
 (MOUSE)//P05142
 10 F-NT2RP5003506//MALE SPECIFIC SPERM PROTEIN MST87F//0.53:21:38//DROSOPHILA MELANOGASTER
 (FRUIT FLY)//P08175
 F-NT2RP5003512//HYPOTHETICAL PROTEIN IN CYCB 3'REGION PRECURSOR (ORF2) (FRAGMENT)//0.92:
 49:32//PARACOCCLUS DENITRIFICANS//P29969
 F-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR)//2.7e-18:165:39//PHASE-
 15 OLUS AUREUS (MUNG BEAN) (VIGNA RADIATA)//P37116
 F-NT2RP5003524//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//6.0e-08:125:41//RATTUS NORVEGICUS
 (RAT)//P02454
 F-NT2RP5003534//ATP SYNTHASE, SUBUNIT F (EC 3.6.1.34)//0.88:37:45//HALOBACTERIUM VOLCANII
 (HALOFERAX VOLCANII)//Q48331
 20 F-OVARC1000001//GAR22 PROTEIN//1.9e-05:41:58//HOMO SAPIENS (HUMAN)//Q99501
 F-OVARC1000004//70 KD EXOCYST COMPLEX PROTEIN//3.7e-08:186:25//SACCHAROMYCES CEREVI-
 SIAE (BAKER'S YEAST)//P19658
 F-OVARC1000006//HISTONE H2A.1//4.7e-55:117:98//RATTUS NORVEGICUS (RAT)//P02262
 F-OVARC1000013//WD-REPEAT PROTEIN POP1//0.00022:126:28//SCHIZOSACCHAROMYCES POMBE
 25 (FISSION YEAST)//P87060
 F-OVARC1000014//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//2.3e-05:220:30//GALLUS GALLUS
 (CHICKEN)//P02457
 F-OVARC1000017//CUTICLE COLLAGEN DPY-13//2.6e-05:97:30//CAENORHABDITIS ELEGANS//P17657
 F-OVARC1000035
 30 F-OVARC1000058//RAS-RELATED PROTEIN RABC//0.00015:110:24//DICTYOSTELIUM DISCOIDEUM
 (SLIME MOLD)//P34143
 F-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE)//6.8e-09:
 60:45//LYCOPERSICON ESCULENTUM (TOMATO)//P80022
 F-OVARC1000068//CYTOTOXIN 4 (CARDIOTOXIN V-II-4)//1.0:27:44//NAJA MOSSAMBICA (MOZAMBIQUE
 35 COBRA)//P01452
 F-OVARC1000071//NUCLEAR TRANSPORT FACTOR 2 (NTF-2) (PLACENTAL PROTEIN 15) (PP15)//5.2e-06:
 115:29//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT)//P13662
 F-OVARC1000085
 F-OVARC1000087//HISTONE MACRO-H2A.1//1.2e-13:174:26//RATTUS NORVEGICUS (RAT)//Q02874
 40 F-OVARC1000091//OCTAPEPTIDE-REPEAT PROTEIN T2//0.0013:137:32//MUS MUSCULUS (MOUSE)//
 Q06666
 F-OVARC1000092//MITOCHONDRIAL RIBOSOMAL PROTEIN S7//0.97:46:39//ACANTHAMOEBA CASTELLA-
 NII (AMOEBA)//P46756
 F-OVARC1000106//HYPOTHETICAL 141.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC REGION//0.0012:165:
 45 29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53935
 F-OVARC1000109//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT)//0.18:
 35:34//DAUCUS CAROTA (CARROT)//P06600
 F-OVARC1000113//HYPOTHETICAL PROTEIN C18//1.0:26:26//SWINEPOX VIRUS (STRAIN KASZA) (SPV)//
 P32217
 50 F-OVARC1000114//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-28:57:63//HOMO SAPIENS (HUMAN)//
 P39194
 F-OVARC1000133
 F-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-
 RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-
 55 TOUS NUCLEAR PROTEIN HOMOLOG)//1.9e-09:200:29//HOMO SAPIENS (HUMAN)//Q13107
 F-OVARC1000145//HOMEBOX PROTEIN DLX-3//1.0:65:30//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA
 DANIO)//Q01702
 F-OVARC1000148//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2)//0.12:175:29//CANDIDA AL-

BICANS (YEAST)//P46593
 F-OVARC1000151//HYPOTHETICAL PROTEIN KIAA0161//5.6e-20:197:30//HOMO SAPIENS (HUMAN)//
 P50876
 F-OVARC1000168//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0030:77:38//HOMO SAPIENS (HUMAN)//
 5 P39188
 F-OVARC1000191//COLANIC ACID BIOSYNTHESIS PROTEIN WCAH//0.95:56:35//ESCHERICHIA COLI//
 P32056
 F-OVARC1000198//HISTONE H1.C2//0.96:70:25//TRYPANOSOMA CRUZI//P40268
 F-OVARC1000209//HYPOTHETICAL 20.9 KD PROTEIN IN PLB1-HXT2 INTERGENIC REGION//2.5e-33:178:
 10 44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03677
 F-OVARC1000212//PROLINE-RICH PROTEIN MP-2 PRECURSOR//1.7e-05:66:46//MUS MUSCULUS
 (MOUSE)//P05142
 F-OVARC1000240//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.8e-10:41:78//HOMO SAPIENS (HUMAN)//
 P39193
 15 F-OVARC1000241//ENDOTHELIAL PAS DOMAIN PROTEIN 1 (EPAS-1) (HIF-1 ALPHA-LIKE FACTOR) (MHLF)
 (HIF-RELATED FACTOR) (HRF)//7.4e-54:177:54//MUS MUSCULUS (MOUSE)//P97481
 F-OVARC1000288//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//2.9e-20:115:
 45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38821
 F-OVARC1000302//CORTICOSTEROID-BINDING GLOBULIN PRECURSOR (CBG) (TRANSCORTIN)//1.0:79:
 20 25//MUS MUSCULUS (MOUSE)//Q06770
 F-OVARC1000304//PROTEIN MOV-10//1.6e-79:181:83//MUS MUSCULUS (MOUSE)//P23249
 F-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2)//6.9e-36:156:42//ASHBYA GOSSYPYII (EREMOTH-
 ECIIUM GOSSYPYII)//Q00063
 F-OVARC1000321//HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME I//5.2e-45:159:53//
 25 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14179
 F-OVARC1000326//BASIC PROLINE-RICH PEPTIDE IB-1//0.036:67:35//HOMO SAPIENS (HUMAN)//P04281
 F-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION//1.2e-16:200:
 27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40004
 F-OVARC1000347//HYPOTHETICAL 7.6 KD PROTEIN YCF33//0.69:41:43//CYANOPHORA PARADOXA//
 30 P48273
 F-OVARC1000384//ANTIFREEZE PEPTIDE 4 PRECURSOR//0.98:49:34//PSEUDOPLEURONECTA AMERI-
 CANUS (WINTER FLOUNDER)//P02734
 F-OVARC1000408//INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT)//8.1e-05:115:33//XENOPUS LAE-
 VIS (AFRICAN CLAWED FROG)//Q05049
 35 F-OVARC1000411//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150)
 (DAP-150) (P150-GLUED)//0.00076:100:29//RATTUS NORVEGICUS (RAT)//P28023
 F-OVARC1000414//HYPOTHETICAL 7.0 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION//1.0:46:34//
 BACILLUS SUBTILIS//P54431
 F-OVARC1000420//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT)//0.0028:97:
 40 37//HOMO SAPIENS (HUMAN)//P25067
 F-OVARC1000427//HYPOTHETICAL 13.9 KD PROTEIN IN PRFA-SPOIIR INTERGENIC REGION//0.70:21:47//
 BACILLUS SUBTILIS//P39150
 F-OVARC1000431
 F-OVARC1000437//TENSIN//9.2e-42:195:52//GALLUS GALLUS (CHICKEN)//Q04205
 45 F-OVARC1000440//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN)//3.4e-31:37:
 97//HOMO SAPIENS (HUMAN)//P48059
 F-OVARC1000442
 F-OVARC1000443//CUTICLE COLLAGEN 2C (FRAGMENT)//0.0056:163:34//HAEMONCHUS CONTORTUS//
 P16252
 50 F-OVARC1000461//FIXU PROTEIN//0.36:36:44//RHIZOBIUM LEGUMINOSARUM (BIOVAR TRIFOLII)//
 P42710
 F-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7//2.4e-14:222:26//SACCHAROMYCES CEREVI-
 SIAE (BAKER'S YEAST)//P11075
 F-OVARC1000466//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.3e-08:29:93//HOMO SAPIENS (HUMAN)//
 55 P39192
 F-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-
 CIFICITY PROTEIN PHOSPHATASE MKP-X) (FRAGMENT)//2.8e-06:96:36//RATTUS NORVEGICUS (RAT)//
 Q63340

- F-OVARC1000479//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K)//0.99:48:37//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA)//P31567 F-OVARC1000486
 F-OVARC1000496//HYPOTHETICAL PROTEIN MJ1213//1.0:62:32//METHANOCOCCUS JANNASCHII//Q58610
- 5 F-OVARC1000520//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT)//0.0011:66:40//EIMERIA ACERVULINA//P09125
 F-OVARC1000526//PROTEIN Q300//1.2e-05:51:43//MUS MUSCULUS (MOUSE)//Q02722
 F-OVARC1000533//NEURONAL PROTEIN 3.1 (P311 PROTEIN)//0.74:43:41//HOMO SAPIENS (HUMAN)//Q16612
- 10 F-OVARC1000543//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)//2.3e-23:192:35//HOMO SAPIENS (HUMAN)//Q10472
 F-OVARC1000556
 F-OVARC1000557//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.6e-08:80:47//HOMO SAPIENS (HUMAN)//P39188
- 15 F-OVARC1000564//VPX PROTEIN (X ORF PROTEIN) (VIRAL ACCESSORY PROTEIN)//0.45:32:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194) (HIV-2)//P17760
 F-OVARC1000573
 F-OVARC1000576//BETA-DEFENSIN 1 (BNDB-1)//0.47:29:41//BOS TAURUS (BOVINE)//P46159
- 20 F-OVARC1000578//COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS)//0.023:96:36//BOS TAURUS (BOVINE)//P02459
 F-OVARC1000588//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3//0.75:57:29//HOMO SAPIENS (HUMAN)//P09001
 F-OVARC1000605//AUTOLYSIN PRECURSOR (EC 3.4.24.38) (GAMETE LYTIC ENZYME) (GLE)//0.91:134:28//CHLAMYDOMONAS REINHARDTII//P31178
- 25 F-OVARC1000622//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.6e-36:100:80//HOMO SAPIENS (HUMAN)//P39189
 F-OVARC1000640//HYPOTHETICAL 8.5 KD PROTEIN YCF40 (ORF73)//0.96:34:38//ODONTELLA SINENSIS//P49535
- 30 F-OVARC1000649//ANTHER-SPECIFIC PROTEIN SF18 PRECURSOR (FRAGMENT)//0.0036:64:37//HELIANTHUS ANNUUS (COMMON SUNFLOWER)//P22357
 F-OVARC1000661//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS)//0.21:53:47//RATTUS NORVEGICUS (RAT)//P02466
 F-OVARC1000678//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17)//1.0:17:58//ESCHERICHIA COLI//P05834
- 35 F-OVARC1000679//DNA-DIRECTED RNA POLYMERASE OMEGA CHAIN (EC 2.7.7.6) (TRANSCRIPTASE OMEGA CHAIN) (RNA POLYMERASE OMEGA SUBUNIT)//0.096:67:29//ESCHERICHIA COLI//P08374
 F-OVARC1000681//PROTEIN Q300//0.72:16:43//MUS MUSCULUS (MOUSE)//Q02722
 F-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B)//7.6e-70:102:99//MUS MUSCULUS (MOUSE)//P39098
- 40 F-OVARC1000689//CADMIUM-METALLOTHIONEIN (CD-MT)//0.032:30:40//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL)//P33187
 F-OVARC1000700//BRAIN NEURON CYTOPLASMIC PROTEIN 2//0.17:60:40//RATTUS NORVEGICUS (RAT)//P02684
- 45 F-OVARC1000703//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.57:42:42//HOMO SAPIENS (HUMAN)//P02811
 F-OVARC1000722//N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1->4) GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT)//1.1e-20:44:70//BOS TAURUS (BOVINE)//P08037
- 50 F-OVARC1000730//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III//5.2e-29:224:36//CAENORHABDITIS ELEGANS//Q18262
 F-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN//6.2e-12:78:48//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25159
 F-OVARC1000769
- 55 F-OVARC1000771//RAS-RELATED PROTEIN RAB-2//1.1e-46:121:79//HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG)//P08886
 F-OVARC1000781//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2)//0.81:36:52//HOMO SAPIENS (HUMAN)//P52951

F-OVARC1000787//40S RIBOSOMAL PROTEIN S14 (FRAGMENT)//0.96:37:48//SUS SCROFA (PIG)//Q29303
 F-OVARC1000800/////ALU SUBFAMILY SB WARNING ENTRY !!!!!2.5e-31:47:82//HOMO SAPIENS (HUMAN)//
 P39189
 5 F-OVARC1000802//HYPOTHETICAL 8.8 KD PROTEIN B0302.2 IN CHROMOSOME X//0.16:55:40//
 CAENORHABDITIS ELEGANS//Q10926
 F-OVARC1000834//SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21- ACTI-
 VATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2)//0.87:140:31//RATTUS NORVEGICUS (RAT)//
 P35465
 10 F-OVARC1000846//NUCLEOLIN (PROTEIN C23)//7.0e-07:109:30//MESOCRICETUS AURATUS (GOLDEN
 HAMSTER)//P08199
 F-OVARC1000850//HYPOTHETICAL 56.2 KD PROTEIN IN ERG8-UBP8 INTERGENIC REGION//6.9e-09:180:
 28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04991
 F-OVARC1000862//UBIQUITIN-CONJUGATING ENZYME E2-17.5 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
 LIGASE) (UBIQUITIN CARRIER PROTEIN)//0.0020:74:28//SACCHAROMYCES CEREVISIAE (BAKER'S
 15 YEAST)//P52490
 F-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1)//9.8e-39:154:55//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//P40484
 F-OVARC1000883//METALLOTHIONEIN-I//0.87:38:36//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLA-
 BRATA)//P15113
 20 F-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-)//2.8e-18:170:34//ESCHERICHIA COLI//P37440
 F-OVARC1000886//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT)//0.00033:60:45//BOS TAURUS (BOVINE)//
 P02465
 F-OVARC1000890//PROBABLE E5 PROTEIN//0.92:7:71//HUMAN PAPILLOMAVIRUS TYPE 70//P50774
 F-OVARC1000891//HYPOTHETICAL 8.3 KD PROTEIN (ORF5)//1.0:36:36//PARAMECIUM TETRAURELIA//
 25 P15606
 F-OVARC1000897//HYPOTHETICAL 6.1 KD PROTEIN PRECURSOR (ORF87)//1.0:34:44//ORGYIA PSEU-
 DOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10337
 F-OVARC1000912//PUTATIVE CUTICLE COLLAGEN C09G5.4//4.0e-07:98:35//CAENORHABDITIS ELE-
 GANS//Q09455
 30 F-OVARC1000915//HYPOTHETICAL PROTEIN KIAA0288 (HA6116)//1.7e-47:115:76//HOMO SAPIENS (HU-
 MAN)//P56524
 F-OVARC1000924//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT)//0.99:54:24//BOA CONSTRICTOR (BOA)//
 P92848
 35 F-OVARC1000936//HYPOTHETICAL 7.5 KD PROTEIN IN INAA-GLPQ INTERGENIC REGION//1.0:48:33//ES-
 CHERICHIA COLI//P45505
 F-OVARC1000937//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//1.0:135:31//HOMO SAPIENS (HU-
 MAN)//P02452
 F-OVARC1000945//EARLY E1A 11 KD PROTEIN//0.087:81:24//MOUSE ADENOVIRUS TYPE 1 (MAV-1)//
 P12533
 40 F-OVARC1000948
 F-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933//0.99:67:28//METHANOCOCCUS JANNASCHII//
 Q58343
 F-OVARC1000960/////ALU SUBFAMILY SP WARNING ENTRY !!!!!1.8e-32:56:75//HOMO SAPIENS (HUMAN)//
 P39193
 45 F-OVARC1000964//MAMBIN (GLYCOPROTEIN IIB-IIA ANTAGONIST) (PLATELET AGGREGATION INHIBITOR)
 (DENDROASPIN)//1.0:30:36//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA)//
 P28375
 F-OVARC1000971
 F-OVARC1000984//HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-ERG24 INTERGENIC REGION PRECUR-
 50 SOR//0.093:36:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53832
 F-OVARC1000996//MO25 PROTEIN//1.9e-39:80:95//MUS MUSCULUS (MOUSE)//Q06138
 F-OVARC1000999//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 1 (BRN-1 PROTEIN)//0.00020:50:
 40//HOMO SAPIENS (HUMAN)//P20264
 F-OVARC1001000/////ALU SUBFAMILY SX WARNING ENTRY !!!!!1.4e-16:43:90//HOMO SAPIENS (HUMAN)//
 55 P39195
 F-OVARC1001004//MALE SPECIFIC SPERM PROTEIN MST84DA//0.95:33:42//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01642
 F-OVARC1001010//HYPOTHETICAL PROTEIN MJ0926//0.50:71:23//METHANOCOCCUS JANNASCHII//

Q58336
 F-OVARC1001011//CORTISTATIN PRECURSOR//0.81:45:37//RATTUS NORVEGICUS (RAT)//Q62949
 F-OVARC1001032//FERREDOXIN LIKE PROTEIN//1.0:26:46//RHIZOBIUM LEGUMINOSARUM (BIOVAR PHA-
 SEOLI)//Q05561
 5 F-OVARC1001034//METALLOTHIONEIN-IG (MT-1G)//0.14:9:77//HOMO SAPIENS (HUMAN)//P13640
 F-OVARC1001038//NUCLEOLIN (PROTEIN C23)//3.2e-07:36:80//HOMO SAPIENS (HUMAN)//P19338
 F-OVARC1001040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-18:45:60//HOMO SAPIENS (HUMAN)//
 P39194
 10 F-OVARC1001044//BIS(5'-NUCLEOSYL)-TETRAPHOSPHATASE (SYMMETRICAL) (EC 3.6.1.41) (DIADENOS-
 INE TETRAPHOSPHATASE)//0.88:43:39//ESCHERICHIA COLI//P05637
 F-OVARC1001051//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN)//0.34:
 117:25//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q05319
 F-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR//1.6e-33:43:97//HOMO SAPIENS (HU-
 MAN)//P43490
 15 F-OVARC1001062
 F-OVARC1001065//METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE--TRNA LIGASE)
 (METRS)//0.79:76:39//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)//Q44951
 F-OVARC1001068//GTP-BINDING PROTEIN ERA HOMOLOG (FRAGMENT)//5.3e-15:100:44//BRADYRHIZO-
 BIUM JAPONICUM//O69162
 20 F-OVARC1001072//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0076:41:56//HOMO SAPIENS (HUMAN)//
 P39188
 F-OVARC1001074//60S RIBOSOMAL PROTEIN L38//1.0:32:40//LYCOPERSICON ESCULENTUM (TOMATO)//
 P46291
 F-OVARC1001085//HYPOTHETICAL 126.5 KD PROTEIN C13F4.06 IN CHROMOSOME I//0.73:135:25//
 25 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10197
 F-OVARC1001092//HYPOTHETICAL 51.2 KD PROTEIN IN PET54-DIE2 INTERGENIC REGION//5.6e-05:30:
 56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P50079
 F-OVARC1001107//SHK1 KINASE-BINDING PROTEIN 1//1.8e-08:52:51//SCHIZOSACCHAROMYCES POMBE
 (FISSION YEAST)//P78963
 30 F-OVARC1001113//DIAPHANOUS PROTEIN//1.9e-33:218:35//DROSOPHILA MELANOGASTER (FRUIT
 FLY)//P48608
 F-OVARC1001117//GENE 7 PROTEIN//0.68:12:50//SPIROPLASMA VIRUS 4 (SPV4)//P11339
 F-OVARC1001118
 F-OVARC1001129//30S RIBOSOMAL PROTEIN S17//0.15:57:22//AQUIFEX AEOLICUS//O66439
 35 F-OVARC1001154//GRANULINS PRECURSOR (ACROGRANIN)//2.3e-95:99:77//MUS MUSCULUS
 (MOUSE)//P28798
 F-OVARC1001161//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT//0.17:87:34//ARABIDOPSIS
 THALIANA (MOUSE-EAR CRESS)//P49177
 F-OVARC1001162
 40 F-OVARC1001167//TRBD PROTEIN//0.92:24:45//ESCHERICHIA COLI//P41070
 F-OVARC1001169//FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,6-BISPHOSPHATE
 1-PHOSPHOHYDROLASE) (FBPASE) (FRAGMENT)//0.82:35:40//MUS MUSCULUS (MOUSE)//P97323
 F-OVARC1001170//PROLINE-RICH PEPTIDE P-B//0.17:27:37//HOMO SAPIENS (HUMAN)//P02814
 F-OVARC1001171//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00023:28:75//HOMO SAPIENS (HUMAN)//
 45 P39188
 F-OVARC1001173
 F-OVARC1001176//HYPOTHETICAL BHLF1 PROTEIN//2.7e-05:158:31//EPSTEIN-BARR VIRUS (STRAIN
 B95-8) (HUMAN HERPESVIRUS 4)//P03181
 F-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2//1.4e-12:208:25//SACCHAROMYCES CEREVISIAE
 50 (BAKER'S YEAST)//P48510
 F-OVARC1001188//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//3.3e-31:
 129:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53215
 F-OVARC1001200//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION//0.018:148:26//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47057
 55 F-OVARC1001232//HYPOTHETICAL PROTEIN MJ1236//2.5e-27:141:39//METHANOCOCCUS JANNASCHII//
 Q58633
 F-OVARC1001240
 F-OVARC1001243

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F-OVARC1001244//RING3 PROTEIN (KIAA9001)//1.7e-13:37:91//HOMO SAPIENS (HUMAN)//P25440
 F-OVARC1001261//OCTAPEPTIDE-REPEAT PROTEIN T2//1.3e-07:109:35//MUS MUSCULUS (MOUSE)//
 Q06666
 5 F-OVARC1001268//HYPOTHETICAL 57.4 KD PROTEIN IN PILT REGION (ORF4)//0.71:43:41//PSEU-
 DOMONAS AERUGINOSA//P24563
 F-OVARC1001270//HYPOTHETICAL 9.0 KD PROTEIN IN UVSW-UVSY INTERGENIC REGION//1.0:44:29//
 BACTERIOPHAGE T4//P32281
 F-OVARC1001271//HYPOTHETICAL 104.7 KD PROTEIN F23F12.8 IN CHROMOSOME III PRECURSOR//
 0.00015:188:23//CAENORHABDITIS ELEGANS//P46504
 10 F-OVARC1001282
 F-OVARC1001296//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31)//0.022:101:31//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P38968
 F-OVARC1001306//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I//0.023:
 134:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O13695
 15 F-OVARC1001329//CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)//1.3e-14:
 150:28//ZEA MAYS (MAIZE)//P49133
 F-OVARC1001330
 F-OVARC1001339//RIBONUCLEOPROTEIN RB97D//0.0013:55:38//DROSOPHILA MELANOGASTER (FRUIT
 FLY)//Q02926
 20 F-OVARC1001341//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION//4.9e-17:110:
 43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40032
 F-OVARC1001342
 F-OVARC1001344//PREPROTEIN TRANSLOCASE SECE SUBUNIT//0.99:39:23//STAPHYLOCOCCUS CAR-
 NOSUS//P36253
 25 F-OVARC1001357//METALLOTHIONEIN//0.99:28:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//
 Q05890
 F-OVARC1001360//LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)//0.86:109:
 31//HOMO SAPIENS (HUMAN)//P48634
 F-OVARC1001369//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT)//6.7e-05:124:36//BOS TAURUS (BOVINE)//
 P02465
 30 F-OVARC1001372//HYPOTHETICAL 34.5 KD PROTEIN IN CLCB-CLCD INTERGENIC REGION PRECUR-
 SOR//0.75:33:48//PSEUDOMONAS PUTIDA, AND PSEUDOMONAS SP. (STRAIN B13)//Q47100
 F-OVARC1001376//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.8e-24:96:61//HOMO SAPIENS (HUMAN)//
 P39188
 35 F-OVARC1001381//MEMBRANE-ASSOCIATED ATPASE EPSILON CHAIN (EC 3.6.1.34) (SUL-ATPASE EPSI-
 LON)//0.96:46:39//SULFOLOBUS ACIDOCALDARIUS//P23039
 F-OVARC1001391//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-
 MENT)//0.00024:189:29//HOMO SAPIENS (HUMAN)//P10162
 F-OVARC1001399//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.062:18:77//HOMO SAPIENS (HUMAN)//
 P39195
 40 F-OVARC1001417//HYPOTHETICAL 157.0 KD PROTEIN C38C10.5 IN CHROMOSOME III//0.010:185:23//
 CAENORHABDITIS ELEGANS//Q03570
 F-OVARC1001419//A-TYPE INCLUSION PROTEIN (ATI)//0.50:135:28//CAMELPOX VIRUS (STRAIN CP-1)//
 Q05482
 45 F-OVARC1001425//COLLAGEN ALPHA 1(X) CHAIN PRECURSOR//0.43:85:40//HOMO SAPIENS (HUMAN)//
 Q03692
 F-OVARC1001436//HYPOTHETICAL 11.4 KD PROTEIN (C4 PROTEIN)//0.031:100:30//TOMATO YELLOW
 LEAF CURL VIRUS (STRAIN AUSTRALIA) (TYLCV)//P36283
 F-OVARC1001442//HOMEBOX PROTEIN HTR-A2 (FRAGMENT)//1.0:32:34//HELOBDELLA TRISERIALIS
 50 (LEECH)//P17138
 F-OVARC1001453//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF)//0.74:19:47//MUS
 MUSCULUS (MOUSE)//P28184
 F-OVARC1001476//GTP-BINDING PROTEIN GTR2//3.0e-12:114:34//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P53290
 55 F-OVARC1001480//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR//0.00019:134:32//MUS MUSCULUS
 (MOUSE)//Q02788
 F-OVARC1001489//HYPOTHETICAL PROTEIN HI1270//0.98:30:43//HAEMOPHILUS INFLUENZAE//P44149
 F-OVARC1001496//C-TERMINAL BINDING PROTEIN 2//4.0e-65:132:100//HOMO SAPIENS (HUMAN)//

P56545
 F-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1)//3.2e-70:159:94//HOMO SAPIENS (HUMAN)//P98161
 F-OVARC1001525//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN14)//1.0:36:33//MUS MUSCULUS (MOUSE)//Q61077
 5 F-OVARC1001542//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B)//0.69:57:33//HOMO SAPIENS (HUMAN)//P35325
 F-OVARC1001547
 F-OVARC1001555//NGG1-INTERACTING FACTOR 3//7.6e-16:148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53081
 10 F-OVARC1001577//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)//8.8e-38:94:81//GALLUS GALLUS (CHICKEN)//P30352
 F-OVARC1001600//GENE 7 PROTEIN//0.80:38:39//SPIROPLASMA VIRUS SPV1-R8A2 B//P15898
 F-OVARC1001610//DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2- DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT)//1.6e-22:122:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P17898
 15 F-OVARC1001611
 F-OVARC1001615//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X//0.30:43:34//CAENORHABDITIS ELEGANS//Q11116
 20 F-OVARC1001668//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.0e-19:45:82//HOMO SAPIENS (HUMAN)//P39192
 F-OVARC1001702//SOX-20 PROTEIN//2.4e-28:71:83//HOMO SAPIENS (HUMAN)//O60248
 F-OVARC1001703//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1) (INTERFERON-GAMMA INDUCIBLE PROTEIN MAG-1)//0.00018:88:36//MUS MUSCULUS (MOUSE)//Q01514
 25 F-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B)//2.7e-05:98:32//MUS MUSCULUS (MOUSE)//Q62267
 F-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI)//4.5e-20:46:67//BOS TAURUS (BOVINE)//P07106
 30 F-OVARC1001726//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES I)//0.59:23:56//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII)//P09921
 F-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE//2.1e-75:176:87//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q01173
 35 F-OVARC1001745//GENE 11 PROTEIN//0.31:36:52//SPIROPLASMA VIRUS SPV1-R8A2 B//P15902
 F-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1)//2.8e-23:197:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P12945
 F-OVARC1001766//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70)//2.2e-06:99:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38911
 40 F-OVARC1001767//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X)//0.99:113:27//ESCHERICHIA COLI//P23839
 F-OVARC1001768
 45 F-OVARC1001791//HYPOTHETICAL 63.3 KD PROTEIN IN MPT5-SAE2 INTERGENIC REGION//0.090:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P46945
 F-OVARC1001795//HYPOTHETICAL 7.5 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION//0.81:21:38//BACTERIOPHAGE T4//P07878
 F-OVARC1001802//PLECTOXIN VIII (PLT-VIII) (PLTVIII)//0.41:19:36//PLECTREURYS TRISTIS (SPIDER)//P36984
 50 F-OVARC1001805//60S RIBOSOMAL PROTEIN L40 (CEP52)//0.67:24:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P14796
 F-OVARC1001809//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.23:111:31//RATTUS NORVEGICUS (RAT)//P02454
 55 F-OVARC1001812//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.99:28:42//HALICHOERUS GRYPUS (GRAY SEAL)//P38592
 F-OVARC1001813//HYPOTHETICAL 9.9 KD PROTEIN//0.41:36:30//VACCINIA VIRUS (STRAIN COPENHAGEN)//P20562

F-OVARC1001820//HYPOTHETICAL PROTEIN ORF-1137//0.80:58:29//MUS MUSCULUS (MOUSE)//P11260
 F-OVARC1001828
 F-OVARC1001846
 F-OVARC1001861//METALLOTHIONEIN (MT)//0.18:11:54//PLEURONECTES PLATESSA (PLAICE)//P07216
 5 F-OVARC1001873
 F-OVARC1001879//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II//2.3e-05:73:31//
 CAENORHABDITIS ELEGANS//Q09296
 F-OVARC1001880//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC
 PEPTIDE P-F] (FRAGMENT)//2.4e-11:203:32//HOMO SAPIENS (HUMAN)//P02812
 10 F-OVARC1001883//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-16:86:59//HOMO SAPIENS (HUMAN)//
 P39188
 F-OVARC1001900//HYPOTHETICAL 105.9 KD PROTEIN F22B7.5 IN CHROMOSOME III//0.0053:48:47//
 CAENORHABDITIS ELEGANS//P34408
 F-OVARC1001901
 15 F-OVARC1001911//40S RIBOSOMAL PROTEIN S28//1.0:33:36//ARABIDOPSIS THALIANA (MOUSE-EAR
 CRESS)//P34789
 F-OVARC1001916//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
 CIOGENITAL DYSPLASIA PROTEIN)//0.00082:114:27//HOMO SAPIENS (HUMAN)//P98174
 F-OVARC1001928//FERREDOXIN III (FDIII)//1.0:64:29//ANABAENA VARIABILIS//P46050
 20 F-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-
 NO, ACETYLTRANSFERASE 1)//3.0e-07:93:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P12945
 F-OVARC1001943//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III//1.7e-23:147:43//
 CAENORHABDITIS ELEGANS//P34664
 25 F-OVARC1001949//ZINC FINGER PROTEIN 177//2.0e-23:56:66//HOMO SAPIENS (HUMAN)//Q13360
 F-OVARC1001950//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.011:57:47//HOMO SAPIENS (HUMAN)//
 P39188
 F-OVARC1001987//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE)//0.39:14:64//MUS MUSCULUS
 (MOUSE)//P02319
 30 F-OVARC1001989//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-13:55:72//HOMO SAPIENS (HUMAN)//
 P39188
 F-OVARC1002044
 F-OVARC1002050//UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP)//3.6e-12:221:25//HOMO
 SAPIENS (HUMAN)//P46939
 35 F-OVARC1002066
 F-OVARC1002082
 F-OVARC1002107//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//0.99:149:24//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P25386
 F-OVARC1002112//HISTONE MACRO-H2A.1//2.8e-64:133:98//RATTUS NORVEGICUS (RAT)//Q02874
 40 F-OVARC1002127//60S RIBOSOMAL PROTEIN L22//0.0023:95:35//DROSOPHILA MELANOGASTER (FRUIT
 FLY)//P50887
 F-OVARC1002138//PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6)//6.4e-51:198:
 56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40328
 F-OVARC1002143
 45 F-OVARC1002156//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION//0.00010:64:
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53915
 F-OVARC1002158//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//8.2e-07:119:35//
 AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41479
 F-OVARC1002165//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B)//0.00023:90:45//EPSTEIN-BARR VI-
 50 RUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03204
 F-OVARC1002182//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHRO-
 MOSOME II//1.3e-34:165:35//CAENORHABDITIS ELEGANS//Q18964
 F-PLACE1000004//HYPOTHETICAL 180.2 KD PROTEIN C31A2.05C IN CHROMOSOME I//8.8e-05:148:25//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09725
 55 F-PLACE1000005//PROTEIN Q300//0.30:10:100//MUS MUSCULUS (MOUSE)//Q02722
 F-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-
 ZYME)//2.3e-39:134:62//CAENORHABDITIS ELEGANS//P34547

EP 1 074 617 A2

F-PLACE1000014//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//
 0.00036:63:39//HOMO SAPIENS (HUMAN)//P19474
 F-PLACE1000031
 F-PLACE1000040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-12:97:41//HOMO SAPIENS (HUMAN)//
 5 P39194
 F-PLACE1000048//50S RIBOSOMAL PROTEIN L15 (FRAGMENT)//0.98:31:38//BACILLUS SP. (STRAIN C-
 125)//P38373
 F-PLACE1000050//COLLAGEN ALPHA 1(III) CHAIN//0.00062:190:33//BOS TAURUS (BOVINE)//P04258
 F-PLACE1000061//60S RIBOSOMAL PROTEIN L37A//6.4e-19:51:86//GALLUS GALLUS (CHICKEN)//P32046
 10 F-PLACE1000066//SSU72 PROTEIN//2.3e-39:165:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P53538
 F-PLACE1000078//BAD PROTEIN (BCL-2 BINDING COMPONENT 6)//1.7e-06:21:95//HOMO SAPIENS (HU-
 MAN)//Q92934
 F-PLACE1000081//HOMEODOMAIN PROTEIN HOX-A4 (HOX-1.4) (MH-3)//0.0053:146:33//MUS MUSCULUS
 15 (MOUSE)//P06798
 F-PLACE1000094
 F-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3)//
 1.8e-62:158:81//HOMO SAPIENS (HUMAN)//P20290
 F-PLACE1000142//ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.17) (SHORT CHAIN
 20 ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1)//9.8e-12:104:34//HOMO SAPIENS (HU-
 MAN)//P30084
 F-PLACE1000184//AC PROTEIN//0.44:31:29//BACTERIOPHAGE T4//P18924
 F-PLACE1000185//HYPOTHETICAL GLYCINE-RICH 49.6 KD PROTEIN CY130.10C PRECURSOR//0.11:48:
 33//MYCOBACTERIUM TUBERCULOSIS//Q10637
 25 F-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//3.4e-05:194:26//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//P08640
 F-PLACE1000214
 F-PLACE1000236//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//0.027:63:34//GALLUS GALLUS
 30 (CHICKEN)//P02457
 F-PLACE1000246//TEGUMENT PROTEIN (GENE 11 PROTEIN)//0.78:100:26//EQUINE HERPESVIRUS TYPE
 4 (STRAIN 1942) (EHV-4) (EQUINE HERPESVIRUS TYPE 1 SUBTYPE 2)//Q00039
 F-PLACE1000292
 F-PLACE1000308//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT)//0.049:28:42//MEDICAGO SATIVA
 35 (ALFALFA)//P11728
 F-PLACE1000332
 F-PLACE1000347//HYPOTHETICAL PROTEIN TP0420//0.15:24:54//TREPONEMA PALLIDUM//O83435
 F-PLACE1000374//LYSOZYME C (EC 3.2.1.17) (1,4-BETA-N-ACETYLMURAMIDASE C)//1.0:63:25//ORYC-
 TOLAGUS CUNICULUS (RABBIT)//P16973
 40 F-PLACE1000380//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE
 A INTERFERENCE PROTEIN)//0.018:169:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36027
 F-PLACE1000383//MYOTUBULARIN//1.2e-65:215:57//HOMO SAPIENS (HUMAN)//Q13496
 F-PLACE1000401//ELASTIN PRECURSOR (TROPOELASTIN)//0.00023:145:30//MUS MUSCULUS
 (MOUSE)//P54320
 45 F-PLACE1000406//54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB))//3.4e-27:90:63//HOMO SAPIENS
 (HUMAN)//Q15233
 F-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE)//4.7e-
 07:134:29//MUS MUSCULUS (MOUSE)//P53368
 F-PLACE1000421//HYPOTHETICAL 8.8 KD PROTEIN C11D3.01C IN CHROMOSOME I//0.48:72:27//
 50 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10080
 F-PLACE1000424
 F-PLACE1000435
 F-PLACE1000444//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.0e-31:129:63//HOMO SAPIENS (HU-
 MAN)//P39195
 55 F-PLACE1000453//PROTEIN Q300//0.013:16:68//MUS MUSCULUS (MOUSE)//Q02722
 F-PLACE1000481//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.14:63:36//HOMO SAPIENS (HU-
 MAN)//P08547
 F-PLACE1000492//BASP1 PROTEIN//0.17:114:28//HOMO SAPIENS (HUMAN)//P80723

F-PLACE1000540
 F-PLACE1000547//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE)//1.8e-21:87:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P41940
 5 F-PLACE1000562//HYPOTHETICAL PROTEIN MJ0562//1.0:35:34//METHANOCOCCUS JANNASCHII//Q57982
 F-PLACE1000564//ADRENAL SPECIFIC 30 KD PROTEIN (CLONE PG2)//0.13:66:37//HOMO SAPIENS (HUMAN)//P15803
 F-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//7.0e-45:192:47//HOMO SAPIENS (HUMAN)//P51522
 10 F-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1)//5.3e-63:122:88//HOMO SAPIENS (HUMAN)//P32455
 F-PLACE1000596//RING CANAL PROTEIN (KELCH PROTEIN)//2.6e-12:120:38//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652
 15 F-PLACE1000599//EARLY E3B 12.7 KD PROTEIN PRECURSOR//0.83:53:32//HUMAN ADENOVIRUS TYPE 12//P36707
 F-PLACE1000610
 F-PLACE1000611//HYPOTHETICAL 33.6 KD PROTEIN IN MCK1-RPS19B INTERGENIC REGION//9.4e-07:64:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48558
 20 F-PLACE1000636//MALE STERILITY PROTEIN 2//3.7e-09:83:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//Q08891
 F-PLACE1000653//PUTATIVE PHOSPHOACETYLGUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGUCOSAMINE-PHOSPHATE MUTASE)//1.9e-30:203:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09687
 25 F-PLACE1000656//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//0.0029:75:33//NICOTIANA TABACUM (COMMON TOBACCO)//P13983
 F-PLACE1000706//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1)//1.1e-38:180:42//HOMO SAPIENS (HUMAN)//Q13263
 F-PLACE1000712//VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSOR//0.93:49:34//MYCOBACTERIUM TUBERCULOSIS//P71934
 30 F-PLACE1000716
 F-PLACE1000748//HYPOTHETICAL 10.4 KD PROTEIN IN SPAT 3'REGION (ORF-11)//0.90:53:37//SHIGELLA FLEXNERI//P55794
 F-PLACE1000749//HYPOTHETICAL PROTEIN MG148//0.0014:142:27//MYCOPLASMA GENITALIUM//P47394
 35 F-PLACE1000755//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III//1.1e-15:98:48//CAENORHABDITIS ELEGANS//P34529
 F-PLACE1000769//VIGILIN//0.51:60:33//GALLUS GALLUS (CHICKEN)//P81021
 F-PLACE1000785//PROBABLE COLD SHOCK PROTEIN CY15C10.04//1.0:22:45//MYCOBACTERIUM TUBERCULOSIS//Q06360
 40 F-PLACE1000786//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III//2.6e-38:159:51//CAENORHABDITIS ELEGANS//P34657
 F-PLACE1000793//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP)//0.0097:128:30//HOMO SAPIENS (HUMAN)//P50552
 45 F-PLACE1000798//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.4e-07:47:61//HOMO SAPIENS (HUMAN)//P39188
 F-PLACE1000841
 F-PLACE1000849//ELAV PROTEIN//3.5e-05:140:35//DROSOPHILA VIRILIS (FRUIT FLY)//P23241
 F-PLACE1000856//HYPOTHETICAL PROTEIN MJ0008//0.95:100:23//METHANOCOCCUS JANNASCHII//Q60319
 50 F-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W//2.3e-46:172:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32899
 F-PLACE1000909//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//0.00022:105:35//HOMO SAPIENS (HUMAN)//P16157
 55 F-PLACE1000931//KILLER TOXIN HM-1//0.95:24:33//WILLIOPSIS MRAKII (YEAST) (HANSENULA MRAKII)//P10410
 F-PLACE1000948//SL CYTOKINE PRECURSOR (FLT3 LIGAND)//0.97:52:40//HOMO SAPIENS (HUMAN)//P49771

EP 1 074 617 A2

F-PLACE1000972//MYOSIN ID HEAVY CHAIN//1.9e-06:79:43//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P34109

F-PLACE1000977//HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME III//2.5e-23:105:41//CAENORHABDITIS ELEGANS//P46941

5 F-PLACE1000979//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF. 16)//0.91:83:30//HOMO SAPIENS (HUMAN)//P17097

F-PLACE1000987//HYPOTHETICAL 111.5 KD PROTEIN C22G7.02 IN CHROMOSOME I//0.10:128:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09796

F-PLACE1001000

10 F-PLACE1001007//ZYXIN//2.2e-05:135:30//GALLUS GALLUS (CHICKEN)//Q04584

F-PLACE1001010//BETA-1 BUNGAROTOXIN B CHAIN, MAJOR COMPONENT PRECURSOR (BUNGAROTOXIN, B1 CHAIN)//1.0:30:40//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT)//P00987

F-PLACE1001015

F-PLACE1001024

15 F-PLACE1001036

F-PLACE1001054//HOLOTRICIN 3 PRECURSOR//0.0044:56:39//HOLOTRICHIA DIOMPHALIA//Q25055

F-PLACE1001062//SACCHAROPINE DEHYDROGENASE [NADP+, L-GLUTAMATE FORMING] (EC 1.5.1.10)//0.0013:38:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38999

F-PLACE1001076

20 F-PLACE1001088//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT)//0.95:32:50//MEDICAGO SATIVA (ALFALFA)//P11728

F-PLACE1001092//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION//0.0026:81:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47057

F-PLACE1001104//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X//0.00063:125:32//CAENORHABDITIS ELEGANS//Q11102

25 F-PLACE1001118//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46)//2.6e-77:209:63//MUS MUSCULUS (MOUSE)//Q03309

F-PLACE1001136//ALPHA-N-ACETYLGALACTOSAMINIDASE PRECURSOR (EC 3.2.1.49) (ALPHA-GALACTOSIDASE B)//0.99:107:30//HOMO SAPIENS (HUMAN)//P17050

30 F-PLACE1001168

F-PLACE1001171//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT)//0.00012:37:59//HOMO SAPIENS (HUMAN)//P12895

F-PLACE1001185//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION//3.6e-12:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53867

35 F-PLACE1001238

F-PLACE1001241//METALLOTHIONEIN B (MTB) (FRAGMENT)//0.13:30:53//COLINUS VIRGINIANUS (BOBWHITE QUAIL) (COMMON BOBWHITE)//P27087

F-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN)//4.1e-24:125:46//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

40 F-PLACE1001272//HYPOTHETICAL PROTEIN IN KSGA 3'REGION (ORF L5) (FRAGMENT)//1.0:24:45//MYCOPLASMA CAPRICOLUM//P43040

F-PLACE1001279//CYTOTOXIN 3 (CYTOTOXIN V-II-3)//0.98:31:41//NAJA MOSSAMBICA (MOZAMBIQUE COBRA)//P01470

F-PLACE1001280//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN]//0.0051:156:32//MUS MUSCULUS (MOUSE)//P28481

45 F-PLACE1001294//GAMETOGENESIS EXPRESSED PROTEIN GEG-154//3.7e-56:109:93//MUS MUSCULUS (MOUSE)//P50636

F-PLACE1001304//ZINC FINGER PROTEIN 35 (ZFP-35)//3.2e-30:75:57//MUS MUSCULUS (MOUSE)//P15620

F-PLACE1001311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.7e-31:66:66//HOMO SAPIENS (HUMAN)//P39189

50 F-PLACE1001323

F-PLACE1001351//REV PROTEIN (ANTI-REPRESSION TRANSACTIVATOR PROTEIN) (ART/TRS)//0.11:66:27//SIMIAN IMMUNODEFICIENCY VIRUS (AGM155 ISOLATE) (SIV-AGM)//P27971

F-PLACE1001366//SHORT NEUROTOXIN 2 (TOXIN CM-14) (TOXIN V-N-12)//0.070:18:33//NAJA HAJE ANNULLIFERA (BANDED EGYPTIAN COBRA)//P01422

55 F-PLACE1001377//DISINTEGRIN TRIGRAMIN BETA (PLATELET AGGREGATION ACTIVATION INHIBITOR)//4.9e-06:50:46//TRIMERESURUS GRAMINEUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE)//P17495

F-PLACE1001383//M PROTEIN, SEROTYPE 49 PRECURSOR.//0.080:136:24//STREPTOCOCCUS PYO-
 GENES.//P16947
 F-PLACE1001384
 5 F-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//1.9e-22:142:
 39//HOMO SAPIENS (HUMAN).//Q12929
 F-PLACE1001395//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION.//0.98:67:34//
 BACTERIOPHAGE T4.//P22917
 F-PLACE1001399//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.1e-32:47:74//HOMO SAPIENS (HUMAN).//
 P39194
 10 F-PLACE1001412//GLYCOPHORIN C (PAS-2') (GLYCOPROTEIN BETA) (GLPC) (GLYCOCONNECTIN)
 (SIALOGLYCOPROTEIN D) (GLYCOPHORIN D) (GPD).//0.00021:125:36//HOMO SAPIENS (HUMAN).//P04921
 F-PLACE1001414//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//0.99:37:35//ASCARIS SUUM (PIG
 ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852
 F-PLACE1001440//PROLINE-RICH PEPTIDE P-B.//0.35:16:50//HOMO SAPIENS (HUMAN).//P02814
 15 F-PLACE1001456//RELAXIN.//0.48:38:36//BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER
 RORQUAL).//P11184
 F-PLACE1001468//HYPOTHETICAL PROTEIN MJ0602.//0.10:86:32//METHANOCOCCUS JANNASCHII.//
 Q58019
 F-PLACE1001484//HYPOTHETICAL 7.5 KD PROTEIN IN DNAC-RPLI INTERGENIC REGION.//1.0:47:34//BA-
 20 CILLUS SUBTILIS.//P37480
 F-PLACE1001502//COLLAGEN 1(X) CHAIN PRECURSOR.//0.00029:118:34//BOS TAURUS (BOVINE).//P23206
 F-PLACE1001503//HYPOTHETICAL 77.3 KD PROTEIN T05G5.8 IN CHROMOSOME III.//2.2e-07:107:30//
 CAENORHABDITIS ELEGANS.//P34561
 F-PLACE1001517//SMALL PROTEIN INHIBITOR OF INSECT ALPHA-AMYLASES 2 (SI ALPHA-2).//0.56:22:45//
 25 SORGHUM BICOLOR MILO (SORGHUM).//P21924
 F-PLACE1001534//PUTATIVE GENE PROTEIN 54.//0.43:44:40//BACTERIOPHAGE SP01.//O48408
 F-PLACE1001545//HYPOTHETICAL 7.9 KD PROTEIN IN CELF-KATE INTERGENIC REGION.//0.99:70:32//ES-
 CHERICHIA COLI.//P37795
 F-PLACE1001551//CHLOROPLAST 50S RIBOSOMAL PROTEIN L32.//1.0:66:28//MARCHANTIA POLYMOR-
 30 PHA (LIVERWORT).//P12196
 F-PLACE1001570//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//0.024:120:27//HOMO SAPI-
 ENS (HUMAN).//Q15431
 F-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.1e-30:90:78//MUS MUSCULUS (MOUSE).//
 Q60809
 35 F-PLACE1001603//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.054:
 77:33//RATTUS NORVEGICUS (RAT).//P10164
 F-PLACE1001608
 F-PLACE1001610//PROBABLE E4 PROTEIN.//0.90:58:29//HUMAN PAPILLOMAVIRUS TYPE 28.//P51896
 F-PLACE1001611//METALLOTHIONEIN-IG (MT-1G).//0.35:30:40//HOMO SAPIENS (HUMAN).//P13640
 40 F-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.6e-28:144:43//HOMO SA-
 PIENS (HUMAN).//P51523
 F-PLACE1001634//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//1.0:36:41//CYANIDIUM CALDARIUM
 (GALDIERIA SULPHURARIA).//O19926
 F-PLACE1001640//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.24:47:38//HUMAN IMMU-
 45 NODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804
 F-PLACE1001672//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.0:27:66//HOMO SAPIENS (HUMAN).//
 P39188
 F-PLACE1001691//HYPOTHETICAL 15.5 KD PROTEIN IN PIK1-POL2 INTERGENIC REGION.//0.40:81:33//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53842
 50 F-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)
 (THIOESTERASE II).//8.3e-41:103:55//RATTUS NORVEGICUS (RAT).//P08635
 F-PLACE1001705
 F-PLACE1001716//HYPOTHETICAL 138.5 KD PROTEIN C17H9.01 IN CHROMOSOME L.//6.1e-07:157:29//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13798
 55 F-PLACE1001720
 F-PLACE1001729//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//6.5e-05:196:32//MUS MUSCULUS
 (MOUSE).//P05143
 F-PLACE1001739//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//

EP 1 074 617 A2

0.00050:213:23//RATTUS NORVEGICUS (RAT)//P12839
 F-PLACE1001740//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.4e-17:90:56//HOMO SAPIENS (HUMAN)//
 P39188
 F-PLACE1001745//HYPOTHETICAL PROTEIN KIAA0125//0.96:38:36//HOMO SAPIENS (HUMAN)//Q14138
 5 F-PLACE1001746//CONGLUTIN DELTA-2 SMALL CHAIN//0.98:23:43//LUPINUS ANGUSTIFOLIUS (NARROW-
 LEAVED BLUE LUPINE)//P09930
 F-PLACE1001748//HYPOTHETICAL 99.0 KD PROTEIN SPBC119:17//2.9e-28:167:38//SCHIZOSACCHARO-
 MYCES POMBE (FISSION YEAST)//O42908
 F-PLACE1001756//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.2e-43:126:77//HOMO SAPIENS (HU-
 10 MAN)//P39189
 F-PLACE1001761//50S RIBOSOMAL PROTEIN L35//0.26:42:38//HELICOBACTER PYLORI (CAMPYLO-
 BACTER PYLORI)//P56057
 F-PLACE1001771//TRANSIENT-RECEPTOR-POTENTIAL LIKE PROTEIN//4.8e-35:223:40//DROSOPHILA
 MELANOGASTER (FRUIT FLY)//P48994
 15 F-PLACE1001781//HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION//9.5e-41:194:
 46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03262
 F-PLACE1001799
 F-PLACE1001810
 F-PLACE1001817//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUC-
 20 CINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA)//2.8e-40:115:61//NEOCALLIMASTIX FRONTALIS (RU-
 MEN FUNGUS)//P53587
 F-PLACE1001821
 F-PLACE1001844//IG KAPPA CHAIN V-I REGION (HAU)//0.59:89:35//HOMO SAPIENS (HUMAN)//P01600
 F-PLACE1001845
 25 F-PLACE1001869//MPA43 PROTEIN//3.5e-14:153:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P53583
 F-PLACE1001897//LIGATOXIN A//1.0:43:27//PHORADENDRON LIGA (ARGENTINE MISTLETOE)//P01540
 F-PLACE1001912//LONG NEUROTOXIN 2 (TOXIN C)//0.57:44:45//ASTROTIA STOKESI (STOKES'S SEA
 SNAKE) (DSTEIRA STOKESI)//P01381
 30 F-PLACE1001920//LATE GENES ACTIVATOR (EARLY PROTEIN GP4) (GPF)//0.89:75:29//BACTERIOPHAGE
 NF//P09877
 F-PLACE1001928
 F-PLACE1001983//IMMEDIATE-EARLY PROTEIN IE180//0.0049:51:45//PSEUDORABIES VIRUS (STRAIN KA-
 PLAN) (PRV)//P33479
 35 F-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4)//8.9e-08:125:36//MORAXELLA CATARRHALIS//Q49091
 F-PLACE1002004
 F-PLACE1002046//LIGATIN (FRAGMENT)//1.6e-84:191:84//MUS MUSCULUS (MOUSE)//Q61211
 F-PLACE1002052
 F-PLACE1002066
 40 F-PLACE1002072//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR//0.16:77:31//ARABIDOP-
 SIS THALIANA (MOUSE-EAR CRESS)//P40602
 F-PLACE1002073//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III//4.0e-11:174:28//
 CAENORHABDITIS ELEGANS//Q09564
 F-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72)//2.8e-57:112:99//HOMO SA-
 45 PIENS (HUMAN)//O76094
 F-PLACE1002115//P8 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE A) (MTCP-1 TYPE A)
 (P8MTCP1)//1.0:49:30//MUS MUSCULUS (MOUSE)//Q61908
 F-PLACE1002119//T-LYMPHOCYTE ACTIVATED PROTEIN (CYCLOHEXIMIDE-INDUCED) (CHX1) (IMMEDI-
 50 ATE EARLY RESPONSE 2 PROTEIN)//2.7e-11:118:36//MUS MUSCULUS (MOUSE)//P17950
 F-PLACE1002140//HYPOTHETICAL 12.3 KD PROTEIN IN MOBL 3'REGION (ORF 4)//0.0086:39:46//THIOBA-
 CILLUS FERROOXIDANS//P20088
 F-PLACE1002150
 F-PLACE1002157//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.4e-34:56:82//HOMO SAPIENS (HUMAN)//
 P39189
 55 F-PLACE1002163//NEUROTOXIN 1//1.0:17:52//CENTRUROIDES SCULPTURATUS (BARK SCORPION)//
 P01492
 F-PLACE1002170
 F-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT

SWI3) (TRANSCRIPTION FACTOR
 TYE2)//0.00023:179:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32591
 F-PLACE1002205//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION//0.77:21:47//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40490
 5 F-PLACE1002213//HISTONE H4 (FRAGMENT)//0.62:31:32//BLEPHARISMA JAPONICUM//P80738
 F-PLACE1002227//HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION//0.41:49:36//RHIZOBIUM LEGUMI-
 NOSARUM//P14310
 F-PLACE1002256//CYTOCHROME B (EC 1.10.2.2)//0.61:95:29//CAENORHABDITIS ELEGANS//P24890
 F-PLACE1002259//HYPOTHETICAL 9.2 KD PROTEIN IN SPS1-QCR7 INTERGENIC REGION//0.99:22:45//
 10 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P56508
 F-PLACE1002319//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION//0.91:18:72//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53867
 F-PLACE1002342//HYPOTHETICAL PROTEIN C16//1.0:53:32//SWINEPOX VIRUS (STRAIN KASZA) (SPV)//
 P32219
 15 F-PLACE1002395//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)//6.4e-05:127:37//PLASMODIUM
 VIVAX//P08677
 F-PLACE1002399
 F-PLACE1002433//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150)
 (DAP-150) (P150-GLUED)//0.00094:182:25//RATTUS NORVEGICUS (RAT)//P28023
 20 F-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1//4.5e-19:62:77//MUS MUSCULUS
 (MOUSE)//P41233
 F-PLACE1002438//HYPOTHETICAL 141.5 KD ZINC FINGER PROTEIN IN TUB1-CPR3 INTERGENIC RE-
 GION//0.014:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04545
 F-PLACE1002450//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT)//3.9e-28:159:38//XENOPUS
 25 LAEVIS (AFRICAN CLAWED FROG)//P18749
 F-PLACE1002465//LARIAT DEBRANCHING ENZYME (EC 3.1.-.-)//0.0014:148:28//SCHIZOSACCHAROMY-
 CES POMBE (FISSION YEAST)//O13765
 F-PLACE1002474//FIBRILLIN 2 PRECURSOR//2.1e-24:203:33//MUS MUSCULUS (MOUSE)//Q61555
 F-PLACE1002477//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.15:65:41//HOMO SAPIENS (HUMAN)//
 30 P39193
 F-PLACE1002493//SEMENOGELIN II PRECURSOR (SGII)//1.0:72:31//MACACA MULATTA (RHESUS
 MACAQUE)//Q95196
 F-PLACE1002499//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X//2.9e-11:67:35//
 CAENORHABDITIS ELEGANS//Q11096
 35 F-PLACE1002500//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PRO-
 TEIN CZCD)//8.4e-11:143:32//ALCALIGENES EUTROPHUS//P13512
 F-PLACE1002514//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (O71)//1.0:15:
 60//ESCHERICHIA COLI//P46878
 F-PLACE1002529
 40 F-PLACE1002532//HOMEOBOX PROTEIN DLX-5//1.1e-76:183:81//MUS MUSCULUS (MOUSE)//P70396
 F-PLACE1002537//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-18:51:86//HOMO SAPIENS (HUMAN)//
 P39195
 F-PLACE1002571//ACTIN-LIKE PROTEIN 13E//6.0e-56:140:47//DROSOPHILA MELANOGASTER (FRUIT
 FLY)//P45890
 45 F-PLACE1002578
 F-PLACE1002583
 F-PLACE1002591//CORONIN-LIKE PROTEIN P57//5.5e-26:78:69//BOS TAURUS (BOVINE)//Q92176
 F-PLACE1002598
 F-PLACE1002604
 50 F-PLACE1002625//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION//6.4e-08:193:
 23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04781
 F-PLACE1002655//ADSEVERIN (GELSOLIN-LIKE PROTEIN)//7.1e-100:210:89//MUS MUSCULUS (MOUSE)//
 Q60604
 F-PLACE1002665//MOBILIZATION PROTEIN MOBS//0.35:60:30//THIOBACILLUS FERROOXIDANS//P20086
 55 F-PLACE1002685//ACTIN BINDING PROTEIN//0.052:115:29//SACCHAROMYCES EXIGUUS (YEAST)//
 P38479
 F-PLACE1002714//CIS-GOLGI MATRIX PROTEIN GM130//1.8e-06:214:30//RATTUS NORVEGICUS (RAT)//
 Q62839

EP 1 074 617 A2

F-PLACE1002722//THROMBIN RECEPTOR PRECURSOR//2.0e-19:134:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P47749

F-PLACE1002768//FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) (FRAGMENT)//0.43:40:35//MUS MUSCULUS (MOUSE)//P35378

5 F-PLACE1002772

F-PLACE1002775//CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5)//4.8e-07:96:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14007

10 F-PLACE1002782//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PROTEIN CZCD)//1.1e-07:114:35//ALCALIGENES EUTROPHUS//P13512

F-PLACE1002794//CUTICLE COLLAGEN 12 PRECURSOR//0.0068:98:39//CAENORHABDITIS ELEGANS//P20630

F-PLACE1002811//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C)//1.1e-09:137:34//MUS MUSCULUS (MOUSE)//Q60772

15 F-PLACE1002815//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT)//0.46:35:42//HORDEUM VULGARE (BARLEY)//P17991

F-PLACE1002816//HYPOTHETICAL PROTEIN KIAA0288 (HA6116)//1.0e-86:201:74//HOMO SAPIENS (HUMAN)//P56524

20 F-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//1.6e-30:54:96//HOMO SAPIENS (HUMAN)//P51522

F-PLACE1002839//METALLOTHIONEIN-I (MT-I)//1.0:43:37//MUS MUSCULUS (MOUSE)//P02802

F-PLACE1002851//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (VAI)//0.77:35:37//VICIA ANGUSTIFOLIA (COMMON VETCH)//P01065

25 F-PLACE1002853//HYPOTHETICAL 7.9 KD PROTEIN IN PE 5'REGION (ORF1)//1.0:18:55//LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYHEDROSIS VIRUS (LDMNPV)//P36866

F-PLACE1002881//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.1e-27:91:70//HOMO SAPIENS (HUMAN)//P39188

F-PLACE1002908//HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III//2.0e-31:148:46//CAENORHABDITIS ELEGANS//P34548

30 F-PLACE1002941//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.6e-11:40:85//HOMO SAPIENS (HUMAN)//P39195

F-PLACE1002962//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT)//0.90:38:36//CANIS FAMILIARIS (DOG)//P13206

35 F-PLACE1002968//TOXIN IV-5 PRECURSOR (TITYUSTOXIN) (FRAGMENT)//0.97:26:38//TITYUS SERRULATUS (BRAZILIAN SCORPION)//P01496

F-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4)//3.3e-20:120:41//METHANOCOCCUS JANNASCHII//Q58560

F-PLACE1002993//HYPOTHETICAL 17.8 KD PROTEIN IN SMPA-SMPB INTERGENIC REGION (F158)//0.00045:93:23//ESCHERICHIA COLI//P52121

40 F-PLACE1002996//PUTATIVE REGULATORY PROTEIN TSC-22 (TGFB STIMULATED CLONE 22 HOMOLOG)//0.17:91:29//GALLUS GALLUS (CHICKEN)//Q91012

F-PLACE1003025//SUPPRESSOR PROTEIN SRP40//0.0079:214:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583

45 F-PLACE1003027//HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III//1.3e-49:167:63//CAENORHABDITIS ELEGANS//P34609

F-PLACE1003044//SPORE COAT PROTEIN D//0.97:24:45//BACILLUS SUBTILIS//P07791

F-PLACE1003045

F-PLACE1003092

50 F-PLACE1003100//HEP27 PROTEIN (PROTEIN D)//3.9e-51:188:57//HOMO SAPIENS (HUMAN)//Q13268

F-PLACE1003108

F-PLACE1003136

F-PLACE1003145//BUTYROPHILIN PRECURSOR (BT)//0.00024:170:24//BOS TAURUS (BOVINE)//P18892

F-PLACE1003153//HUNCHBACK PROTEIN (FRAGMENT)//1.0:32:37//LOCUSTA MIGRATORIA (MIGRATORY LOCUST)//Q01777

55 F-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)//6.3e-05:54:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P42743

F-PLACE1003176//HYPOTHETICAL 62.3 KD PROTEIN IN PCS60-ABD1 INTERGENIC REGION//0.24:74:36//

EP 1 074 617 A2

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38319
 F-PLACE1003190//SOF1 PROTEIN//1.0e-52:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
 P33750
 F-PLACE1003200
 5 F-PLACE1003205//SPERM PROTAMINE P1//0.074:20:45//CAENOLESTES FULIGINOSUS//P42131
 F-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001//0.013:20:55//HOMO SAPIENS
 (HUMAN).//Q15391
 F-PLACE1003249//HYPOTHETICAL PROTEIN KIAA0125//0.98:48:37//HOMO SAPIENS (HUMAN).//Q14138
 F-PLACE1003256//OMEGA-CONOTOXINS GVIA, GVIB AND GVIC PRECURSOR (SHAKER PEPTIDE).//0.84:
 10 53:30//CONUS GEOGRAPHUS (GEOGRAPHY CONE).//P01522
 F-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//4.1e-18:70:47//CAENORHABDITIS ELE-
 GANS.//P21541
 F-PLACE1003296//SPECTRIN BETA CHAIN, ERYTHROCYTE.//0.063:160:24//HOMO SAPIENS (HUMAN).//
 P11277
 15 F-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//9.4e-69:84:94//HOMO SAPI-
 ENS (HUMAN).//P51522
 F-PLACE1003334//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN).//
 0.029:125:24//RATTUS NORVEGICUS (RAT).//Q63083
 F-PLACE1003342//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.97:44:40//DROSOPHILA MELA-
 20 NOGASTER (FRUIT FLY).//Q01643
 F-PLACE1003343//GENE 11 PROTEIN.//1.0:37:37//SPIROPLASMA VIRUS SPV1-R8A2 B//P15902
 F-PLACE1003353//SH2/SH3 ADAPTOR CRK (ADAPTER MOLECULE CRK) (CRK2).//6.4e-05:69:40//XENOPUS
 LAEVIS (AFRICAN CLAWED FROG).//P87378
 F-PLACE1003361//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.6e-23:66:75//HOMO SAPIENS (HUMAN).//
 25 P39192
 F-PLACE1003366//SMALL PROLINE-RICH PROTEIN 2-1.//0.62:19:57//HOMO SAPIENS (HUMAN).//P35326
 F-PLACE1003369//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.3e-06:102:42//SACCHAROMY-
 CES CEREVISIAE (BAKER'S YEAST).//P32323
 F-PLACE1003373//PROTEIN Q300.//0.042:29:37//MUS MUSCULUS (MOUSE).//Q02722
 30 F-PLACE1003375//OLFACTORY RECEPTOR 11 (M49) (FRAGMENT).//0.99:46:34//MUS MUSCULUS
 (MOUSE).//Q60890
 F-PLACE1003383
 F-PLACE1003394//RAS-RELATED PROTEIN RAB-14.//2.8e-80:166:89//RATTUS NORVEGICUS (RAT).//
 P35287
 35 F-PLACE1003401
 F-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//8.1e-17:138:37//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//P40556
 F-PLACE1003454
 F-PLACE1003478
 40 F-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//3.4e-11:123:32//HOMO SAPIENS (HU-
 MAN).//Q13201
 F-PLACE1003516//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.0e-32:68:76//HOMO SAPIENS (HU-
 MAN).//P08547
 F-PLACE1003519//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.2e-17:77:50//HOMO SAPIENS (HUMAN).//
 45 P39188
 F-PLACE1003521//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:38:42//FOWLPOX VIRUS (ISOLATE HP-438
 [MUNICH]).//P14366
 F-PLACE1003528//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:32:40//XENOPUS LAEVIS (AFRI-
 CAN CLAWED FROG).//P03931
 50 F-PLACE1003537//CEF PROTEIN.//0.92:47:29//BACTERIOPHAGE T4.//Q01436
 F-PLACE1003553
 F-PLACE1003566//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:32:34//FOWLPOX VIRUS (ISOLATE HP-438
 [MUNICH]).//P14366
 F-PLACE1003575
 55 F-PLACE1003583//PROBABLE E5 PROTEIN.//0.16:64:31//HUMAN PAPILLOMAVIRUS TYPE 35.//P27226
 F-PLACE1003584
 F-PLACE1003592//EXCISIONASE.//0.26:19:52//BACTERIOPHAGE PHI-80.//P05998
 F-PLACE1003593//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:30//OVIS ARIES (SHEEP).//

O78751

F-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG//6.3e-87:238:67//CAENORHABDITIS ELEGANS//P46975

F-PLACE1003602//HYPOTHETICAL 11.0 KD PROTEIN IN FAA3-MAS3 INTERGENIC REGION//8.4e-17:98:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40554

F-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR//2.0e-09:82:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q02516

F-PLACE1003611//PANCREATIC SECRETORY TRYPSIN INHIBITOR//0.99:32:43//CANIS FAMILIARIS (DOG)//P04542

F-PLACE1003618//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.7e-65:229:58//HOMO SAPIENS (HUMAN)//P08547

F-PLACE1003625//30S RIBOSOMAL PROTEIN S20 (FRAGMENT)//1.0:56:26//PROTEUS MIRABILIS//P42275

F-PLACE1003638//PROTEIN Q300//0.079:41:39//MUS MUSCULUS (MOUSE)//Q02722

F-PLACE1003669//TRICHOHYALIN//2.9e-07:180:30//OVIS ARIES (SHEEP)//P22793

F-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75)//3.3e-16:98:40//HOMO SAPIENS (HUMAN)//Q08170

F-PLACE1003709//HYPOTHETICAL 59.5 KD PROTEIN IN CCT3-CCT8 INTERGENIC REGION//2.8e-07:128:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47074

F-PLACE1003711//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-IV)//5.0e-05:88:30//TRITICUM AESTIVUM (WHEAT)//P04724

F-PLACE1003723//TYROSINE-PROTEIN KINASE SRM (EC 2.7.1.112) (PTK70)//6.0e-06:98:36//MUS MUSCULUS (MOUSE)//Q62270

F-PLACE1003738//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT)//2.5e-45:147:46//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P18749

F-PLACE1003760//CYTOCHROME B (EC 1.10.2.2)//0.91:49:34//TRYPANOSOMA BRUCEI BRUCEI//P00164

F-PLACE1003762//METALLOTHIONEIN-LIKE PROTEIN TYPE 2//0.98:28:32//MALUS DOMESTICA (APPLE) (MALUS SYLVESTRIS)//Q24058

F-PLACE1003768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//8.5e-19:123:37//HOMO SAPIENS (HUMAN)//P08547

F-PLACE1003771

F-PLACE1003783//SRY-RELATED PROTEIN ADW2 (FRAGMENT)//1.0:29:37//ALLIGATOR MISSISSIPPIENSIS (AMERICAN ALLIGATOR)//P40634

F-PLACE1003784//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION//1.2e-13:199:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40164

F-PLACE1003795//EC PROTEIN I/II (ZINC-METALLOTHIONEIN CLASS II)//0.67:53:30//TRITICUM AESTIVUM (WHEAT)//P30569

F-PLACE1003833//METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9)//0.99:158:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS)//P43523

F-PLACE1003850

F-PLACE1003858//HUNCHBACK PROTEIN (FRAGMENT)//0.37:28:42//LITHOBIUS FORFICATUS//Q02030

F-PLACE1003864//OUTER MEMBRANE LIPOPROTEIN LOLB PRECURSOR//0.0046:116:31//ACTINOBACILLUS ACTINOMYCETEMCOMITANS (HAEMOPHILUS ACTINOMYCETEMCOMITANS)//Q52727

F-PLACE1003870

F-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT)//1.6e-92:166:75//HOMO SAPIENS (HUMAN)//P51003

F-PLACE1003886//IMMEDIATE-EARLY PROTEIN IE180//0.54:96:34//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV)//P11675

F-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT)//8.8e-54:260:46//BOS TAURUS (BOVINE)//P10895

F-PLACE1003892//PROBABLE E5 PROTEIN//1.0:13:61//HUMAN PAPILLOMAVIRUS TYPE 18//P06792

F-PLACE1003900//BETA-FRUCTOFURANOSIDASE, SOLUBLE ISOENZYME I (EC 3.2.1.26) (SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) (FRAGMENTS)//0.58:49:36//DAUCUS CAROTA (CARROT)//P80065

F-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE)//3.8e-52:92:85//HOMO SAPIENS (HUMAN)//P17812

F-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE-TRNA LIGASE) (ARGRS)//2.6e-26:202:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q05506

F-PLACE1003923//HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS)//0.94:
 65:29//STREPTOCOCCUS EQUISIMILIS//P30053
 F-PLACE1003932//HYPOTHETICAL 17.3 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION//0.098:79:31//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53074
 5 F-PLACE1003936
 F-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN)//
 4.7e-68:164:78//RATTUS NORVEGICUS (RAT)//P80385
 F-PLACE1004103//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.9e-14:60:73//HOMO SAPIENS (HUMAN)//
 P39192
 10 F-PLACE1004104//EXOCYST COMPLEX COMPONENT SEC5//0.020:202:20//SACCHAROMYCES CEREVI-
 SIAE (BAKER'S YEAST)//P89102
 F-PLACE1004114//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.1e-15:69:60//HOMO SAPIENS (HUMAN)//
 P39188
 F-PLACE1004118//REGULATORY PROTEIN E2//0.73:58:36//CANINE ORAL PAPILLOMAVIRUS (COPV)//
 15 Q89420
 F-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA
 CHAIN 4)//7.7e-62:108:100//MUS MUSCULUS (MOUSE)//P29387
 F-PLACE1004149//PROBABLE NUCLEAR ANTIGEN//0.0011:73:42//PSEUDORABIES VIRUS (STRAIN KAP-
 LAN) (PRV)//P33485
 20 F-PLACE1004156//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//0.00061:39:48//OWENIA FUSI-
 FORMIS//P21260
 F-PLACE1004161//PLASMINOGEN-BINDING PROTEIN PAM PRECURSOR (FRAGMENT)//0.033:108:27//
 STREPTOCOCCUS PYOGENES//P49054
 F-PLACE1004183//HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-ERP5 INTERGENIC REGION//4.0e-07:146:
 25 35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38817
 F-PLACE1004197//BUTYROPHILIN PRECURSOR (BT)//5.9e-11:208:27//MUS MUSCULUS (MOUSE)//
 Q62556
 F-PLACE1004203//PROTEIN A39//8.5e-18:139:33//VACCINIA VIRUS (STRAIN COPENHAGEN)//P21062
 F-PLACE1004242//PHOTOSYSTEM II REACTION CENTRE J PROTEIN//1.0:28:42//PISUM SATIVUM (GAR-
 30 DEN PEA)//P13555
 F-PLACE1004256//MYOSIN HEAVY CHAIN D (MHC D)//0.73:134:25//CAENORHABDITIS ELEGANS//P02567
 F-PLACE1004257//HYPOTHETICAL PROTEIN HI0490//0.13:75:29//HAEMOPHILUS INFLUENZAE//P44006
 F-PLACE1004258//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT)//0.027:128:
 35 35//HOMO SAPIENS (HUMAN)//P25067
 F-PLACE1004270//LARGE TEGUMENT PROTEIN//1.8e-10:100:44//EPSTEIN-BARR VIRUS (STRAIN B95-8)
 (HUMAN HERPESVIRUS 4)//P03186
 F-PLACE1004274//HYPOTHETICAL PROTEIN E-95//0.44:61:42//HUMAN ADENOVIRUS TYPE 2//P03286
 F-PLACE1004277//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.0013:55:38//BOS TAURUS (BOVINE)//
 P25508
 40 F-PLACE1004284//7 KD PROTEIN (ORF 4)//1.0:63:23//CHRYSANTHEMUM VIRUS B (CVB)//P37990
 F-PLACE1004289//SPERM PROTAMINE P3//0.00057:22:77//MUS MUSCULUS (MOUSE)//Q62100
 F-PLACE1004302//SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-)//0.0065:148:29//STREPTOMY-
 CES COELICOLOR//P54741
 F-PLACE1004316//AUTOPHAGY PROTEIN APG5//8.8e-06:117:29//SACCHAROMYCES CEREVISIAE (BAK-
 45 ER'S YEAST)//Q12380
 F-PLACE1004336//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR//0.0027:83:36//HOMO SAPIENS (HU-
 MAN)//P53420
 F-PLACE1004358//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//2.9e-05:200:33//GALLUS GALLUS
 (CHICKEN)//P02457
 50 F-PLACE1004376//AXONEME-ASSOCIATED PROTEIN MST101(2)//2.4e-05:179:29//DROSOPHILA HYDEI
 (FRUIT FLY)//Q08696
 F-PLACE1004384//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.6e-28:46:76//HOMO SAPIENS (HUMAN)//
 P39194
 F-PLACE1004388//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION//5.7e-34:202:
 55 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39722
 F-PLACE1004405//NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMINYLLAC-
 TOSE- BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH) (FLAGELLAR
 SHEATH ADHESIN) (ADHESIN A) (FRAGMENT)//0.93:74:33//HELICOBACTER ACINONYX//Q47947

F-PLACE1004425//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.81:70:42//HOMO SAPIENS (HUMAN)//
 P39195
 F-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-)//1.9e-31:203:39//RATTUS NORVEGICUS
 (RAT)//Q63448
 5 F-PLACE1004437//ISOCITRATE DEHYDROGENASE [NAD], MITOCHONDRIAL SUBUNIT BETA PRECURSOR
 (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD⁺-SPECIFIC ICDH) (FRAGMENT)//4.2e-93:140:100//
 MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY)//Q28479
 F-PLACE1004451//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00013:40:62//HOMO SAPIENS (HUMAN)//
 P39188
 10 F-PLACE1004460//MATERNAL TUDOR PROTEIN//0.0066:218:23//DROSOPHILA MELANOGASTER (FRUIT
 FLY)//P25823
 F-PLACE1004467//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.8e-10:33:87//HOMO SAPIENS (HUMAN)//
 P39193
 15 F-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//7.0e-56:92:58//HOMO SAPI-
 ENS (HUMAN)//P51522
 F-PLACE1004473//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I//0.019:136:27//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09844
 F-PLACE1004491//LYSIS PROTEIN//0.95:53:30//BACTERIOPHAGE FR//P19903
 F-PLACE1004506//AUTOIMMUNOGENIC CANCER/TESTIS ANTIGEN NY-ESO-1 (LAGE-1)//0.58:66:34//HO-
 20 MO SAPIENS (HUMAN)//P78358
 F-PLACE1004510//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150)//
 3.0e-07:63:46//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24325
 F-PLACE1004516//HYPOTHETICAL PROTEIN 5' TO ASP-RICH AND HIS-RICH PROTEINS (FRAGMENT)//
 0.95:62:29//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL)//P14587
 25 F-PLACE1004518//METALLOTHIONEIN 10-III (MT-10-III)//0.91:28:42//MYTILUS EDULIS (BLUE MUSSEL)//
 P80248
 F-PLACE1004548//DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAM-
 MA SUBUNIT//0.94:75:32//ORYCTOLAGUS CUNICULUS (RABBIT)//P19518
 F-PLACE1004550//CUTICLE COLLAGEN 2//0.90:155:31//CAENORHABDITIS ELEGANS//P17656
 30 F-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100
 KD SUBUNIT)//3.2e-70:121:100//BOS TAURUS (BOVINE)//Q10568
 F-PLACE1004629//PROTEIN OS-9 PRECURSOR//1.7e-10:132:36//HOMO SAPIENS (HUMAN)//Q13438
 F-PLACE1004645//TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (TFIIB)//0.00036:100:30//PYRO-
 COCCUS FURIOSUS//Q51731
 35 F-PLACE1004646//PROBABLE UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)//0.91:58:29//KLEBSIELLA
 PNEUMONIAE//Q48481
 F-PLACE1004658//GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 4 PRECURSOR (N-METHYL D-AS-
 PARTATE RECEPTOR SUBTYPE 2D) (NR2D) (NMDAR2D)//0.031:134:32//MUS MUSCULUS (MOUSE)//
 Q03391
 40 F-PLACE1004664//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION//0.025:125:
 20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04781
 F-PLACE1004672//HYPOTHETICAL 36.7 KD PROTEIN C2F7:14C IN CHROMOSOME I//7.6e-52:158:56//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09704
 F-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257)//1.4e-88:144:93//
 45 MUS MUSCULUS (MOUSE)//P12815
 F-PLACE1004681//CCR4-ASSOCIATED FACTOR 1 (CAF1)//1.0e-34:70:100//MUS MUSCULUS (MOUSE)//
 Q60809
 F-PLACE1004686//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.4e-08:48:62//HOMO SAPIENS (HUMAN)//
 P39192
 50 F-PLACE1004691//METALLOTHIONEIN (MT)//0.064:24:45//ARIANTA ARBUSTORUM//P55946
 F-PLACE1004693
 F-PLACE1004716//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:27:37//PAN PANISCUS (PYGMY
 CHIMPANZEE) (BONOBO)//Q35587
 F-PLACE1004722//HYPOTHETICAL 61.5 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION//0.95:53:33//
 55 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48565
 F-PLACE1004736//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22//0.014:163:30//RATTUS NORVEGI-
 CUS (RAT)//Q05175
 F-PLACE1004740//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.9e-09:37:70//HOMO SAPIENS (HUMAN)//

P39194
 F-PLACE1004743//HYPOTHETICAL 12.6 KD PROTEIN IN ALGR3 3'REGION.//0.99:72:33//PSEUDOMONAS
 AERUGINOSA.//P21484
 5 F-PLACE1004751//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANS-
 FERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST)
 (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4).//2.2e-08:90:38//HOMO SAPIENS (HUMAN).//Q11206
 F-PLACE1004773//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.2e-25:233:32//HOMO
 SAPIENS (HUMAN).//P16157
 10 F-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//8.1e-26:210:30//
 RATTUS NORVEGICUS (RAT).//P30337
 F-PLACE1004793//ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36].//0.00062:
 106:25//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10259
 F-PLACE1004804
 15 F-PLACE1004813//HYPOTHETICAL PROTEIN UL12.//1.0:22:40//HUMAN CYTOMEGALOVIRUS (STRAIN
 AD169).//P16777
 F-PLACE1004814//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//2.8e-06:136:25//
 CAENORHABDITIS ELEGANS.//Q09217
 F-PLACE1004815
 20 F-PLACE1004824//HYPOTHETICAL 106.7 KD PROTEIN IN MUP1-SPR3 INTERGENIC REGION.//2.3e-09:70:
 38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53236
 F-PLACE1004827//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3'REGION (ORF3).//0.54:25:56//BACILLUS LI-
 CHENIFORMIS.//P22754
 F-PLACE1004836//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.0066:12:66//BOS TAURUS (BOVINE).//P20072
 F-PLACE1004838
 25 F-PLACE1004840
 F-PLACE1004868//MALE STERILITY PROTEIN 2.//4.0e-16:172:30//ARABIDOPSIS THALIANA (MOUSE-EAR
 CRESS).//Q08891
 F-PLACE1004885
 30 F-PLACE1004900//MAST CELL DEGRANULATING PEPTIDE PRECURSOR (MCDP) (MCD) (PEPTIDE 401).//
 1.0:23:47//APIS MELLIFERA (HONEYBEE).//P01499
 F-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE
 SPAC10F6.02C.//7.3e-15:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42643
 F-PLACE1004913//HYPOTHETICAL 7.2 KD PROTEIN IN BCSA-DEGR INTERGENIC REGION.//1.0:42:33//BA-
 CILLUS SUBTILIS.//P54165
 35 F-PLACE1004918//HYPOTHETICAL 12.4 KD PROTEIN IN RPS21B-MRS3 INTERGENIC REGION.//0.98:50:34//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47012
 F-PLACE1004930//HYPOTHETICAL PROTEIN MJ0562.//0.82:44:36//METHANOCOCCUS JANNASCHII.//
 Q57982
 F-PLACE1004934
 40 F-PLACE1004937//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN
 CHROMOSOME I.//9.0e-10:87:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053
 F-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4.0e-14:184:25//
 CAENORHABDITIS ELEGANS.//Q11073
 F-PLACE1004972//BROMELAIN INHIBITOR 2 (BI-II) (BROMELAIN INHIBITOR VI) (BI-VI).//1.0:35:37//ANANAS
 COMOSUS (PINEAPPLE).//P27478
 45 F-PLACE1004979//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//5.3e-30:55:72//HOMO SAPIENS (HUMAN).//
 P39192
 F-PLACE1004982//M PROTEIN, SEROTYPE 12 PRECURSOR (FRAGMENT).//0.00049:124:27//STREPTO-
 COCCUS PYOGENES.//P19401
 50 F-PLACE1004985//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:26:34//LUMBRICUS TERRESTRIS
 (COMMON EARTHWORM).//Q34942
 F-PLACE1005026//TELOMERE-BINDING PROTEIN HOMOLOG.//0.0011:179:27//EUPLOTES CRASSUS.//
 Q06183
 F-PLACE1005027
 55 F-PLACE1005046//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.082:44:36//BOS TAURUS (BOVINE).//P20072
 F-PLACE1005052//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.38:36:44//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY).//Q01645
 F-PLACE1005055

EP 1 074 617 A2

F-PLACE1005066//RING CANAL PROTEIN (KELCH PROTEIN)//2.9e-38:194:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652
F-PLACE1005077
5 F-PLACE1005085//INSECT TOXIN 1 (BOT IT1)//0.85:36:33//BUTHUS OCCITANUS TUNETANUS (COMMON EUROPEAN SCORPION)//P55902
F-PLACE1005086//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/8.5e-38:93:76//HOMO SAPIENS (HUMAN)//P39194
F-PLACE1005101//HYPOTHETICAL PROTEIN ZAP128 (FRAGMENT)//1.6e-11:35:100//HOMO SAPIENS (HUMAN)//P49753
10 F-PLACE1005102//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13)//3.0e-14:110:38//MUS MUSCULUS (MOUSE)//Q60821
F-PLACE1005108//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF)//0.41:35:34//BOS TAURUS (BOVINE)//P37359
15 F-PLACE1005111//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) (CHARGERIN II)//1.0:29:41//RATTUS NORVEGICUS (RAT)//P11608
F-PLACE1005128//RABPHILIN-3A (FRAGMENT)//5.9e-05:95:36//MUS MUSCULUS (MOUSE)//P47708
F-PLACE1005146//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 15 (FIN15)//0.17:48:35//MUS MUSCULUS (MOUSE)//Q61075
20 F-PLACE1005162//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.0e-31:60:76//HOMO SAPIENS (HUMAN)//P39189
F-PLACE1005176
F-PLACE1005181//HYPOTHETICAL 7 KD PROTEIN//1.0:31:45//MEASLES VIRUS (STRAIN HALLE) (SUBACUTE SCLEROSE PANENCEPHALITIS VIRUS)//P06831
25 F-PLACE1005187//GLUCAN SYNTHASE-1 (EC 2.4.1.34) (1,3-BETA-GLUCAN SYNTHASE) (UDP-GLUCOSE-1,3-BETA-D-GLUCAN GLUCOSYLTRANSFERASE)//0.0025:58:34//NEUROSPORA CRASSA//P38678
F-PLACE1005206//HYPOTHETICAL 10.7 KD PROTEIN//0.34:57:42//VACCINIA VIRUS (STRAIN COPENHAGEN)//P20511
F-PLACE1005232//AMELOGENIN, Y ISOFORM PRECURSOR//0.70:60:35//HOMO SAPIENS (HUMAN)//Q99218
30 F-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-)//0.0017:114:27//PHYCOMYCES BLAKESLEEANUS//Q01577
F-PLACE1005261//HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II//1.2e-38:206:41//CAENORHABDITIS ELEGANS//Q10003
F-PLACE1005266
35 F-PLACE1005277//PROTEIN GURKEN PRECURSOR//0.58:95:29//DROSOPHILA MELANOGASTER (FRUIT FLY)//P42287
F-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP)//2.0e-12:211:29//GALLUS GALLUS (CHICKEN)//P53352
F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3)//1.8e-78:205:78//BOS TAURUS (BOVINE)//P08760
40 F-PLACE1005308//WOUND-INDUCED BASIC PROTEIN//0.99:40:40//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN)//Q09020
F-PLACE1005313//HYPOTHETICAL 8.7 KD PROTEIN IN LEUX-FECE INTERGENIC REGION (O67)//0.15:36:41//ESCHERICHIA COLI//P39355
45 F-PLACE1005327//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//1.0:19:52//HOMO SAPIENS (HUMAN)//P30808
F-PLACE1005331//BREAKPOINT CLUSTER REGION PROTEIN//0.00021:98:35//HOMO SAPIENS (HUMAN)//P11274
F-PLACE1005335//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3//0.37:98:33//MUS MUSCULUS (MOUSE)//P81067
50 F-PLACE1005373//PSEUDOURIDYLATE SYNTHASE 4 (EC 4.2.1.70) (PSEUDOURIDINE SYNTHASE 4) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLASE)//0.010:96:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48567
F-PLACE1005374
55 F-PLACE1005409
F-PLACE1005453//LICHENASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE)//1.0:50:32//NICOTIANA PLUMBAGINIFOLIA (LEADWORT-LEAVED TOBACCO)//P07979
F-PLACE1005467//KERATIN, FEATHER (F-KER)//0.0095:42:35//LARUS NOVAE-HOLLANDIAE (SILVER

GULL)//P02451
 F-PLACE1005471//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0.23:49:32//PHYTOPH-
 THORA INFESTANS (POTATO LATE BLIGHT FUNGUS)//Q37598
 F-PLACE1005477//HYPOTHETICAL PROTEIN ORF-1137//9.6e-13:115:38//MUS MUSCULUS (MOUSE)//
 5 P11260
 F-PLACE1005480//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT)//0.97:33:30//HORDEUM VULGARE (BAR-
 LEY)//P17991
 F-PLACE1005481//HUNCHBACK PROTEIN (FRAGMENT)//0.30:52:38//APIS MELLIFERA (HONEYBEE)//
 P31504
 10 F-PLACE1005494//TRANSIENT-RECEPTOR-POTENTIAL PROTEIN//3.9e-05:87:33//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//P19334
 F-PLACE1005502
 F-PLACE1005526//IMMEDIATE-EARLY PROTEIN IE180//4.6e-05:132:32//PSEUDORABIES VIRUS (STRAIN
 KAPLAN) (PRV)//P33479
 15 F-PLACE1005528//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.4e-09:31:74//HOMO SAPIENS (HUMAN)//
 P39195
 F-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III//9.7e-50:148:58//
 CAENORHABDITIS ELEGANS//Q09251
 F-PLACE1005550//HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III//3.0e-21:127:37//
 20 CAENORHABDITIS ELEGANS//P34524
 F-PLACE1005554//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT)//0.84:38:31//DIPODOMYS CALIFORNICUS
 (KANGAROO RAT)//P16359
 F-PLACE1005557//60S RIBOSOMAL PROTEIN L27//4.8e-09:60:48//CRYPTOCOCCUS NEOFORMANS (FILO-
 BASIDIELLA NEOFORMANS)//P46288
 25 F-PLACE1005574//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.89:44:29//BOS TAURUS (BOVINE)//
 P03929
 F-PLACE1005584//MALE SPECIFIC SPERM PROTEIN MST87F//0.00030:33:48//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//P08175
 F-PLACE1005595//IMMEDIATE-EARLY PROTEIN IE180//0.00048:162:30//PSEUDORABIES VIRUS (STRAIN
 30 INDIANA-FUNKHAUSER / BECKER) (PRV)//P11675
 F-PLACE1005603//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN)//
 0.00034:83:30//TETRAHYMENA PYRIFORMIS//P40625
 F-PLACE1005611//DNAJ PROTEIN//8.6e-20:108:48//CLOSTRIDIUM ACETOBUTYLICUM//P30725
 F-PLACE1005623//EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.-) (ERK5) (ERK4) (BMK1 KI-
 35 NASE)//0.80:116:31//HOMO SAPIENS (HUMAN)//Q13164
 F-PLACE1005630//INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT B-CELL GROWTH
 FACTOR) (HMW-BCGF)//0.0024:74:39//HOMO SAPIENS (HUMAN)//P40222
 F-PLACE1005639//EXTRACELLULAR MATRIX PROTEIN 1 (SECRETORY COMPONENT P85) (FRAGMENT)//
 0.72:18:61//RATTUS NORVEGICUS (RAT)//Q62894
 40 F-PLACE1005646//RNA HELICASE-LIKE PROTEIN DB10//4.8e-29:172:45//NICOTIANA SYLVESTRIS (WOOD
 TOBACCO)//P46942
 F-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLE-
 OTIDE REDUCTASE)//3.7e-64:133:75//MESOCRICETUS AURATUS (GOLDEN HAMSTER)//Q60561
 F-PLACE1005666//CHLOROPLAST 50S RIBOSOMAL PROTEIN L28//0.57:36.41//PORPHYRA PURPUREA//
 45 P51224
 F-PLACE1005698//HYPOTHETICAL PROTEIN IN SIGD 3'REGION (ORFC) (FRAGMENT)//0.50:61:29//BACIL-
 LUS SUBTILIS//P40405
 F-PLACE1005727//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT)//0.46:
 27:51//BRASSICA NAPUS (RAPE)//P40603
 50 F-PLACE1005730//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT)//0.95:21:52//ORYCTOLAGUS CUNICULUS
 (RABBIT)//P02456
 F-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11//3.4e-46:111:53//MUS MUSCULUS
 (MOUSE)//Q60710
 F-PLACE1005755//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION//2.6e-12:66:
 51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P42951
 55 F-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)
 (THIOESTERASE II)//1.5e-26:69:57//RATTUS NORVEGICUS (RAT)//P08635
 F-PLACE1005799//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN)//0.028:96:32//HOMO

SAPIENS (HUMAN)//P26371
 F-PLACE1005802//PROTEIN PROSPERO//0.86:64:42//DROSOPHILA MELANOGASTER (FRUIT FLY)//
 P29617
 F-PLACE1005803//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116//1.0:95:25//MUS
 5 MUSCULUS (MOUSE)//P17564
 F-PLACE1005804//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B)//
 2.8e-73:198:73//MUS MUSCULUS (MOUSE)//P39098
 F-PLACE1005813//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION//0.022:78:38//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47057
 10 F-PLACE1005828//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.8e-23:56:76//HOMO SAPIENS (HUMAN)//
 P39195
 F-PLACE1005834//LATE CONTROL GENE B PROTEIN (GPB)//0.97:33:39//BACTERIOPHAGE 186//P08711
 F-PLACE1005845
 F-PLACE1005850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.5e-28:96:73//HOMO SAPIENS (HUMAN)//
 15 P39194
 F-PLACE1005851
 F-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100
 KD SUBUNIT)//2.2e-99:155:95//BOS TAURUS (BOVINE)//Q10568
 F-PLACE1005884
 20 F-PLACE1005890//BEM46 PROTEIN (FRAGMENT)//1.8e-33:137:49//SCHIZOSACCHAROMYCES POMBE
 (FISSION YEAST)//P54069
 F-PLACE1005898//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3)
 (COMPLEX I-MLRQ) (CI-MLRQ)//0.77:58:34//HOMO SAPIENS (HUMAN)//O00483
 F-PLACE1005921//AIG1 PROTEIN//1.4e-23:165:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//
 25 P54120
 F-PLACE1005923//HYPOTHETICAL 22.4 KD PROTEIN (ORF16)//0.90:118:28//PARAMECIUM TETRAURE-
 LIA//P15617
 F-PLACE1005925//HYPOTHETICAL GENE 30 PROTEIN//0.94:57:29//HERPESVIRUS SAIMIRI (STRAIN 11)//
 Q01010
 30 F-PLACE1005932//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//
 0.42:128:32//NICOTIANA TABACUM (COMMON TOBACCO)//P13983
 F-PLACE1005934//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6)(RPB1) (FRAG-
 MENT)//0.40:76:35//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414
 F-PLACE1005936//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)//0.50:15:66//HUMAN IMMU-
 35 NODEFICIENCY VIRUS TYPE 1 (CLONE 12) (HIV-1)//P04326
 F-PLACE1005951//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//
 0.0025:135:32//NICOTIANA TABACUM (COMMON TOBACCO)//P13983
 F-PLACE1005953//HIGH POTENTIAL IRON-SULFUR PROTEIN (HIPIP)//0.64:57:33//RHODOFERAX FER-
 40 MENTANS//P80882
 F-PLACE1005955//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//1.0e-32:110:
 50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38821
 F-PLACE1005966//TACHYPLESIN II PRECURSOR//0.97:31:35//TACHYPLEUS TRIDENTATUS (JAPANESE
 HORSESHOE CRAB)//P14214
 F-PLACE1005968//GATA FACTOR SREP//0.17:52:40//PENICILLIUM CHRYSOGENUM//Q92259
 45 F-PLACE1005990//CELL PATTERN FORMATION-ASSOCIATED PROTEIN//0.36:55:36//EMERICELLA NIDU-
 LANS (ASPERGILLUS NIDULANS)//P36011
 F-PLACE1006002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.5e-36:102:75//HOMO SAPIENS (HU-
 MAN)//P39192
 F-PLACE1006003//HYPOTHETICAL 6.8 KD PROTEIN IN COX3-NAD1 INTERGENIC REGION (ORF 61)//1.0:
 50 22:40//MARCHANTIA POLYMORPHA (LIVERWORT)//P38473
 F-PLACE1006011//POLY [ADP-RIBOSE] POLYMERASE (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+)) ADP- RIBO-
 SYLTRANSFERASE) (POLY[ADP-RIBOSE] SYNTHETASE)//2.8e-21:163:36//ARABIDOPSIS THALIANA
 (MOUSE-EAR CRESS)//Q11207
 F-PLACE1006017//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-10:43:67//HOMO SAPIENS (HUMAN)//
 55 P39192
 F-PLACE1006037//VITELLOGENIN I PRECURSOR (VTG I) [CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN
 (PV); LIPOVITELLIN 2 (LV2)]//0.00019:123:37//FUNDULUS HETEROCLITUS (KILLIFISH) (MUMMICHOG)//
 Q90508

F-PLACE1006040//CAMP-REGULATED PHOSPHOPROTEIN 19 (ARPP-19)//3.2e-40:110:76//HOMO SAPIENS (HUMAN)//P56211
 F-PLACE1006076//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR A-II//0.99:30:40//ARACHIS HYPOGAEA (PEANUT)//P01066
 5 F-PLACE1006119//IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT) (RAN-BINDING PROTEIN 5)//8.8e-94:218:76//HOMO SAPIENS (HUMAN)//O00410
 F-PLACE1006129//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.00092:228:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323
 F-PLACE1006139//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION//5.9e-55:128:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43616
 10 F-PLACE1006143//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.4e-25:107:63//HOMO SAPIENS (HUMAN)//P39194
 F-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)//1.3e-21:168:32//SUS SCROFA (PIG)//P98110
 15 F-PLACE1006159//COLD SHOCK INDUCED PROTEIN TIR1 PRECURSOR (SERINE-RICH PROTEIN 1)//0.46:98:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P10863
 F-PLACE1006164//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0:70:28:42//ARTEMIA SALINA (BRINE SHRIMP)//P19049
 20 F-PLACE1006167//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//8.9e-05:167:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P08640
 F-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT)//1.1e-67:157:88//MUS MUSCULUS (MOUSE)//P17427
 25 F-PLACE1006187//G1/S-SPECIFIC CYCLIN E//5.6e-75:224:62//HOMO SAPIENS (HUMAN)//P24864
 F-PLACE1006195//T-RELATED PROTEIN (TRP) (BRACHYENTERON PROTEIN)//0.99:177:29//DROSOPHILA MELANOGASTER (FRUIT FLY)//P55965
 F-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06//2.0e-33:183:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09747
 30 F-PLACE1006205
 F-PLACE1006223//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.00015:22:50//MUS MUSCULUS (MOUSE)//P15265
 F-PLACE1006225//VIRION INFECTIVITY FACTOR (SOR PROTEIN)//1.0:63:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1)//P18805
 35 F-PLACE1006236
 F-PLACE1006239//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT)//0.48:23:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P51407
 F-PLACE1006246//CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR)//0.012:84:30//MUS MUSCULUS (MOUSE)//Q61420
 40 F-PLACE1006248//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140)//0.017:203:22//RATTUS NORVEGICUS (RAT)//P41777
 F-PLACE1006262//L-FUCULOSE PHOSPHATE ALDOLASE (EC 4.1.2.17)//0.84:25:52//HAEMOPHILUS INFLUENZAE//P44777
 45 F-PLACE1006288
 F-PLACE1006318//CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 (AFP1) (M1)//1.0:29:48//SINAPIS ALBA (WHITE MUSTARD) (BRASSICA HIRTA)//P30231
 F-PLACE1006325//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2)//0.99:97:32//HOMO SAPIENS (HUMAN)//P49918
 50 F-PLACE1006335//PROLINE-RICH PEPTIDE P-B//0.56:19:52//HOMO SAPIENS (HUMAN)//P02814
 F-PLACE1006357
 F-PLACE1006360
 F-PLACE1006368//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110)//0.0057:122:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32380
 55 F-PLACE1006371//ARS BINDING PROTEIN 1//0.00030:142:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P49777
 F-PLACE1006382//NEUROTOXIN V//0.85:28:39//ANDROCTONUS MAURETANICUS MAURETANICUS (SCORPION)//P01482

- F-PLACE1006385//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION//3.1e-35:165:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47160
F-PLACE1006412//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.3e-08:40:47//HOMO SAPIENS (HUMAN)//P08547
- 5 F-PLACE1006414//FORKHEAD-RELATED TRANSCRIPTION FACTOR 4 (FREAC-4)//3.8e-05:123:39//HOMO SAPIENS (HUMAN)//Q16676
F-PLACE1006438//ZINC FINGER PROTEIN 165//2.8e-21:76:64//HOMO SAPIENS (HUMAN)//P49910
F-PLACE1006445//SUPPRESSOR OF HAIRY WING PROTEIN//0.058:99:29//DROSOPHILA VIRILIS (FRUIT FLY)//Q08876
- 10 F-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME)//1.8e-64:177:50//ESCHERICHIA COLI//P27550
F-PLACE1006470
F-PLACE1006482//TRANSCRIPTION FACTOR MAFF//2.0e-47:120:85//GALLUS GALLUS (CHICKEN)//Q90595
- 15 F-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)//1.8e-85:173:95//CANIS FAMILIARIS (DOG)//Q00004
F-PLACE1006492//VERY HYPOTHETICAL 11.2 KD PROTEIN C56F8.13 IN CHROMOSOME I//0.75:32:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10261
F-PLACE1006506
F-PLACE1006521
- 20 F-PLACE1006531//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III//1.3e-53:167:61//CAENORHABDITIS ELEGANS//P34681
F-PLACE1006534
F-PLACE1006540
- 25 F-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT)//1.3e-07:242:23//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS)//P39922
F-PLACE1006598//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//0.17:43:51//HOMO SAPIENS (HUMAN)//P39190
F-PLACE1006615//ACROSIN PRECURSOR (EC 3.4.21.10)//3.6e-05:66:43//ORYCTOLAGUS CUNICULUS (RABBIT)//P48038
- 30 F-PLACE1006617//HYPOTHETICAL 14.6 KD PROTEIN (READING FRAME C) (REPUCATION)//1.0:74:29//STAPHYLOCOCCUS AUREUS//P03861
F-PLACE1006626//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III//2.9e-10:73:46//CAENORHABDITIS ELEGANS//P34529
- 35 F-PLACE1006629//HYPOTHETICAL PROTEIN BB0410//1.0:23:43//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)//Q051371
F-PLACE1006640
F-PLACE1006673
- 40 F-PLACE1006678//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT)//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT)//P02456
F-PLACE1006704//BROAD-COMPLEX CORE-TNT1-Q1-Z1 PROTEIN (BRCORE-TNT1-Q1-Z1) [CONTAINS: BROAD-COMPLEX CORE-Q1-Z1 PROTEIN]//0.00062:157:26//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01295
- 45 F-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE)//1.3e-07:127:36//CORYNEBACTERIUM AMMONIAGENES (BREVIBACTERIUM AMMONIAGENES)//Q59263
F-PLACE1006754//CARCINOEMBRYONIC ANTIGEN CGM1 PRECURSOR (CD66D ANTIGEN)//1.9e-19:78:53//HOMO SAPIENS (HUMAN)//P40198
- 50 F-PLACE1006760//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT)//0.21:107:30//RATTUS NORVEGICUS (RAT)//P13941
F-PLACE1006779//CYTOTOXIN 5 (CTXV)//1.0:20:30//NAJA MOSSAMBICA (MOZAMBIQUE COBRA)//P25517
F-PLACE1006782//ZINC FINGER PROTEIN 1//0.00052:178:28//CANDIDA ALBICANS (YEAST)//P28875
F-PLACE1006792
- 55 F-PLACE1006795//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAW (SHAW2)//1:0:80:30//DROSOPHILA MELANOGASTER (FRUIT FLY)//P17972
F-PLACE1006800//HYPOTHETICAL 9.4 KD PROTEIN//0.99:62:33//VACCINIA VIRUS (STRAIN COPENHAGEN)//P20569
F-PLACE1006805

- F-PLACE1006815//HYPOTHETICAL PROTEIN UL61//0.038:146:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169)//P16818
- F-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//7.3e-98:239:76//HOMO SAPIENS (HUMAN)//P08547
- 5 F-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8)//0.061:34:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P50102
- F-PLACE1006860
- F-PLACE1006867
- 10 F-PLACE1006878//HYPOTHETICAL 8.2 KD PROTEIN IN MOBL 3'REGION (ORF 3)//0.85:27:37//THIOBACILLUS FERROOXIDANS//P20087
- F-PLACE1006883//VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR)//0.78:51:37//MUS MUSCULUS (MOUSE)//P48281
- F-PLACE1006901//HYPOTHETICAL 8.1 KD PROTEIN//0.99:55:23//VACCINIA VIRUS (STRAIN COPENHAGEN)//P20567
- 15 F-PLACE1006904//MATING-TYPE LOCUS ALLELE B1 PROTEIN//0.95:86:26//USTILAGO MAYDIS (SMUT FUNGUS)//P22015
- F-PLACE1006917//HYPOTHETICAL 40.9 KD PROTEIN C08B11.5 IN CHROMOSOME II//6.9e-15:101:45//CAENORHABDITIS ELEGANS//Q09442
- 20 F-PLACE1006932//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE//0.089:28:39//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI)//Q48251
- F-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III//0.93:35:48//CAENORHABDITIS ELEGANS//Q10000
- F-PLACE1006956//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130)//0.00079:122:36//HOMO SAPIENS (HUMAN)//O00268
- 25 F-PLACE1006958//OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG-1)//8.8e-70:140:98//MUS MUSCULUS (MOUSE)//P48722
- F-PLACE1006961
- F-PLACE1006962//APOLOPOPROTEIN C-I PRECURSOR (APO-C1)//1.0:25:40//PAPIO HAMADRYAS (HAMADRYAS BABOON)//P34929
- 30 F-PLACE1006966//HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC REGION//1.6e-47:221:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40160
- F-PLACE1006989//HYPOTHETICAL 13.1 KD HIT-LIKE PROTEIN IN P37 5'REGION//0.15:46:32//MYCOPLASMA HYORHINIS//P32083
- 35 F-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12)//3.4e-09:120:29//HOMO SAPIENS (HUMAN)//Q14542
- F-PLACE1007021//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00046:42:59//HOMO SAPIENS (HUMAN)//P39188
- F-PLACE1007045//HYPOTHETICAL PROTEIN ORF-1137//8.1e-14:115:35//MUS MUSCULUS (MOUSE)//P11260
- 40 F-PLACE1007053//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.038:48:39//HOMO SAPIENS (HUMAN)//P22531
- F-PLACE1007068//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE)//0.0040:113:39//GALLUS GALLUS (CHICKEN)//Q05063
- 45 F-PLACE1007097//HYPOTHETICAL 6.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION//0.97:47:29//AUTOGRAPH A CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41663
- F-PLACE1007105//HYPOTHETICAL 83.6 KD PROTEIN C15A10.10 IN CHROMOSOME L//2.9e-33:219:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q13730
- F-PLACE1007111
- 50 F-PLACE1007112//HYPOTHETICAL 9.2 KD PROTEIN//0.47:75:28//ESCHERICHIA COLI//P03853
- F-PLACE1007132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.8e-11:56:57//HOMO SAPIENS (HUMAN)//P39188
- F-PLACE1007140//GAR2 PROTEIN//0.72:185:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P41891
- 55 F-PLACE1007178//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C//0.97:79:30//MYCOBACTERIUM TUBERCULOSIS//Q10826
- F-PLACE1007226//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION (O378)//1.9e-15:123:32//ESCHERICHIA COLI//P52062

F-PLACE1007238//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)//5.5e-10:98:44//ACANTHAMOEBA
 CASTELLANII (AMOEBA)//P19706
 F-PLACE1007239//TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR
 A)//3.9e-19:96:57//HOMO SAPIENS (HUMAN)//P23193
 5 F-PLACE1007242//GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM B (RALGEF)//1.0:
 132:30//RATTUS NORVEGICUS (RAT)//Q03386
 F-PLACE1007243//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION//0.041:114:29//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39981
 F-PLACE1007257//DIAPHANOUS PROTEIN//1.3e-42:205:46//DROSOPHILA MELANOGASTER (FRUIT
 10 FLY)//P48608
 F-PLACE1007274//CADMIUM-METALLOTHIONEIN (CD-MT)//0.054:60:30//HELIX POMATIA (ROMAN SNAIL)
 (EDIBLE SNAIL)//P33187
 F-PLACE1007276//BETA-DEFENSIN 1 PRECURSOR (RHBD-1) (DEFENSIN, BETA 1)//1.0:42:28//SUS SCRO-
 FA (PIG)//O62697
 15 F-PLACE1007282//OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CON-
 TAINS: OUTER CAPSID PROTEINS VP5 AND VP8]//0.070:126:27//HUMAN ROTAVIRUS (SEROTYPE 4 /
 STRAIN ST. THOMAS 3)//P11200
 F-PLACE1007286
 F-PLACE1007301//HYPOTHETICAL PROTEIN KIAA0168//0.042:61:39//HOMO SAPIENS (HUMAN)//P50749
 20 F-PLACE1007317
 F-PLACE1007342//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIV-
 ITY) (TRANSCRIPTION FACTOR NTF-1)//1.7e-06:77:36//DROSOPHILA MELANOGASTER (FRUIT FLY)//
 P13002
 F-PLACE1007346//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN)
 25 (KRIP-1)//0.0026:147:27//MUS MUSCULUS (MOUSE)//Q62318
 F-PLACE1007367//ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.3e-37:110:76//HOMO SAPIENS (HU-
 MAN)//P39189
 F-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13//4.7e-07:71:39//
 CAENORHABDITIS ELEGANS//P27715
 30 F-PLACE1007386//HYPOTHETICAL 7.6 KD PROTEIN IN FLO1-PHO11 INTERGENIC REGION//0.74:48:29//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39561
 F-PLACE1007402//TRANSCRIPTIONAL REGULATORY PROTEIN ENTR (ENTERICIDIN R)//0.99:63:36//CIT-
 ROBACTER FREUNDII//O69280
 F-PLACE1007409//WHITE PROTEIN//7.9e-38:179:41//DROSOPHILA MELANOGASTER (FRUIT FLY)//
 35 P10090
 F-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26)
 (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP)//0.031:159:23//HOMO SAPIENS
 (HUMAN)//P27487
 F-PLACE1007450//ZINC FINGER PROTEIN 39 (ZINC FINGER PROTEIN KOX27) (FRAGMENT)//0.023:36:50//
 40 HOMO SAPIENS (HUMAN)//P17038
 F-PLACE1007452//HYPOTHETICAL 22.1 KD PROTEIN IN CCP1-MET1 INTERGENIC REGION//2.2e-18:85:
 54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36149
 F-PLACE1007454//PHOTOSYSTEM II REACTION CENTRE N PROTEIN//0.66:13:53//CHLAMYDOMONAS RE-
 INHARDTII//Q06480
 45 F-PLACE1007460//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.93:45:33//SUS SCROFA (PIG)//Q35914
 F-PLACE1007478//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE
 (EC 2.7.7.49); ENDONUCLEASE]//5.3e-08:50:56//MUS MUSCULUS (MOUSE)//P11369
 F-PLACE1007484//HYPOTHETICAL 6.8 KD PROTEIN IN REPLICATION ORIGIN REGION//0.87:43:37//ES-
 CHERICHIA COLI//P03849
 50 F-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
 CIOGENITAL DYSPLASIA PROTEIN)//1.2e-25:202:31//HOMO SAPIENS (HUMAN)//P98174
 F-PLACE1007507//HYPOTHETICAL 16.0 KD PROTEIN IN TAF60-G4P1 INTERGENIC REGION//0.12:128:25//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53139
 F-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19)//2.1e-45:209:48//
 55 BOS TAURUS (BOVINE)//P08728
 F-PLACE1007524//HYPOTHETICAL 9.2 KD PROTEIN//0.74:80:30//VACCINIA VIRUS (STRAIN COPENHA-
 GEN)//P20550
 F-PLACE1007525

F-PLACE1007537//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN) //0.045:92:
 30//MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT) //P80144
 F-PLACE1007544//IMMEDIATE-EARLY PROTEIN IE180 //1.5e-07:59:50//PSEUDORABIES VIRUS (STRAIN
 KAPLAN) (PRV) //P33479
 5 F-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III //2.5e-16:188:34//
 CAENORHABDITIS ELEGANS //P34537
 F-PLACE1007557
 F-PLACE1007583//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT) //0.98:
 72:33//DAUCUS CAROTA (CARROT) //P06600
 10 F-PLACE1007598//ZINC FINGER PROTEIN 92 (ZINC FINGER PROTEIN HTF12) (FRAGMENT) //1.7e-11:88:
 43//HOMO SAPIENS (HUMAN) //Q03936
 F-PLACE1007618//ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (B3RP) //0.19:
 109:27//MUS MUSCULUS (MOUSE) //P13808
 F-PLACE1007621//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT) //0.98:34:
 15 41//PSEUDOMONAS AERUGINOSA //P23621
 F-PLACE1007632//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT) //0.70:110:34//BOS TAURUS (BOVINE) //
 P02465
 F-PLACE1007645//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) //0.99:20:45//STRUTHIO CAMELUS (OS-
 TRICH) //O21401
 20 F-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) //8.1e-06:197:26//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST) //P08640
 F-PLACE1007677//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!! //1.0:47:46//HOMO SAPIENS (HUMAN) //
 P39192
 25 F-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG) //
 2.7e-06:116:28//AEDES ALBOPICTUS (FOREST DAY MOSQUITO) //Q26457
 F-PLACE1007690//SPERM PROTAMINE P1 //0.12:26:50//TACHYGLOSSUS ACULEATUS ACULEATUS (AUS-
 TRALIAN ECHIDNA) //P35311
 F-PLACE1007697//SPERM PROTAMINE P1 //0.19:34:52//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH
 30 AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM) //P35305
 F-PLACE1007705//BIOH PROTEIN //0.015:97:29//ESCHERICHIA COLI //P13001
 F-PLACE1007706//HYPOTHETICAL 112.2 KD PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF1) //5.3e-
 55:190:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P32898
 F-PLACE1007725
 35 F-PLACE1007729//PROTEASE (EC 3.4.23.-) //1.8e-21:136:42//MOUSE MAMMARY TUMOR VIRUS (STRAIN
 BR6) //P10271
 F-PLACE1007730//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT) //0.0031:77:40//HOMO SAPIENS
 (HUMAN) //P81489
 F-PLACE1007737//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! //0.78:39:56//HOMO SAPIENS (HUMAN) //
 40 P39195
 F-PLACE1007743
 F-PLACE1007746//RRP5 PROTEIN HOMOLOG (KIAA0185) (FRAGMENT) //0.0066:168:25//HOMO SAPIENS
 (HUMAN) //Q14690
 F-PLACE1007791//KRUEPPEL PROTEIN (FRAGMENT) //0.62:17:41//LITHOBIUS FORFICATUS //Q01872
 45 F-PLACE1007807//HYPOTHETICAL 6.4 KD PROTEIN IN BLTR-SPOIII INTERGENIC REGION //1.0:40:30//BA-
 CILLUS SUBTILIS //P54446
 F-PLACE1007810//ANTHOPLEURIN A (TOXIN AP-A) //0.79:28:46//ANTHOPLEURA XANTHOGRAMMICA (GI-
 ANT GREEN SEA ANEMONE) //P01530
 F-PLACE1007829//SPORE COAT PROTEIN G //1.0:65:38//BACILLUS SUBTILIS //P39801
 50 F-PLACE1007843
 F-PLACE1007846//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //1.5e-32:37:94//HOMO SAPIENS (HU-
 MAN) //P08547
 F-PLACE1007852//RHO-RELATED GTP-BINDING PROTEIN RHOH (GTP-BINDING PROTEIN TTF) //8.7e-05:
 138:30//HOMO SAPIENS (HUMAN) //Q15669
 55 F-PLACE1007858//ANAPHASE SPINDLE ELONGATION PROTEIN //0.0039:127:25//SACCHAROMYCES CER-
 EVISIAE (BAKER'S YEAST) //P50275
 F-PLACE1007866
 F-PLACE1007877

F-PLACE1007897//CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EX-
 TRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR)
 (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (HAM1 ANTI-
 GEN)//0.44:128:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER)//Q60522
 5 F-PLACE1007908//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.5e-28:61:65//HOMO SAPIENS (HUMAN)//
 P39192
 F-PLACE1007946//HYPOTHETICAL MERCURIC RESISTANCE .PROTEIN MERC//0.84:48:37//PSEU-
 DOMONAS AERUGINOSA//P04139
 F-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION//0.00070:96:29//
 10 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38226
 F-PLACE1007955//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II//0.00027:255:23//
 CAENORHABDITIS ELEGANS//Q09625
 F-PLACE1007958//HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17)//
 1.7e-09:127:30//MUS MUSCULUS (MOUSE)//P70453
 15 F-PLACE1007969//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//2.4e-05:104:37//
 AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV)//P41479
 F-PLACE1007990//SPERM PROTAMINE P1//0.78:36:47//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLAT-
 YPUS)//P35307
 F-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DEN-
 20 SITY PROTEIN PSD-93)//1.2e-16:128:39//RATTUS NORVEGICUS (RAT)//Q63622
 F-PLACE1008002
 F-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NU-
 CLEOPORIN) (P105)//3.9e-106:208:93//RATTUS NORVEGICUS (RAT)//P52590
 F-PLACE1008045//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//3.9e-09:49:53//BOS TAURUS (BO-
 25 VINE)//P25508
 F-PLACE1008080//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48)//0.00025:100:27//EGGPLANT MOSAIC VI-
 RUS//P20126
 F-PLACE1008095//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO)//0.90:74:25//MYCOBACTERIUM
 TUBERCULOSIS//O53230
 30 F-PLACE1008111//HYPOTHETICAL PROTEIN MJCS12//0.30:38:42//METHANOCOCCUS JANNASCHII//
 Q60311
 F-PLACE1008122//PEA2 PROTEIN (PPF2 PROTEIN)//0.0085:117:34//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//P40091
 F-PLACE1008129//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS)//1.8e-06:154:36//GAL-
 35 LUS GALLUS (CHICKEN)//P02467
 F-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III//1.4e-13:227:36//
 CAENORHABDITIS ELEGANS//Q09531
 F-PLACE1008177//TRICHOHYALIN//2.7e-10:230:26//OVIS ARIES (SHEEP)//P22793
 F-PLACE1008181
 40 F-PLACE1008198//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//0.00044:121:34//
 XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437
 F-PLACE1008201//ZINC FINGER PROTEIN ZFMSA12A//3.0e-05:82:37//MICROPTERUS SALMOIDES
 (LARGEMOUTH BASS)//P38621
 F-PLACE1008209//METALLOTHIONEIN-I (MT-I)//0.95:39:35//CERCOPITHECUS AETHIOPS (GREEN MON-
 45 KEY) (GRIVET)//P02797
 F-PLACE1008231//PROCYCLIC FORM SPECIFIC POLYPEPTIDE B1-ALPHA PRECURSOR (PROCYCLIN)
 (PARP)//0.028:23:52//TRYPANOSOMA BRUCEI BRUCEI//P08469
 F-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//2.2e-23:148:38//PODOSPORA AN-
 SERINA//Q00808
 50 F-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//1.1e-97:222:
 81//BOS TAURUS (BOVINE)//P53620
 F-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-)//5.8e-20:161:37//SACCHAROMYCES CEREVI-
 SIAE (BAKER'S YEAST)//P12689
 F-PLACE1008280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.1e-23:124:42//HOMO SAPIENS (HU-
 55 MAN)//P08547
 F-PLACE1008309//HYPOTHETICAL 98.3 KD PROTEIN C9G1.06C IN CHROMOSOME I//0.47:99:37//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14302
 F-PLACE1008329//PUTATIVE Z PROTEIN//0.73:52:28//OVIS ARIES (SHEEP)//P08105

F-PLACE1008330//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-37:75:81//HOMO SAPIENS (HUMAN)//
 P39194
 F-PLACE1008331//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.1e-08:70:50//HOMO SAPIENS (HUMAN)//
 P39188
 5 F-PLACE1008356//FRUIT PROTEIN PKIW1501 //0.0037:148:29//ACTINIDIA CHINENSIS (KIWI) (YANGTAO)//
 P43393
 F-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN)//3.5e-18:205:30//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q04652
 F-PLACE1008369
 10 F-PLACE1008392
 F-PLACE1008398//GENE 33 POLYPEPTIDE//1.5e-102:225:84//RATTUS NORVEGICUS (RAT)//P05432
 F-PLACE1008401//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//2.9e-08:186:34//MUS MUSCULUS
 (MOUSE)//P05143
 F-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED
 15 PROTEIN) (TAP)//9.4e-105:207:98//BOS TAURUS (BOVINE)//P41541
 F-PLACE1008405
 F-PLACE1008424//PROTEIN UL56//1.0:65:33//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN HFEM)//P36297
 F-PLACE1008426//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II)//4.4e-05:185:28//
 DROSOPHILA MELANOGASTER (FRUIT FLY)//Q09323
 20 F-PLACE1008429//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22//0.00054:172:25//RATTUS NOR-
 VEGICUS (RAT)//Q05175
 F-PLACE1008437//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III//1.9e-23:226:34//
 CAENORHABDITIS ELEGANS//P34681
 F-PLACE1008455//DNA-BINDING PROTEIN (AGNOPROTEIN)//0.97:23:52//BUDGERIGAR FLEDGLING DIS-
 25 EASE VIRUS (BFDV)//P13893
 F-PLACE1008457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.1e-12:89:47//HOMO SAPIENS (HUMAN)//
 P39188
 F-PLACE1008465//ZINC FINGER PROTEIN 31 (ZINC FINGER PROTEIN KOX29) (FRAGMENT)//0.00017:23:
 43//HOMO SAPIENS (HUMAN)//P17040
 30 F-PLACE1008488//HYPOTHETICAL PROTEIN UL61//9.1e-05:204:30//HUMAN CYTOMEGALOVIRUS
 (STRAIN AD169)//P16818
 F-PLACE1008524//HOMEODOMAIN PROTEIN HLX1 (HOMEODOMAIN PROTEIN HB24)//0.95:74:36//HOMO SAPIENS
 (HUMAN)//Q14774
 F-PLACE1008531//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.1e-05:86:45//HOMO SAPIENS (HUMAN)//
 35 P39192
 F-PLACE1008532//HYPOTHETICAL 36.4 KD PROTEIN IN SMP1-MBA1 INTERGENIC REGION//3.9e-21:62:
 45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38298
 F-PLACE1008533//HYPOTHETICAL 86.2 KD PROTEIN C4G8.04 IN CHROMOSOME I//3.5e-06:118:29//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09830
 40 F-PLACE1008568//NEURONATIN//0.046:34:52//HOMO SAPIENS (HUMAN)//Q16517
 F-PLACE1008584//HUNCHBACK PROTEIN (FRAGMENT)//0.94:30:43//LITHOBIUS FORFICATUS//Q02030
 F-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NU-
 CLEOPORIN) (P140)//3.9e-123:224:96//RATTUS NORVEGICUS (RAT)//P37199
 F-PLACE1008621//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD)//5.0e-05:31:67//HOMO SAPIENS
 45 (HUMAN)//P20931
 F-PLACE1008625//DISAGREGIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)//0.87:17:52//ORNI-
 THODOROS MOUBATA (SOFT TICK)//P36235
 F-PLACE1008626//METALLOTHIONEIN-I (MT-I)//0.77:33:36//SCYLLA SERRATA (MUD CRAB)//P02805
 F-PLACE1008627//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB)//0.14:44:
 50 31//HOMO SAPIENS (HUMAN)//P25713
 F-PLACE1008629
 F-PLACE1008630//PROTAMINE Z3 (SCYLLIORHININE Z3)//0.78:33:36//SCYLLIORHINUS CANICULA (SPOT-
 TED DOGFISH) (SPOTTED CATSHARK)//P30258
 F-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN
 55 H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN
 SENSITIVE GLYCOPROTEIN 120) (PK-120)//1.7e-30:220:41//HOMO SAPIENS (HUMAN)//Q14624
 F-PLACE1008650//PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1//2.5e-10:106:31//ARABI-
 DOPSIS THALIANA (MOUSE-EAR CRESS)//Q42384

F-PLACE1008693//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI)//1.0:36:38//MEDICAGO SCUTEL-
 LATA (SNAIL MEDIC)//P80321
 F-PLACE1008696//NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC
 1.6.99.3) (COMPLEX I-23KD) (CI-23KD) (TYKY SUBUNIT)//4.8e-14:47:80//HOMO SAPIENS (HUMAN)//
 5 O00217
 F-PLACE1008715//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION//0.66:105:24//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38834
 F-PLACE1008748//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//0.10:178:
 26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214
 10 F-PLACE1008757//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3)//0.60:
 44:34//ESCHERICHIA COLI//P33669
 F-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA
 S2)//3.0e-69:191:80//MUS MUSCULUS (MOUSE)//O35345
 F-PLACE1008798//BACTERIOCIN LACTOBIN A//1.0:34:41//LACTOBACILLUS AMYLOVORUS //P80696
 15 F-PLACE1008807//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.91:77:36//HOMO SAPIENS (HU-
 MAN)//P08547
 F-PLACE1008808//REC1 PROTEIN//0.45:39:30//USTILAGO MAYDIS (SMUT FUNGUS)//P14746
 F-PLACE1008813
 F-PLACE1008851//VERY HYPOTHETICAL 11.8 KD PROTEIN IN KTR3-DUR1,2 INTERGENIC REGION//1.0:
 20 62:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38309
 F-PLACE1008854//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION//1.0:82:26//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47170
 F-PLACE1008867//PATATIN T5 PRECURSOR (POTATO TUBER PROTEIN)//0.65:61:36//SOLANUM TUBERO-
 SUM (POTATO)//P15478
 25 F-PLACE1008887//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.5e-56:180:54//NYCTICEBUS COU-
 CANG (SLOW LORIS)//P08548
 F-PLACE1008902
 F-PLACE1008920
 F-PLACE1008925//HYPOTHETICAL 41.2 KD PROTEIN IN GAPA-RND INTERGENIC REGION//0.90:77:33//ES-
 30 CHERICHIA COLI//P76242
 F-PLACE1008934//HYPOTHETICAL PROTEIN IN ADHS 5'REGION (ORF3) (FRAGMENT)//0.14:77:45//GLU-
 CONOBACTER SUBOXIDANS//O05543
 F-PLACE1008941//ZINC FINGER PROTEIN 141//1.1e-17:45:95//HOMO SAPIENS (HUMAN)//Q15928
 F-PLACE1008947//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)//4.1e-
 14:136:39//MUS MUSCULUS (MOUSE)//P27790
 35 F-PLACE1009020//ANNEXIN VII (SYNEXIN) (FRAGMENT)//0.74:37:48//BOS TAURUS (BOVINE)//P20072
 F-PLACE1009027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0.39:57:36//BALAENOP-
 TERA MUSCULUS (BLUE WHALE)//P41301
 F-PLACE1009039
 40 F-PLACE1009045//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83)//0.48:32:
 43//ESCHERICHIA COLI//P46879
 F-PLACE1009048
 F-PLACE1009050
 F-PLACE1009060//HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III//4.9e-23:244:31//
 45 CAENORHABDITIS ELEGANS//P34552
 F-PLACE1009090//50S RIBOSOMAL PROTEIN L35//1.0:27:51//MYCOPLASMA GENITALIUM//P47439
 F-PLACE1009091
 F-PLACE1009094//NEL-LIKE PROTEIN (FRAGMENT)//3.6e-15:180:30//HOMO SAPIENS (HUMAN)//Q92832
 F-PLACE1009099//ZINC FINGER PROTEIN 27 (ZFP-27) (MKR4 PROTEIN) (FRAGMENT)//1.4e-94:228:71//
 50 MUS MUSCULUS (MOUSE)//P10077
 F-PLACE1009110//HIRUDIN HV1 (BUFRUDIN)//1.0:49:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH)//
 P81492
 F-PLACE1009111//!!!! ALU SUBFAMILY SX WARNING ENTRY!!!!//1.4e-05:30:83//HOMO SAPIENS (HUMAN)//
 P39195
 55 F-PLACE1009113//ANNEXIN VII (SYNEXIN) (FRAGMENT)//0.032:40:52//BOS TAURUS (BOVINE)//P20072
 F-PLACE1009130//HYPOTHETICAL PROTEIN KIAA0032//3.3e-37:214:38//HOMO SAPIENS (HUMAN)//
 Q15034
 F-PLACE1009150//!!!! ALU SUBFAMILY SX WARNING ENTRY!!!!//1.6e-32:56:76//HOMO SAPIENS (HUMAN)//

P39195
 F-PLACE1009155//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-17:101:57//HOMO SAPIENS (HUMAN)//P39194
 5 F-PLACE1009158//HYPOTHETICAL PROTEIN HKRFX (J11)//0.0058:73:42//HUMAN CYTOMEGALOVIRUS (STRAIN AD169)//P09711
 F-PLACE1009166//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5)//0.0086:96:30//HOMO SAPIENS (HUMAN)//P49902
 F-PLACE1009172//HYPOTHETICAL 8.7 KD PROTEIN IN GAPA-RND INTERGENIC REGION//1.0:19:52//ESCHERICHIA COLI//P76246
 10 F-PLACE1009174//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-17:47:82//HOMO SAPIENS (HUMAN)//P39194
 F-PLACE1009183
 F-PLACE1009186//HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOME I//0.019:62:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09783
 15 F-PLACE1009190//PALMITOYL-COA HYDROLASE (EC 3.1.2.2) (LONG-CHAIN FATTY-ACYL-COA HYDROLASE) (FRAGMENT)//0.027:53:28//RATTUS NORVEGICUS (RAT)//P80250
 F-PLACE1009200//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.4e-28:84:71//HOMO SAPIENS (HUMAN)//P39194
 F-PLACE1009230//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.8e-12:50:74//HOMO SAPIENS (HUMAN)//P39189
 20 F-PLACE1009246//UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (EC 1.10.2.2) (MITOCHONDRIAL HINGE PROTEIN) (CR7)//1.0:17:52//SOLANUM TUBEROSUM (POTATO)//P48504
 F-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35//6.6e-41:177:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P34110
 25 F-PLACE1009308//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN)//0.00034:108:33//HOMO SAPIENS (HUMAN)//P26371
 F-PLACE1009319//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95)//5.3e-16:84:50//HOMO SAPIENS (HUMAN)//P78352
 F-PLACE1009328//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.9e-82:263:67//HOMO SAPIENS (HUMAN)//P08547
 30 F-PLACE1009335//60S RIBOSOMAL PROTEIN L32//0.95:71:36//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT)//P02433
 F-PLACE1009338//TRANSCRIPTION FACTOR HES-5 (HAIRY AND ENHANCER OF SPLIT 5)//0.90:42:40//MUS MUSCULUS (MOUSE)//P70120
 35 F-PLACE1009368//BASIC PROLINE-RICH PEPTIDE IB-1//0.013:33:48//HOMO SAPIENS (HUMAN)//P04281
 F-PLACE1009375//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III//0.0022:135:21//CAENORHABDITIS ELEGANS//P34492
 F-PLACE1009388//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-22:73:65//HOMO SAPIENS (HUMAN)//P39195
 40 F-PLACE1009398//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//8.1e-83:223:65//HOMO SAPIENS (HUMAN)//P51523
 F-PLACE1009404//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR//0.047:145:29//TRITICUM AESTIVUM (WHEAT)//P08489
 F-PLACE1009410//TOXIN C13S1C1 PRECURSOR//0.22:21:47//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA)//P18329
 45 F-PLACE1009434//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K (EC 1.6.5.3) (FRAGMENT)//0.81:61:29//ANTHOCEROS FORMOSAE//Q31791
 F-PLACE1009443//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//9.1e-05:93:32//MUS MUSCULUS (MOUSE)//Q62203
 50 F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA)//6.4e-15:41:97//HOMO SAPIENS (HUMAN)//P42356
 F-PLACE1009459//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I//0.0011:119:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09874
 F-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP)//4.2e-34:101:75//RATTUS NORVEGICUS (RAT)//P54319
 55 F-PLACE1009476//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.086:21:52//HOMO SAPIENS (HUMAN)//P30808
 F-PLACE1009477

F-PLACE1009493//HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOME X.//1.4e-18:138:39//
 CAENORHABDITIS ELEGANS.//Q11069
 F-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FAC-
 TOR).//9.4e-80:155:85//HOMO SAPIENS (HUMAN).//Q99418
 5 F-PLACE1009539//GTP-BINDING NUCLEAR PROTEIN RAN/TC4.//1.0:76:26//GIARDIA LAMBLIA (GIARDIA IN-
 TESTINALIS).//P38543
 F-PLACE1009542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00016:31:77//HOMO SAPIENS (HUMAN).//
 P39188
 F-PLACE1009571//ATP SYNTHASE B CHAIN (EC 3.6.1.34) (SUBUNIT I).//0.88:116:29//STREPTOCOCCUS
 10 PNEUMONIAE.//Q59952
 F-PLACE1009581//50S RIBOSOMAL PROTEIN L32.//0.00023:37:51//RHODOBACTER CAPSULATUS (RHO-
 DOPSEUDOMONAS CAPSULATA).//P30788
 F-PLACE1009595
 F-PLACE1009596//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHRO-
 15 MOSOME III.//2.1e-36:116:49//CAENORHABDITIS ELEGANS.//Q17963
 F-PLACE1009607//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.8e-43:73:69//HOMO SAPIENS (HUMAN).//
 P39188
 F-PLACE1009613
 F-PLACE1009621//TRANSCRIPTION FACTOR BTF3 HOMOLOG 2.//0.91:29:44//HOMO SAPIENS (HUMAN).//
 20 Q13891
 F-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3e-22:132:47//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY).//P25159
 F-PLACE1009637//HYPOTHETICAL 18.1 KD PROTEIN IN CFXA 3'REGION.//0.30:28:57//BACTEROIDES VUL-
 GATUS.//P30905
 25 F-PLACE1009639//LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN).//0.23:79:31//PSEU-
 DOMONAS AERUGINOSA.//Q04591
 F-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (BRAIN PROTEIN H19) (MH19) (FRAG-
 MENT).//3.9e-126:227:96//MUS MUSCULUS (MOUSE).//P28660
 F-PLACE1009665//IG KAPPA CHAIN V-I REGION (HAU).//0.52:89:35//HOMO SAPIENS (HUMAN).//P01600
 30 F-PLACE1009670//CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19) (CYCLO-
 DEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).//0.16:114:29//PAENIBACILLUS MACERANS (BACILLUS
 MACERANS).//P31835
 F-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN
 CHROMOSOME I.//9.6e-19:156:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09876
 35 F-PLACE1009721//MSF1 PROTEIN.//7.7e-23:176:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
 P35200
 F-PLACE1009731//AIG1 PROTEIN.//1.1e-09:91:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//
 P54120
 F-PLACE1009763//HYPOTHETICAL 48.9 KD PROTEIN C24H6.12C IN CHROMOSOME I.//8.3e-42:171:51//
 40 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09765
 F-PLACE1009794//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.99:36:33//HORDEUM VULGARE (BAR-
 LEY).//P17991
 F-PLACE1009798//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT).//2.6e-34:191:
 38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779
 45 F-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.2e-19:190:33//SACCHA-
 ROMYCES CEREVISIAE (BAKER'S YEAST).//P38968
 F-PLACE1009861//CATHEPSIN B PRECURSOR (EC 3.4.22.1).//4.4e-20:171:33//BOS TAURUS (BOVINE).//
 P07688
 F-PLACE1009879//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.99:
 50 30:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779
 F-PLACE1009886
 F-PLACE1009888//NONSTRUCTURAL POLYPROTEIN [CONTAINS: NONSTRUCTURAL PROTEIN NSP4]
 (FRAGMENT).//1.0:33:42//WESTERN EQUINE ENCEPHALITIS VIRUS.//P13896
 F-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN CHROMOSOME I.//3.1e-42:205:
 55 46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10190
 F-PLACE1009921
 F-PLACE1009924//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.70:128:29//TRYPANOSOMA BRU-
 CEI BRUCEI.//P24499

- F-PLACE1009925//ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34)//0.99:111:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P30902
- F-PLACE1009935//HYPOTHETICAL PROTEIN MJ0258//0.063:75:32//METHANOCOCCUS JANNASCHII//Q57706
- 5 F-PLACE1009947//NEUROGRANIN (NG) (P17) (B-50 IMMUNOREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT)//0.33:51:45//BOS TAURUS (BOVINE)//P35722
- F-PLACE1009971//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN)//0.022:84:27//MUS MUSCULUS (MOUSE)//P28575
- F-PLACE1009992//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1)//0.00011:35:51//HOMO SAPIENS (HUMAN)//P13497
- 10 F-PLACE1009995//TROPOMYOSIN, SMOOTH MUSCLE/FIBROBLAST CTM1//0.052:185:22//CIONA INTESTINALIS//Q07068
- F-PLACE1009997//TRANSCRIPTION ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FACTOR DMS-II) (TFIIS)//0.68:98:28//DROSOPHILA MELANOGASTER (FRUIT FLY)//P20232
- 15 F-PLACE1010023//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III//6.6e-06:111:32//CAENORHABDITIS ELEGANS//Q18262
- F-PLACE1010031//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//0.0024:72:33//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV)//P41479
- F-PLACE1010053//HYPOTHETICAL PROTEIN HI0593//0.83:24:45//HAEMOPHILUS INFLUENZAE//P44022
- 20 F-PLACE1010069
- F-PLACE1010074//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5//0.00027:192:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q92331
- F-PLACE1010076//HUNCHBACK PROTEIN (FRAGMENT)//0.80:39:30//SCIARA COPROPHILA (FUNGUS GNAT)//Q01790
- 25 F-PLACE1010083//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131)//2.7e-48:177:46//HOMO SAPIENS (HUMAN)//P98171
- F-PLACE1010089//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 11) (KIAA0055)//7.9e-07:55:43//HOMO SAPIENS (HUMAN)//P40818
- 30 F-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-)//1.0e-107:232:90//RATTUS NORVEGICUS (RAT)//Q62671
- F-PLACE1010102//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6)//1.0:33:45//METHANOCOCCUS JANNASCHII//Q57649
- F-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN)//1.2e-47:200:46//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652
- 35 F-PLACE1010106//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//1.2e-14:94:41//MUS MUSCULUS (MOUSE)//P11369
- F-PLACE1010134//HYPOTHETICAL 171.5 KD HELICASE IN NUT1-ARO2 INTERGENIC REGION//4.0e-28:78:76//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53115
- F-PLACE1010148//GAR2 PROTEIN//2.6e-05:180:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P41891
- 40 F-PLACE1010152//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)//2.1e-59:227:54//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24574
- F-PLACE1010181//MALE SPECIFIC SPERM PROTEIN MST87F//0.39:12:58//DROSOPHILA MELANOGASTER (FRUIT FLY)//P08175
- 45 F-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)//1.4e-07:95:43//GALLUS GALLUS (CHICKEN)//P30352
- F-PLACE1010202//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36)//0.094:109:29//RATTUS NORVEGICUS (RAT)//P47973
- 50 F-PLACE1010231//LANTIBIOTIC NISIN A PRECURSOR//0.99:42:35//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS)//P13068
- F-PLACE1010261//SEGREGATION DISTORTER PROTEIN//6.0e-71:201:62//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25722
- F-PLACE1010270
- 55 F-PLACE1010274//HYPOTHETICAL 16.2 KD PROTEIN C4F8.01 IN CHROMOSOME I//4.4e-08:100:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14177
- F-PLACE1010293//ALU SUBFAMILY J WARNING ENTRY !!!!!//3.9e-26:94:64//HOMO SAPIENS (HUMAN)//P39188

F-PLACE1010310//SYNAPSINS IA AND IB //5.7e-09:89:37//RATTUS NORVEGICUS (RAT)//P09951
 F-PLACE1010321//IMMEDIATE-EARLY PROTEIN IE180//0.033:145:31//PSEUDORABIES VIRUS (STRAIN KA-
 PLAN) (PRV)//P33479
 F-PLACE1010324//MAST CELL DEGRANULATING PEPTIDE (MCDP) (MCD)//0.60:25:48//MEGABOMBUS
 5 PENNSYLVANICUS (AMERICAN COMMON BUMBLEBEE)//P04567
 F-PLACE1010329//TOXIN S5C10//1.0:39:33//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S
 MAMBA)//P01419
 F-PLACE1010341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.0049:49:55//HOMO SAPIENS (HUMAN)//
 P39189
 10 F-PLACE1010362//VARIANT-SURFACE-GLYCOPROTEIN PHOSPHOLIPASE C (EC 3.1.4.47) (VSG LIPASE)
 (GLYCOSYLPHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (GPI-PLC)//0.0034:89:30//
 TRYPANOSOMA CRUZI//015886
 F-PLACE1010364//NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COM-
 PLEX I-B17) (CI-B17)//1.0:40:35//SUS SCROFA (PIG)//Q29259
 15 F-PLACE1010383
 F-PLACE1010401//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140)//0.10:174:22//RATTUS NORVEGI-
 CUS (RAT)//P41777
 F-PLACE1010481//HYPOTHETICAL 71.9 KD PROTEIN B0285.5 IN CHROMOSOME III//1.5e-21:170:35//
 CAENORHABDITIS ELEGANS//P46555
 20 F-PLACE1010491//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION//1.0:31:41//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40490
 F-PLACE1010492//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I//0.77:97:30//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09874
 F-PLACE1010522//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.74:45:37//HOMO SAPIENS
 25 (HUMAN)//P22531
 F-PLACE1010529//DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE
 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE
 (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIAL-
 DEHYDE DEHYDROGENASE)]//0.70:58:39//VIGNA ACONITIFOLIA (MOTHBEAN)//P32296
 30 F-PLACE1010547//HYPOTHETICAL 31.0 KD PROTEIN IN BUD9-RME1 INTERGENIC REGION//0.17:68:39//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53227
 F-PLACE1010562//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33//0.50:48:29//PORPHYRA PURPUREA//
 P51255
 F-PLACE1010579//HYPOTHETICAL PROTEIN HI1571//0.29:37:43//HAEMOPHILUS INFLUENZAE//P44260
 35 F-PLACE1010580//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06//3.3e-38:178:48//SCHIZOSAC-
 CHAROMYCES POMBE (FISSION YEAST)//Q09747
 F-PLACE1010599//PEROXISOMAL MEMBRANE PROTEIN PER10 (PEROXIN-14)//4.6e-17:192:31//PICHIA
 ANGUSTA (YEAST) (HANSENULA POLYMORPHA)//P78723
 F-PLACE1010616//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION//0.44:32:37//PSEUDOMONAS PUT-
 40 IDA//P25753
 F-PLACE1010622//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//5.0e-06:102:42//SACCHAROMY-
 CES CEREVISIAE (BAKER'S YEAST)//P32323
 F-PLACE1010624//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-
 MENT)//0.00036:134:321//HOMO SAPIENS (HUMAN)//P10162
 45 F-PLACE1010628
 F-PLACE1010629//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-12:37:81//HOMO SAPIENS (HUMAN)//
 P39194
 F-PLACE1010630
 F-PLACE1010631//WNT-5B PROTEIN (FRAGMENT)//0.49:62:30//EUMECES SKILTONIANUS (WESTERN
 50 SKINK)//P28118
 F-PLACE1010661//MATERNAL EXUPERANTIA 2 PROTEIN//1.0:95:30//DROSOPHILA PSEUDOOBSCURA
 (FRUIT FLY)//Q24617
 F-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)
 (DUGT)//3.2e-05:117:24//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q09332
 55 F-PLACE1010702//ZINC FINGER PROTEIN 195//1.4e-62:117:62//HOMO SAPIENS (HUMAN)//O14628
 F-PLACE1010714
 F-PLACE1010720//CHROMOSOME ASSEMBLY PROTEIN XCAP-C//1.1e-64:176:76//XENOPUS LAEVIS (AF-
 RICAN CLAWED FROG)//P50532

F-PLACE1010739//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT)//0.97:31:41//
 HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1)//P04612
 F-PLACE1010743//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//3.8e-05:253:30//MUS MUSCULUS
 (MOUSE)//P05143
 5 F-PLACE1010761//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II//1.5e-14:175:25//
 CAENORHABDITIS ELEGANS//Q09217
 F-PLACE1010771//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP//1.3e-120:216:89//MUS MUSCULUS
 (MOUSE)//Q02614
 F-PLACE1010786//CENTROSOMIN (ARROW PROTEIN)//0.97:133:24//DROSOPHILA MELANOGASTER
 10 (FRUIT FLY)//P54623
 F-PLACE1010800//HYPOTHETICAL 31.7 KD PROTEIN IN TRAX-FINO INTERGENIC REGION (ORFC)//
 0.0060:111:31//ESCHERICHIA COLI//Q99390
 F-PLACE1010802//UREASE ACCESSORY PROTEIN UREI//0.82:44:29//BACILLUS SP. (STRAIN TB-90)//
 Q07415
 15 F-PLACE1010811//CYTOCHROME C-551 (C551)//0.99:42:38//ECTOTHIORHODOSPIRA HALOCHLORIS//
 P38587
 F-PLACE1010833//CALTRACTIN, ISOFORM 1 (CENTRIN)//2.8e-09:90:34//HOMO SAPIENS (HUMAN)//
 P41208
 F-PLACE1010856//MOLT-INHIBITING HORMONE (MIH)//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP
 20 CRAYFISH)//P55848
 F-PLACE1010857//IG ALPHA-1 CHAIN C REGION//0.49:73:34//GORILLA GORILLA GORILLA (LOWLAND GO-
 RILLA)//P20758
 F-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.2e-56:173:58//HO-
 MO SAPIENS (HUMAN)//Q05481
 25 F-PLACE1010877//HEAT SHOCK PROTEIN 82//0.13:130:25//ZEA MAYS (MAIZE)//Q08277
 F-PLACE1010891//HYPOTHETICAL 8.2 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION//0.95:51:27//
 BACILLUS SUBTILIS//P54436
 F-PLACE1010896//SERINE/THREONINE-PROTEIN KINASE PTK1/STK1 (EC 2.7.1.)/0.98:71:30//SACCHA-
 ROMYCES CEREVISIAE (BAKER'S YEAST)//P36002
 30 F-PLACE1010900//HYPOTHETICAL PROTEIN HI0840//1.0:42:30//HAEMOPHILUS INFLUENZAE//P44897
 F-PLACE1010916//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB3//0.060:59:35//OVIS ARIES (SHEEP)//
 P02444
 F-PLACE1010917//E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PELOMER PROTEIN)//
 0.71:141:24//BOVINE CORONAVIRUS (STRAIN L9)//P25191
 35 F-PLACE1010925//HYPOTHETICAL 8.1 KD PROTEIN//1.0:17:58//THERMOPROTEUS TENAX VIRUS 1
 (STRAIN KRA1) (TTV1)//P19285
 F-PLACE1010926//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269//0.011:51:45//HOMO SAPIENS (HU-
 MAN)//Q92558
 F-PLACE1010942//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN
 40 EPS15)//3.1e-09:64:37//MUS MUSCULUS (MOUSE)//P42567
 F-PLACE1010944//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44)//0.17:71:38//BOS TAURUS
 (BOVINE)//P41987
 F-PLACE1010947
 F-PLACE1010954//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE//0.011:144:26//HOMO SAPIENS
 45 (HUMAN)//P09493
 F-PLACE1010960//ACTIN-LIKE PROTEIN 13E//1.1 e-60:136:52//DROSOPHILA MELANOGASTER (FRUIT
 FLY)//P45890
 F-PLACE1010965
 F-PLACE1011026//PERIOD CLOCK PROTEIN (FRAGMENT)//1.0:64:31//DROSOPHILA ANANASSAE (FRUIT
 50 FLY)//Q03293
 F-PLACE1011032//RIBONUCLEASE HI (EC 3.1.26.4) (RNASE HI) (RIBONUCLEASE H) (RNASE H)//1.0:32:37//
 SALMONELLA TYPHIMURIUM//P23329
 F-PLACE1011041//HOMEBOX PROTEIN VAB-7//0.36:65:30//CAENORHABDITIS ELEGANS//Q93899
 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC
 55 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154)//1.3e-22:58:93//RATTUS NORVEGI-
 CUS (RAT)//P10687
 F-PLACE1011054//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-07:38:73//HOMO SAPIENS (HUMAN)//
 P39195

F-PLACE1011056//HISTONE H1 //2.2e-10:109:41//PISUM SATIVUM (GARDEN PEA)//P08283
 F-PLACE1011057
 F-PLACE1011090//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLO5 INTERGENIC REGION//1.8e-07:133:
 32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38892
 5 F-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)//5.4e-25:63:88//RAT-
 TUS NORVEGICUS (RAT)//Q07803
 F-PLACE1011114//PUTATIVE ATP-DEPENDENT RNA HELICASE C1F7.02C//8.4e-31:157:45//SCHIZOSAC-
 CHAROMYCES POMBE (FISSION YEAST)//Q09916
 F-PLACE1011133//SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1-GLYCOPRO-
 10 TEIN)//0.92:58:31//HOMO SAPIENS (HUMAN)//P02743
 F-PLACE1011143//PROBABLE E5 PROTEIN//0.24:42:35//HUMAN PAPILLOMAVIRUS TYPE31//P17385
 F-PLACE1011160//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315)//0.88:98:27//GLYCINE MAX
 (SOYBEAN)//Q02917
 F-PLACE1011165//HISTIDINE-RICH PROTEIN//0.013:13:76//PLASMODIUM FALCIPARUM (ISOLATE FCM17 /
 15 SENEGAL)//P14586
 F-PLACE1011185//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.4e-13:98:50//HOMO SAPIENS (HUMAN)//
 P39188
 F-PLACE1011203
 F-PLACE1011214//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:48:27//EQUUS ASINUS (DONKEY)//
 20 P92479
 F-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-)//1.9e-15:162:31//STREPTOMYCES ANTIBI-
 OTICUS//Q03326
 F-PLACE1011221//ANTITHROMBIN-III HOMOLOG//0.84:74:33//FOWLPOX VIRUS (ISOLATE HP-438[MU-
 NICH])//P14369
 25 F-PLACE1011229//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-
 RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-
 TOUS NUCLEAR PROTEIN HOMOLOG)//3.5e-86:218:68//HOMO SAPIENS (HUMAN)//Q13107
 F-PLACE1011263//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT)//
 3.0e-07:99:36//HOMO SAPIENS (HUMAN)//Q01485
 30 F-PLACE1011273
 F-PLACE1011291//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS)//0.011:36:50//RATTUS
 NORVEGICUS (RAT)//P20468
 F-PLACE1011296//HOMEBOX PROTEIN DLX-6//0.76:55:32//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA
 DANIO)//Q98877
 35 F-PLACE1011310//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN)//
 0.46:43:44//PETUNIA SP. (PETUNIA)//Q07060
 F-PLACE1011325//HYPOTHETICAL 222.8 KD PROTEIN C1F3.06C IN CHROMOSOME I//0.00021:171:27//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10411
 F-PLACE1011332//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR//7.3e-27:113:52//
 40 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//Q05211
 F-PLACE1011340//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.6e-07:40:62//HOMO SAPIENS (HUMAN)//
 P39188
 F-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN
 H2)//2.2e-54:227:44//MUS MUSCULUS (MOUSE)//Q61703
 45 F-PLACE1011375//PROBABLE E5 PROTEIN//0.93:28:57//HUMAN PAPILLOMAVIRUS TYPE 51//P26553
 F-PLACE1011399//HISTONE H2B-IV//0.19:129:27//VOLVOX CARTERI//P16868
 F-PLACE1011419
 F-PLACE1011433//ZINC FINGER PROTEIN GLI3 (FRAGMENT)//3.4e-05:133:24//GALLUS GALLUS (CHICK-
 EN)//P55879
 50 F-PLACE1011452//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//3.9e-25:76:63//HOMO SAPIENS (HU-
 MAN)//P08547
 F-PLACE1011465//ECTODERMAL DYSPLASIA PROTEIN (EDA PROTEIN)//0.97:36:41//HOMO SAPIENS (HU-
 MAN)//Q92838
 F-PLACE1011472//METALLOTHIONEIN-1 (CUMT-1)//0.084:55:30//HOMARUS AMERICANUS (AMERICAN
 55 LOBSTER)//P29499
 F-PLACE1011477//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER
 PROTEIN 1)//0.028:129:34//CLOSTRIDIUM THERMOCELLUM//Q06852
 F-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)//

2.9e-13:147:31//BRASSICA OLERACEA (CAULIFLOWER)//P52178
 F-PLACE1011503//PUTATIVE FERREDOXIN-LIKE PROTEIN IN PURL-DPJ INTERGENIC REGION (086)//0.66:
 32:40//ESCHERICHIA COLI//P52102
 F-PLACE1011520
 5 F-PLACE1011563//LORICRIN//0.00023:112:39//HOMO SAPIENS (HUMAN)//P23490
 F-PLACE1011567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.2e-31:78:76//HOMO SAPIENS (HUMAN)//
 P39195
 F-PLACE1011576//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.5e-32:45:86//HO-
 MO SAPIENS (HUMAN)//Q05481
 10 F-PLACE1011586//N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN-SENSITIVE N-
 TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT)//0.26:81:37//HOMO SAPIENS (HUMAN)//Q00975
 F-PLACE1011635//IMMEDIATE-EARLY PROTEIN IE180//0.00045:170:30//PSEUDORABIES VIRUS (STRAIN
 INDIANA-FUNKHAUSER/BECKER) (PRV)//P11675
 F-PLACE1011641
 15 F-PLACE1011643//CUTICLE COLLAGEN 40//1.0:128:32//CAENORHABDITIS ELEGANS//P34804
 F-PLACE1011646//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-15:44:63//HOMO SAPIENS (HUMAN)//
 P39188
 F-PLACE1011649//HYPOTHETICAL PROTEIN F-215//0.48:106:34//HUMAN ADENOVIRUS TYPE 2//P03291
 F-PLACE1011650
 20 F-PLACE1011664//CROOKED NECK PROTEIN//1.2e-79:201:68//DROSOPHILA MELANOGASTER (FRUIT
 FLY)//P17886
 F-PLACE1011675//FERREDOXIN//1.0:44:29//METHANOCOCCUS THERMOLITHOTROPHICUS//P21305
 F-PLACE1011682//HYPOTHETICAL 7.0 KD PROTEIN IN RPS26A-COX4 INTERGENIC REGION//1.0:40:22//
 SAGCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53098
 25 F-PLACE1011719//NEUROTOXIN TX2-6//0.90:31:35//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPI-
 DER)//P29425
 F-PLACE1011725//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN)//
 0.0065:125:25//RATTUS NORVEGICUS (RAT)//Q63083
 F-PLACE1011729//SRV-RELATED PROTEIN LG27 (FRAGMENT)//0.97:48:39//EUBLEPHARIS MACULAR-
 IUS//P40654
 30 F-PLACE1011749
 F-PLACE1011762//D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN)//0.028:91:39//MUS
 MUSCULUS (MOUSE)//Q60925
 F-PLACE1011778
 35 F-PLACE1011783//EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1)//0.97:48:
 43//MUS MUSCULUS (MOUSE)//P20863
 F-PLACE1011858//COLLAGEN 1(X) CHAIN PRECURSOR//0.0027:154:33//BOS TAURUS (BOVINE)//P23206
 F-PLACE1011874//BACTERIOCHLOROPHYLL A PROTEIN (BCHL A PROTEIN) (BCP)//1.0:60:26//PROSTHE-
 COCHLORIS AESTUARII//P11741
 40 F-PLACE1011875//HYPOTHETICAL 6.6 KD PROTEIN IN GP54-ALT INTERGENIC REGION//0.99:34:35//AC-
 TERIOPHAGE T4//P39495
 F-PLACE1011891//SMOOTHELIN//0.018:122:31//HOMO SAPIENS (HUMAN)//P53814
 F-PLACE1011896//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//6.3e-09:203:35//
 XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437
 45 F-PLACE1011922//CRYPTDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C)//0.067:37:48//MUS MUSCU-
 LUS (MOUSE)//P50715
 F-PLACE1011923//SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-) (SERUM INDUCIBLE KINASE)//
 1.5e-83:175:89//MUS MUSCULUS (MOUSE)//P53351
 F-PLACE1011962//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR//0.50:46:41//SCHIZOPHYLLUM
 50 COMMUNE (BRACKET FUNGUS)//Q02593
 F-PLACE1011964//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.6e-05:47:51//NYCTICEBUS COU-
 CANG (SLOW LORIS)//P08548
 F-PLACE1011982//APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN)//0.98:
 83:31//PLASMODIUM FRAGILE//P22622
 55 F-PLACE1011995
 F-PLACE1012031//HYPOTHETICAL PROTEIN KIAA0254//0.032:62:33//HOMO SAPIENS (HUMAN)//Q92543
 F-PLACE2000003//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.4e-18:63:73//HOMO SAPIENS (HUMAN)//
 P39193

F-PLACE2000006//ANNEXIN VII (SYNEXIN) (FRAGMENT)//0.14:20:50//BOS TAURUS (BOVINE)//P20072
 F-PLACE2000007//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.0045:176:30//MUS MUSCULUS
 (MOUSE)//P05143
 F-PLACE2000011//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-25:57:78//HOMO SAPIENS (HUMAN)//
 5 P39194
 F-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III//0.00013:237:27//
 CAENORHABDITIS ELEGANS//Q09475
 F-PLACE2000015//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-33:60:80//HOMO SAPIENS (HUMAN)//
 P39193
 10 F-PLACE2000017//FOLATE RECEPTOR BETA PRECURSOR (FR-BETA) (FOLATE RECEPTOR 2) (FOLATE
 RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP)//1.0:83:31//HOMO SAPI-
 ENS (HUMAN)//P14207
 F-PLACE2000021//EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KI-
 NASE RECEPTOR CEK8)//0.99:103:26//GALLUS GALLUS (CHICKEN)//Q07496
 15 F-PLACE2000030//MALE SPECIFIC SPERM PROTEIN MST84DA//0.69:29:44//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01642
 F-PLACE2000033//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-)//1.1e-05:74:41//STREPTOMYCES ANTIBIOTI-
 CUS//Q03326
 F-PLACE2000034//AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYC-
 OPROTEIN 1)//6.7e-18:191:35//HOMO SAPIENS (HUMAN)//Q02246
 20 F-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C)//4.7e-80:163:96//RATTUS NOR-
 VEGICUS (RAT)//P38650
 F-PLACE2000047//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/6.4e-06:63:49//HOMO SAPIENS (HU-
 MAN)//P39191
 25 F-PLACE2000050//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.2e-22:74:64//HOMO SAPIENS (HUMAN)//
 P39192
 F-PLACE2000061
 F-PLACE2000062//GLUCOSE STARVATION-INDUCIBLE PROTEIN B (GENERAL STRESS PROTEIN B)//1.9e-
 06:108:37//BACILLUS SUBTILIS//P26907
 30 F-PLACE2000072//ZINC FINGER PROTEIN 165//3.5e-34:175:49//HOMO SAPIENS (HUMAN)//P49910
 F-PLACE2000097//RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A)//0.36:39:38//ONDAT-
 RA ZIBETHICUS (MUSKRAT)//P00681
 F-PLACE2000100
 F-PLACE2000103//TUBULIN ALPHA-4 CHAIN (FRAGMENTS)//0.18:32:37//ZEA MAYS (MAIZE)//P33626
 35 F-PLACE2000111//CMRF35 ANTIGEN PRECURSOR//0.056:107:27//HOMO SAPIENS (HUMAN)//Q08708
 F-PLACE2000115//DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7) (DAP EPIMERASE) (FRAGMENT)//1.0:21:
 52//CLOSTRIDIUM PERFRINGENS//Q46185
 F-PLACE2000124//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-37:108:68//HOMO SAPIENS (HU-
 MAN)//P39194
 40 F-PLACE2000132//PROBABLE MEMBRANE ANTIGEN GP85//0.99:133:29//EPSTEIN-BARR VIRUS (STRAIN
 B95-8) (HUMAN HERPESVIRUS 4)//P03224
 F-PLACE2000136//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2) (PITUI-
 TARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR) (PACAP TYPE III RECEP-
 TOR) (PACAP-R-3)//0.83:65:32//MUS MUSCULUS (MOUSE)//P41588
 45 F-PLACE2000140
 F-PLACE2000164//TIPD PROTEIN//5.7e-12:190:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//
 Q15736
 F-PLACE2000170//BACTERIOCIN CARNOBACTERIOCIN BM1 PRECURSOR (CARNOBACTERIOCIN B1)//
 1.0:30:26//CARNOBACTERIUM PISCICOLA//P38579
 50 F-PLACE2000172
 F-PLACE2000176//HYPOTHETICAL PROTEIN AF0526//0.76:44:43//ARCHAEOGLOBUS FULGIDUS//Q02924
 F-PLACE2000187//EM-LIKE PROTEIN GEA6//0.84:42:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//
 Q02973
 F-PLACE2000216
 55 F-PLACE2000223//NEUROTOXIN III (LQQ III)//0.99:38:34//LEIURUS QUINQUESTRIATUS QUINQUESTRIA-
 TUS (EGYPTIAN SCORPION)//P01487
 F-PLACE2000235
 F-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN)//5.1e-37:121:42//DROSOPHILA MELA-

NOGASTER (FRUIT FLY)//Q04652
 F-PLACE2000264//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.4e-05:77:42//HOMO SAPIENS (HUMAN)//P39191
 5 F-PLACE2000274//DYNEIN BETA CHAIN, CILIARY//5.3e-46:232:45//TRIPNEUSTES GRATILLA (HAWAIIAN SEA URCHIN)//P23098
 F-PLACE2000302//TRICHOHYALIN//1.5e-06:215:29//ORYCTOLAGUS CUNICULUS (RABBIT)//P37709
 F-PLACE2000305//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.3e-06:33:66//HOMO SAPIENS (HUMAN)//P39188
 10 F-PLACE2000317//TOXIN C13S1C1 PRECURSOR//0.44:45:33//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA)//P18329
 F-PLACE2000335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.9e-08:35:71//HOMO SAPIENS (HUMAN)//P39195
 F-PLACE2000341//SODIUM/GLUCOSE COTRANSPORTER 1 (NA+)/GLUCOSE COTRANSPORTER 1 (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER)//0.014:141:24//ORYCTOLAGUS CUNICULUS (RABBIT)//P11170
 15 F-PLACE2000342//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//5.7e-09:96:38//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41479
 F-PLACE2000347//ZINC FINGER PROTEIN 177//5.9e-05:49:53//HOMO SAPIENS (HUMAN)//Q13360
 F-PLACE2000359//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.5e-10:69:52//HOMO SAPIENS (HUMAN)//P39194
 20 F-PLACE2000366
 F-PLACE2000371//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)//1.5e-05:216:29//HOMO SAPIENS (HUMAN)//P54259
 F-PLACE2000373//MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT)//0.27:63:33//HOMO SAPIENS (HUMAN)//Q99583
 25 F-PLACE2000379//HYPOTHETICAL GENE 1 PROTEIN//0.72:120:31//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1)//P28978
 F-PLACE2000394//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.95:40:42//HOMO SAPIENS (HUMAN)//P02811
 30 F-PLACE2000398//RIBONUCLEASE PRECURSOR (EC 3.1.27.-)//0.88:88:31//AEROMONAS HYDROPHILA//Q07465
 F-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7)//7.6e-16:180:39//HOMO SAPIENS (HUMAN)//P14209
 F-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS)//1.7e-94:243:64//CAENORHABDITIS ELEGANS//Q09996
 35 F-PLACE2000411//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT)//1.2e-09:78:39//MUS MUSCULUS (MOUSE)//Q60676
 F-PLACE2000419//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-20:61:62//HOMO SAPIENS (HUMAN)//P39188
 40 F-PLACE2000425//HYPOTHETICAL 11.9 KD PROTEIN IN MSB2-UGA1 INTERGENIC REGION//0.98:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53211
 F-PLACE2000427//INSULIN PRECURSOR//0.98:55:34//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET)//P30407
 F-PLACE2000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.5e-07:65:50//HOMO SAPIENS (HUMAN)//P39188
 45 F-PLACE2000435
 F-PLACE2000438//HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III//4.7e-66:178:47//CAENORHABDITIS ELEGANS//P34678
 F-PLACE2000450//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-23:88:62//HOMO SAPIENS (HUMAN)//P39195
 50 F-PLACE2000455//TOXIN II (TOXIN II.10.9.2) (FRAGMENT)//0.093:18:44//CENTRUROIDES LIMPIDUS LIMPIDUS (MEXICAN SCORPION)//P45630
 F-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN)//3.1e-23:165:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//P33450
 55 F-PLACE2000465//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.6e-23:73:63//HOMO SAPIENS (HUMAN)//P39188
 F-PLACE2000477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-37:90:78//HOMO SAPIENS (HUMAN)//P39194

F-PLACE3000004//EYES ABSENT HOMOLOG 3//1.1e-09:27:100//MUS MUSCULUS (MOUSE)//P97480
 F-PLACE3000009//PUTATIVE CUTICLE COLLAGEN C09G5.6//0.0061:148:34//CAENORHABDITIS ELE-
 GANS//Q09457
 5 F-PLACE3000020//ADENYLATE CYCLASE, OLFACTIVE TYPE (EC 4.6.1.1) (TYPE III) (ATP PYROPHOS-
 PHATE-LYASE) (ADENYLYL CYCLASE)//8.8e-93:193:92//RATTUS NORVEGICUS (RAT)//P21932
 F-PLACE3000029//50S RIBOSOMAL PROTEIN L31E//0.15:50:38//METHANOCOCCUS JANNASCHII//P54009
 F-PLACE3000059//TCP1-CHAPERONIN COFACTOR A//0.96:50:34//BOS TAURUS (BOVINE)//P48427
 F-PLACE3000070//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION//0.29:22:59//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST)//P38898
 10 F-PLACE3000103//LYSIS PROTEIN (E PROTEIN) (GPE)//0.99:53:32//BACTERIOPHAGE ALPHA-3//P31280
 F-PLACE3000119//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//5.4e-41:87:78//HOMO SAPIENS (HUMAN)//
 P39189
 F-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC151//1.0e-07:269:22//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST)//P22224
 15 F-PLACE3000124//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.2e-29:97:73//HOMO SAPIENS (HUMAN)//
 P39188
 F-PLACE3000136//PARS INTERCEREBRALIS MAJOR PEPTIDE D1 (PMP-D1)//0.77:26:42//LOCUSTA MIGRA-
 TORIA (MIGRATORY LOCUST)//P80059
 F-PLACE3000142//HYPOTHETICAL 7.1 KD PROTEIN IN NAD2 3'REGION (ORF 63)//0.82:34:41//MARCHAN-
 TIA POLYMORPHA (LIVERWORT)//P38468
 20 F-PLACE3000145//TENSIN//3.5e-91:238:74//GALLUS GALLUS (CHICKEN)//Q04205
 F-PLACE3000147//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-30:61:65//HOMO SAPIENS (HUMAN)//
 P39194
 F-PLACE3000148//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE
 (EC 2.7.7.49); ENDONUCLEASE]//1.4e-18:226:34//GIBBON APE LEUKEMIA VIRUS//P21414
 25 F-PLACE3000155//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.00014:107:33//ZEA MAYS
 (MAIZE)//P14918
 F-PLACE3000156//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE
 (EC 2.7.7.49); ENDONUCLEASE]//2.7e-19:169:30//BABOON ENDOGENOUS VIRUS (STRAIN M7)//P10272
 30 F-PLACE3000157//PROBABLE SERINE/THREONINE-PROTEIN KINASE CY50.16 (EC 2.7.1.-)//0.0061:92:30//
 MYCOBACTERIUM TUBERCULOSIS//Q11053
 F-PLACE3000158//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//5.7e-49:56:80//HOMO SAPIENS (HUMAN)//
 P39189
 F-PLACE3000160//DNA TRANSFORMATION PROTEIN TFOX (COMPETENCE ACTIVATOR) (PROTEIN SXY)//
 0.39:94:34//HAEMOPHILUS INFLUENZAE//P43779
 35 F-PLACE3000169//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.6e-28:99:59//HOMO SAPIENS (HUMAN)//
 P39193
 F-PLACE3000194//PROLINE-RICH PROTEIN LAS17//0.91:80:36//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//Q12446
 40 F-PLACE3000197//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M)//
 0.24:119:32//GALLUS GALLUS (CHICKEN)//P16053
 F-PLACE3000199//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//
 0.76:87:37//NICOTIANA TABACUM (COMMON TOBACCO)//P13983
 F-PLACE3000207//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.5e-09:32:78//HOMO SAPIENS (HUMAN)//
 45 P39188
 F-PLACE3000208
 F-PLACE3000218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.2e-34:96:70//HOMO SAPIENS (HUMAN)//
 P39194
 F-PLACE3000220//OSTEOCALCIN (GAMMA-CARBOXYGLUTAMIC ACID-CONTAINING PROTEIN) (BONE
 GLA- PROTEIN) (BGP)//0.46:13:53//CANIS FAMILIARIS (DOG)//P81455
 50 F-PLACE3000221//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.8e-24:178:45//HOMO SAPIENS (HUMAN)//
 P39188
 F-PLACE3000226//30S RIBOSOMAL PROTEIN S18//0.98:38:34//NEISSERIA GONORRHOEAE//O07815
 F-PLACE3000230//METALLOTHIONEIN (MT)//0.97:25:48//OREOCHROMIS MOSSAMBICUS (MOZAMBIQUE
 55 TILAPIA) (TILAPIA MOSSAMBICA)//P52726
 F-PLACE3000242//MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)//8.0e-21:121:39//HOMO SA-
 PIENS (HUMAN)//P43361
 F-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR)//2.3e-125:264:87//MUS MUS-

CULUS (MOUSE)//P53995
 F-PLACE3000254//RTOA PROTEIN (RATIO-A)//0.99:142:23//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P54681
 F-PLACE3000271//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-12:63:53//HOMO SAPIENS (HUMAN)//P39188
 5 F-PLACE3000276//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN)//1.0:55:38//HOMO SAPIENS (HUMAN)//P27658
 F-PLACE3000304//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.0028:31:54//HOMO SAPIENS (HUMAN)//P30808
 10 F-PLACE3000310//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)//0.98:82:34//RATTUS NORVEGICUS (RAT)//P54258
 F-PLACE3000320
 F-PLACE3000322//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR//2.2e-22:61:52//ORYZA SATIVA (RICE)//P25074
 15 F-PLACE3000331//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//0.32:15:53//HOMO SAPIENS (HUMAN)//P22532
 F-PLACE3000339//CHORION PROTEIN S19//0.34:89:37//DROSOPHILA VIRILIS (FRUIT FLY)//P24516
 F-PLACE3000341//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT)//1.0:47:38//COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL)//P24968
 20 F-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-)//3.9e-50:168:60//CAENORHABDITIS ELEGANS //P46549
 F-PLACE3000352//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.8e-29:76:71//HOMO SAPIENS (HUMAN)//P39194
 F-PLACE3000353//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOS-AMINYLTRANSFERASE) (GALNAC-T1)//3.0e-09:100:41//HOMO SAPIENS (HUMAN)//Q10472
 25 F-PLACE3000362//HYPOTHETICAL PROTEIN TP0064//1.0:75:26//TREPONEMA PALLIDUM//O83103
 F-PLACE3000363//METALLOTHIONEIN (MT)//0.067:42:33//ASTACUS FLUVIATILIS (BROAD-FINGERED CRAYFISH) (ASTACUS ASTACUS)//P55951
 30 F-PLACE3000365//LYSIS PROTEIN (E PROTEIN) (GPE)//1.0:65:27//BACTERIOPHAGE PHI-K//Q38040
 F-PLACE3000373//RETROVIRUS-RELATED ENV POLYPROTEIN//1.5e-18:90:47//HOMO SAPIENS (HUMAN)//P10267
 F-PLACE3000388
 F-PLACE3000399//!!!!ALU SUBFAMILY SP WARNING ENTRY !!!!!/6.3e-45:60:75//HOMO SAPIENS (HUMAN)//P39193
 35 F-PLACE3000400
 F-PLACE3000401//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.6e-09:46:73//HOMO SAPIENS (HUMAN)//P39188
 F-PLACE3000402//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.036:43:44//HOMO SAPIENS (HUMAN)//P39188
 40 F-PLACE3000405//POSTERIOR PITUITARY PEPTIDE //0.70:25:40//BOS TAURUS (BOVINE)//P01154
 F-PLACE3000406//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-09:49:67//HOMO SAPIENS (HUMAN)//P39195
 F-PLACE3000413//MALE SPECIFIC SPERM PROTEIN MST87F//0.12:42:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//P08175
 45 F-PLACE3000416//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I)//0.67:236:21//BOS TAURUS (BOVINE)//P35662
 F-PLACE3000425//PROLINE-RICH PEPTIDE P-B//0.45:19:42//HOMO SAPIENS (HUMAN)//P02814
 F-PLACE3000455//AMELOGENIN, CLASS I PRECURSOR//0.0073:81:43//BOS TAURUS (BOVINE)//P02817
 50 F-PLACE3000475//8.6 KD TRANSGLUTAMINASE SUBSTRATE//1.0:53:32//TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB)//P81281
 F-PLACE3000477//MUSCARINIC TOXIN 7 (MT-7)//0.13:55:32//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA)//P80970
 F-PLACE4000009//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT)//7.0e-19:180:27//HOMO SAPIENS (HUMAN)//P35749
 55 F-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP)//3.2e-15:193:30//HOMO SAPIENS (HUMAN)//P46100
 F-PLACE4000034//BRIDE OF SEVENLESS PROTEIN PRECURSOR//0.0024:97:29//DROSOPHILA MELA-

NOGASTER (FRUIT FLY)//P22815
 F-PLACE4000049//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.8e-32:79:75//HOMO SAPIENS (HUMAN)//
 P39194
 F-PLACE4000052//ATP-BINDING CASSETTE TRANSPORTER 1//2.2e-99:178:97//MUS MUSCULUS
 5 (MOUSE)//P41233
 F-PLACE4000063//IMMEDIATE-EARLY PROTEIN//0.0017:159:25//HERPESVIRUS SAIMIRI (STRAIN 11)//
 Q01042
 F-PLACE4000089
 F-PLACE4000093
 10 F-PLACE4000100//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-14:68:60//HOMO SAPIENS (HUMAN)//
 P39188
 F-PLACE4000106//1A PROTEIN[CONTAINS: HELICASE; METHYLTRANSFERASE]//1.0:46:41//BROAD BEAN
 MOTTLE VIRUS//Q00020
 F-PLACE4000128//HYPOTHETICAL PROTEIN E-115//0.00020:101:30//HUMAN ADENOVIRUS TYPE 2//
 15 P03290
 F-PLACE4000129//CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN)//
 0.15:57:31//HOMO SAPIENS (HUMAN)//P22528
 F-PLACE4000131
 F-PLACE4000147//COMPETENCE PHEROMONE PRECURSOR//1.0:45:24//BACILLUS SUBTILIS//P45453
 20 F-PLACE4000156//ZINC FINGER PROTEIN 136//2.1e-88:194:59//HOMO SAPIENS (HUMAN)//P52737
 F-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654)//0.083:148:26//HOMO SAPIENS (HU-
 MAN)//P52746
 F-PLACE4000211//CALPHOTIN//0.20:43:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q02910
 F-PLACE4000222//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-05:20:85//HOMO SAPIENS (HUMAN)//
 25 P39188
 F-PLACE4000230//DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) / THYMIDYLATE SYNTHASE (EC 2.1.1.45)
 (DHFR-TS)//1.0:96:28//TRYPANOSOMA BRUCEI BRUCEI//Q27783
 F-PLACE4000233
 F-PLACE4000247//METALLOTHIONEIN (MT)//1.0e-05:34:41//PLEURONECTES PLATESSA (PLAICE)//
 30 P07216
 F-PLACE4000250//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN)//0.99:33:42//CAPRINE ARTHRITIS EN-
 CEPHALITIS VIRUS (CAEV)//P31834
 F-PLACE4000252//MALE SPECIFIC SPERM PROTEIN MST84DB//0.42:24:45//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01643
 35 F-PLACE4000259//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-)//3.5e-09:189:32//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST)//P32639
 F-PLACE4000261//PEREGRIN (BR140 PROTEIN)//5.0e-11:103:37//HOMO SAPIENS (HUMAN)//P55201
 F-PLACE4000269//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//0.037:181:25//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P25386
 40 F-PLACE4000270//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21)//1.0:46:39//MUS MUSCULUS
 (MOUSE)//P70375
 F-PLACE4000300//50S RIBOSOMAL PROTEIN L32//0.81:28:46//THERMUS AQUATICUS (SUBSP. THER-
 MOPHILUS)//P80339
 F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN)//
 45 1.6e-29:44:93//HOMO SAPIENS (HUMAN)//P42345
 F-PLACE4000323
 F-PLACE4000326//PARATHYMOSIN//0.0018:54:48//HOMO SAPIENS (HUMAN)//P20962
 F-PLACE4000344//EPIDERMAL GROWTH FACTOR (EGF) (FRAGMENT)//0.97:28:42//SUS SCROFA (PIG)//
 Q00968
 50 F-PLACE4000367//NEUROTOXIN 1 (TOXIN SHP-I) (SHNA) (NEUROTOXIN SHI)//1.0:33:36//STOICHACTIS
 HELIANTHUS (CARRIBEAN SEA ANEMONE) (STICHODACTYLA HELIANTHUS)//P19651
 F-PLACE4000369//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.071:42:42//SORGHUM
 VULGARE (SORGHUM)//P24152
 F-PLACE4000379//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-16:54:77//HOMO SAPIENS (HUMAN)//
 55 P39193
 F-PLACE4000387//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR//0.25:21:52//HOR-
 DEUM VULGARE (BARLEY), AND SECALE CEREALE (RYE)//P25877
 F-PLACE4000392//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE)

(FRAGMENT) //0.91:36:50//YERSINIA PSEUDOTUBERCULOSIS //Q05338
 F-PLACE4000401//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-29:96:67//HOMO SAPIENS (HUMAN) //P39194
 F-PLACE4000411//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.3e-18:41:73//HOMO SAPIENS (HUMAN) //P39188
 5 F-PLACE4000431//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-) //5.4e-21:237:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P32639
 F-PLACE4000445//HYPOTHETICAL 99.7 KD PROTEIN IN SDL1 5'REGION PRECURSOR //0.00081:210:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40442
 10 F-PLACE4000450//TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPTION FACTOR HBP1) //0.020:87:33//TRITICUM AESTIVUM (WHEAT) //P23922
 F-PLACE4000465//METALLOTHIONEIN-IL (MT-1L) (MT1X) //0.20:18:38//HOMO SAPIENS (HUMAN) //P80297
 F-PLACE4000487//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-19:73:52//HOMO SAPIENS (HUMAN) //P39188
 15 F-PLACE4000489
 F-PLACE4000494//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1) //0.17:130:30//MUS MUSCULUS (MOUSE) //Q03173
 F-PLACE4000521//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] (FRAGMENT) //3.0e-05:50:36//MUS MUSCULUS (MOUSE) //P10400
 20 F-PLACE4000522//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR //1.8e-45:231:47//RATTUS NORVEGICUS (RAT) //Q07008
 F-PLACE4000548//CYTOCHROME C-551 (C551) //0.96:50:34//ECTOTHIORHODOSPIRA HALOPHILA //P00122
 F-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN) //1.6e-28:223:36//DROSOPHILA MELANOGASTER (FRUIT FLY) //P55824
 25 F-PLACE000581//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM) (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3) //9.7e-11:166:281//HOMO SAPIENS (HUMAN) //P16109
 F-PLACE4000590//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] //1.6e-17:134:35//GIBBON APE LEUKEMIA VIRUS //P21414
 F-PLACE4000593//GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) //1.0:54:29//RATTUS NORVEGICUS (RAT) //P30969
 30 F-PLACE4000612//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30] //2.6e-14:221:32//MOLONEY MURINE SARCOMA VIRUS (STRAIN TS110) //P32594
 35 F-PLACE4000638//HYPOTHETICAL 9.3 KD PROTEIN IN NRDB-INAA INTERGENIC REGION //0.65:37:40//ESCHERICHIA COLI //P37910
 F-PLACE4000650//ZINC FINGER PROTEIN 16 (ZINC FINGER PROTEIN KOX9) (FRAGMENT) //1.0:33:33//HOMO SAPIENS (HUMAN) //P17020
 40 F-PLACE4000654
 F-PLACE4000670//HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION //1.6e-07:161:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P33313
 F-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT) //7.4e-15:223:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //O60100
 45 F-SKNMC1000013//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6) //0.0013:128:35//GALLUS GALLUS (CHICKEN) //Q98937
 F-SKNMC1000046//CUTICLE COLLAGEN 1 //0.0010:154:33//CAENORHABDITIS ELEGANS //P08124
 F-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE) //3.2e-41:87:98//HOMO SAPIENS (HUMAN) //P17655
 50 F-SKNMC1000091//NTAK PROTEIN (NEURAL- AND THYMUS- DERIVED ACTIVATOR FOR ERBB KINASES) //0.0032:154:35//HOMO SAPIENS (HUMAN) //O14511
 F-THYRO1000017//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE) //1.6e-23:124:37//CAENORHABDITIS ELEGANS //Q20939
 55 F-THYRO1000026//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.0e-13:54:66//HOMO SAPIENS (HUMAN) //P39192
 F-THYRO1000034//HYPOTHETICAL 10.4 KD PROTEIN //0.16:44:34//HEPATITIS B VIRUS (SUBTYPE AYW) //P03163

F-THYRO1000035//CAMPATH-1 ANTIGEN PRECURSOR (CD52 ANTIGEN) (CDW52) (CAMBRIDGE PATHOL-
 OGY 1 ANTIGEN)//0.83:59:37//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MON-
 KEY)//P32763
 5 F-THYRO1000040//60S RIBOSOMAL PROTEIN L37 (FRAGMENT)//0.25:23:39//BOS TAURUS (BOVINE)//
 P79244
 F-THYRO1000070//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//2.3e-11:133:36//ORGYIA PSEUDOTSUGA-
 TA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341
 F-THYRO1000072//C-PROTEIN, SKELETAL MUSCLE SLOW-ISOFORM//1.5e-14:205:29//HOMO SAPIENS
 (HUMAN)//Q00872
 10 F-THYRO1000085
 F-THYRO1000092//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.063:59:33//HOMO SA-
 PIENS (HUMAN)//P49901
 F-THYRO1000107
 F-THYRO1000111//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//5.0e-58:110:67//NYCTICEBUS COU-
 CANG (SLOW LORIS)//P08548
 15 F-THYRO1000121//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//2.6e-06:134:35//MUS
 MUSCULUS (MOUSE)//Q62203
 F-THYRO1000124//TENECIN 3 PRECURSOR//0.047:76:35//TENEBRIO MOLITOR (YELLOW MEALWORM)//
 Q27270
 20 F-THYRO1000129//FBROSIN (FRAGMENT)//0.35:43:34//MUS MUSCULUS (MOUSE)//Q60791
 F-THYRO1000132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.7e-14:104:42//HOMO SAPIENS (HUMAN)//
 P39188
 F-THYRO1000156
 F-THYRO1000163//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.7e-20:71:71//HOMO SAPIENS (HUMAN)//
 25 P39189
 F-THYRO1000173//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN
 AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN
 ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)//6.7e-88:216:76//MUS MUSCULUS (MOUSE)//P35585
 F-THYRO1000186//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.9e-24:72:77//HOMO SAPIENS (HUMAN)//
 30 P39192
 F-THYRO1000187
 F-THYRO1000190//PROTEIN TRANSPORT PROTEIN SEC61 BETA 2 SUBUNIT//0.060:50:42//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P52871
 F-THYRO1000197
 35 F-THYRO1000199//HYPOTHETICAL 49.8 KD PROTEIN D2007.5 IN CHROMOSOME III//2.0e-06:88:35//
 CAENORHABDITIS ELEGANS//34379
 F-THYRO1000206
 F-THYRO1000221
 F-THYRO1000241//HYPOTHETICAL 11.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION//1.0:51:35//
 40 AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41661
 F-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//7.4e-37:137:36//HOMO SA-
 PIENS (HUMAN)//P51523
 F-THYRO1000253//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.11:21:52//HO-
 MO SAPIENS (HUMAN)//P30808
 45 F-THYRO1000270//WDNM1 PROTEIN PRECURSOR//0.40:52:32//MUS MUSCULUS (MOUSE)//Q62477
 F-THYRO1000279//BETA CRYSTALLIN A4//0.97:64:26//BOS TAURUS (BOVINE)//P11842
 F-THYRO1000288//POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC
 ENDOPROTEASE 1) (PPSEP 1)//3.4e-48:142:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//
 Q10071
 50 F-THYRO1000320//ZINC FINGER PROTEIN 14 (ZFP-14) (KROX-9 PROTEIN) (FRAGMENT)//0.87:35:45//MUS
 MUSCULUS (MOUSE)//P10755
 F-THYRO1000327//HYPOTHETICAL 64.7 KD PROTEIN F26E4.11 IN CHROMOSOME I//0.00010:75:26//
 CAENORHABDITIS ELEGANS//P90859
 F-THYRO1000343//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN;
 55 WE-14]//0.88:107:26//MUS MUSCULUS (MOUSE)//P26339
 F-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN//4.6e-25:49:81//MUS MUSCULUS (MOUSE)//
 P17563
 F-THYRO1000368//LOCOMOTION-RELATED PROTEIN HIKARU GENKI PRECURSOR//1.0:136:26//DRO-

SOPHILA MELANOGASTER (FRUIT FLY).//Q09101
 F-THYRO1000381//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12;
 CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].//0.032:99:35//SIMIAN SARCOMA VIRUS.//P03330
 F-THYRO1000387//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.90:46:30//HALICHOERUS GRYPUS
 5 (GRAY SEAL).//P38592
 F-THYRO1000394//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.00019:48:37//HOMO SAPI-
 ENS (HUMAN).//P22531
 F-THYRO1000395//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-33:186:38//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY).//Q04652
 10 F-THYRO1000401//50S RIBOSOMAL PROTEIN L7/L12 (FRAGMENT).//0.57:67:31//STAPHYLOCOCCUS AU-
 REUS.//P48860
 F-THYRO1000438//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:38//STRONGYLOCENTROTUS
 PURPURATUS (PURPLE SEA URCHIN).//P15997
 F-THYRO1000452//BACTERIOCIN CARNOBACTERIOCIN A PRECURSOR (PISCICOLIN 61).//0.31:34:44//
 15 CARNOBACTERIUM PISCICOLA.//P38578
 F-THYRO1000471//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-31:94:72//HOMO SAPIENS (HUMAN).//
 P39194
 F-THYRO1000484//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.9e-08:30:86//HOMO SAPIENS (HUMAN).//
 P39195
 20 F-THYRO1000488//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.93:98:27//GLYCINE MAX
 (SOYBEAN).//Q02917
 F-THYRO1000501//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//2.4e-51:198:50//MUS
 MUSCULUS (MOUSE).//P15533
 F-THYRO1000502//HUNCHBACK PROTEIN (FRAGMENT).//0.84:41:43//APIS MELLIFERA (HONEYBEE).//
 25 P31504
 F-THYRO1000505//HYPOTHETICAL BHLF1 PROTEIN.//0.99:231:33//EPSTEIN-BARR VIRUS (STRAIN B95-8)
 (HUMAN HERPESVIRUS 4).//P03181
 F-THYRO1000558//ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).//0.47:58:37//GALLUS GALLUS
 (CHICKEN).//Q03352
 30 F-THYRO1000569//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00048:64:42//RATTUS NORVEGICUS
 (RAT).//P02454
 F-THYRO1000570//HYPOTHETICAL 11.6 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//0.94:61:32//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39725
 F-THYRO1000585//SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR
 35 SRP55).//0.050:104:36//HOMO SAPIENS (HUMAN).//Q13247
 F-THYRO1000596//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.99:37:40//
 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P37319
 F-THYRO1000602//EAMZP30-47 PROTEIN (FRAGMENT).//0.88:61:34//EIMERIA ACERVULINA.//P21959
 F-THYRO1000605//SUPPRESSOR PROTEIN SRP40.//0.0016:116:26//SACCHAROMYCES CEREVISIAE
 40 (BAKER'S YEAST).//P32583
 F-THYRO1000625//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-33:88:78//HOMO SAPIENS (HUMAN).//
 P39194
 F-THYRO1000637//METALLOTHIONEIN A (MT A).//1.0:23:43//SPARUS AURATA (GILTHEAD SEA BREAM).//
 P52727
 45 F-THYRO1000641//PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN.//0.99:26:46//CYANIDIUM CALDARIUM
 (GALDIERIA SULPHURARIA).//O19925
 F-THYRO1000658//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-49:116:69//HOMO SAPIENS (HU-
 MAN).//P39189
 F-THYRO1000662//DNA-DAMAGE-INDUCIBLE PROTEIN P.//3.7e-15:119:43//ESCHERICHIA COLI.//Q47155
 50 F-THYRO1000666//KINESIN-LIKE PROTEIN KLP1.//1.0e-44:232:41//CHLAMYDOMONAS REINHARDTII.//
 P46870
 F-THYRO1000676//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.1e-15:144:39//HOMO SAPIENS (HU-
 MAN).//P39193
 F-THYRO1000684//HYPOTHETICAL 73.5 KD PROTEIN IN SCS3-RPS2 INTERGENIC REGION.//0.00033:84:
 30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53129
 55 F-THYRO1000699//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.97:20:85//HOMO SAPIENS (HUMAN).//
 P39192
 F-THYRO1000712//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.2e-10:69:59//HOMO SAPIENS (HUMAN).//

P39188
 F-THYRO1000715//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) (CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H)//4.6e-10:204:32//HOMO SAPIENS (HUMAN)//P04280
 F-THYRO1000734
 5 F-THYRO1000748//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT)//1.8e-46:130:70//HOMO SAPIENS (HUMAN)//O43295
 F-THYRO1000756//ALPHA-N-ACETYLGLACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY)//1.1e-06:95:31//RATTUS NORVEGICUS (RAT)//Q64686
 F-THYRO1000777//CUTICLE COLLAGEN 2C (FRAGMENT)//0.0031:119:34//HAEMONCHUS CONTORTUS//
 10 P16252
 F-THYRO1000783//MYOSIN IC HEAVY CHAIN//0.0014:121:37//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569
 F-THYRO1000787//HUNCHBACK PROTEIN (FRAGMENT)//0.54:25:52//PHOLCUS PHALANGIOIDES//Q02031
 15 F-THYRO1000793//PRE-MRNA SPLICING FACTOR PRP9//0.91:3 0:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P19736
 F-THYRO1000796
 F-THYRO1000805//HYPOTHETICAL 7.3 KD PROTEIN IN 100.KD PROTEIN REGION//0.081:31:38//HUMAN ADENOVIRUS TYPE 41//P23691
 20 F-THYRO1000815//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/6.0e-30:81:70//HOMO SAPIENS (HUMAN)//P39195
 F-THYRO1000829//NEUROTOXIN III (BOM III)//0.022:32:34//BUTHUS OCCITANUS MARDOCHEI (MOROC-CAN SCORPION)//P13488
 F-THYRO1000843//HYPOTHETICAL 7.7 KD PROTEIN IN GENES 5-4 INTERGENIC REGION (ORF 109)//0.98:25:44//BACTERIOPHAGE P22//P26750
 25 F-THYRO1000852//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)//7.3e-09:83:42//VOLVOX CART-ERI//P21997
 F-THYRO1000855//ANTIFREEZE PEPTIDE 4 PRECURSOR//1.0:54:35//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER)//P02734
 30 F-THYRO1000865//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!/5.2e-17:66:57//HOMO SAPIENS (HUMAN)//P39188
 F-THYRO1000895//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.0e-12:58:62//HOMO SAPIENS (HUMAN)//P39189
 F-THYRO1000916//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.0e-32:101:69//HOMO SAPIENS (HUMAN)//P39189
 35 F-THYRO1000926//NITROGEN FIXATION REGULATORY PROTEIN//5.5e-05:108:27//KLEBSIELLA OXYTOCA//P56267
 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE)//3.9e-50:147:40//HOMO SAPIENS (HUMAN)//P32322
 40 F-THYRO1000951//DIHYDROXYACETONE KINASE (EC 2.7.1.29) (GLYCERONE KINASE)//1.8e-31:136:56//CITROBACTER FREUNDII//P45510
 F-THYRO1000952//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION//2.4e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47170
 F-THYRO1000974//MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR//1.0:35:40//
 45 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32580
 F-THYRO1000975
 F-THYRO1000983//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X//1.3e-20:96:51//CAENORHABDITIS ELEGANS//Q11076
 F-THYRO1000984//GTP-BINDING ADP-RIBOSYLATION FACTOR HOMOLOG 1 PROTEIN//0.011:76:34//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25160
 50 F-THYRO1000988
 F-THYRO1001003//HYPOTHETICAL 8.1 KD PROTEIN IN MSCL-RPLQ INTERGENIC REGION//0.97:60:31//ESCHERICHIA COLI//P36675
 F-THYRO1001031//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.5e-18:56:66//HOMO SAPIENS (HUMAN)//P39195
 55 F-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521//5.0e-13:126:35//HOMO SAPIENS (HUMAN)//P31948
 F-THYRO1001062//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-35:97:79//HOMO SAPIENS (HUMAN)//

P39194
 F-THYRO1001093//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.4e-13:70:57//HOMO SAPIENS (HUMAN)//
 P39194
 F-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT)//4.2e-63:219:63//HOMO SAPIENS
 5 (HUMAN)//P98168
 F-THYRO1001120//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)//0.00068:160:31//HOMO
 SAPIENS (HUMAN)//Q15427
 F-THYRO1001121//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME I//0.37:158:28//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10263
 10 F-THYRO1001133//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.3e-15:59:66//HOMO SAPIENS (HUMAN)//
 P39188
 F-THYRO1001134//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAG-
 MENT)//0.00088:159:29//HOMO SAPIENS (HUMAN)//P10161
 F-THYRO1001142//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.0e-29:81:71//HOMO SAPIENS (HUMAN)//
 15 P39194
 F-THYRO1001173//CYTOCHROME C OXIDASE POLYPEPTIDE VIIS (EC 1.9.3.1)//0.88:51:35//DICTYOSTEL-
 IUM DISCOIDEUM (SLIME MOLD)//P20610
 F-THYRO1001177//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.0e-24:91:68//HOMO SAPIENS (HUMAN)//
 P39192
 20 F-THYRO1001189//MKR2 PROTEIN (ZINC FINGER PROTEIN 2)//7.3e-27:165:39//MUS MUSCULUS
 (MOUSE)//P08043
 F-THYRO1001204//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.67:42:42//HOMO SAPIENS (HUMAN)//
 P02811
 F-THYRO1001213//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.9e-16:61:68//HOMO SAPIENS (HUMM)//
 25 P39194
 F-THYRO1001262//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-36:50:84//HOMO SAPIENS (HUMAN)//
 P39193
 F-THYRO1001271//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.62:126:30//STREPTO-
 MYCES FRADIAE//P20186
 30 F-THYRO1001287//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC REGION//1.9e-26:208:
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38888
 F-THYRO1001290//GIANT HEMOGLOBIN AIV CHAIN (FRAGMENT)//1.0:31:38//LAMELLIBRACHIA SP.
 (DEEP-SEA GIANT TUBE WORM)//P20413
 F-THYRO1001313//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5//0.00042:105:31//SAC-
 35 CHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q92331
 F-THYRO1001320//COLLAGEN ALPHA 1(III) CHAIN//0.27:57:38//BOS TAURUS (BOVINE)//P04258
 F-THYRO1001321//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.5e-20:74:64//HOMO SAPIENS (HUMAN)//
 P39188
 F-THYRO1001322//HYPOTHETICAL 7.2 KD PROTEIN//0.66:49:30//VACCINIA VIRUS (STRAIN COPENHA-
 40 GEN)//P21123
 F-THYRO1001347//TOXIN F-VIII PRECURSOR (TOXIN TA2) (TOXIN DAF8)//0.94:61:36//DENDROASPIS AN-
 GUSTICEPS (EASTERN GREEN MAMBA)//P01404
 F-THYRO1001363//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0025:23:73//HOMO SAPIENS (HUMAN)//
 45 P39188
 F-THYRO1001365//MERSACIDIN PRECURSOR//0.35:38:42//BACILLUS SP. (STRAIN HIL-Y85/54728)//
 P43683
 F-THYRO1001374//PROTEIN VDLD//1.6e-3:140:31//HELICOBACTER PYLORI (CAMPYLOBACTER PY-
 LORI)//O05729
 F-THYRO1001401//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.047:43:48//HOMO SAPIENS (HUMAN)//
 50 P39192
 F-THYRO1001403
 F-THYRO1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.0068:26:42//HOMO SAPIENS
 (HUMAN)//P22531
 F-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-)//3.1e-81:97:83//MUS MUSCU-
 55 LUS (MOUSE)//O70503
 F-THYRO1001411//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.9e-26:89:74//HOMO SAPIENS (HUMAN)//
 P39193
 F-THYRO1001426//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-09:55:61//HOMO SAPIENS (HUMAN)//

P39193
 F-THYRO1001434//BETA-DEFENSIN 4 PRECURSOR (BNDB-4)//0.68:44:34//BOS TAURUS (BOVINE)//
 P46162
 F-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE
 5 B) (NMMHC-B)//3.8e-64:216:62//HOMO SAPIENS (HUMAN)//P35580
 F-THYRO1001480//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.3e-29:88:75//HOMO SAPIENS (HUMAN)//
 P39194
 F-THYRO1001487//HOMEBOX PROTEIN HOX-B4 (HOX-2.6)//0.99:59:37//MUS MUSCULUS (MOUSE)//
 P10284
 10 F-THYRO1001534//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.4e-14:40:82//HOMO SAPIENS (HUMAN)//
 P39194
 F-THYRO1001537//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLO5 INTERGENIC REGION//2.4e-07:142:
 32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38892
 F-THYRO1001541//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.98:26:61//HOMO SAPIENS (HUMAN)//
 15 P39195
 F-THYRO1001559//PROTEIN Q300//2.6e-05:20:75//MUS MUSCULUS (MOUSE)//Q02722
 F-THYRO1001570
 F-THYRO1001573//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.033:71:36//MUS MUS-
 CULUS (MOUSE)//P15265
 20 F-THYRO1001584//SUPPRESSOR PROTEIN SRP40//2.1e-05:188:27//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//P32583
 F-THYRO1001595//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//6.1e-21:35:91//HO-
 MO SAPIENS (HUMAN)//Q15404
 F-THYRO1001602//TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKH//1.0:57:42//HAEMOPHILUS INFLU-
 25 ENZAE//P44843
 F-THYRO1001605//VENOM BASIC PROTEASE INHIBITORS IX AND VIIIIB//1.0:34:38//BUNGARUS FASCIA-
 TUS (BANDED KRAIT)//P25660
 F-THYRO1001617//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.0e-18:55:81//HOMO SAPIENS (HUMAN)//
 P39194
 30 F-THYRO1001637//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.00020:25:80//HOMO SAPIENS (HU-
 MAN)//P39195
 F-THYRO1001656//PROLINE-RICH PROTEIN MP-2 PRECURSOR//0.0091:54:42//MUS MUSCULUS
 (MOUSE)//P05142
 F-THYRO1001661//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182)//0.033:
 35 77:35//ESCHERICHIA COLI//P09160
 F-THYRO1001671//((2'-5'))OLIGOADENYLATE SYNTHETASE 1 (EC 2.7.7.-) ((2'-5'))OLIGO(A) SYNTHETASE 1)
 (2-5A SYNTHETASE 1) (P46/P41) (E18/E16)//4.3e-34:207:34//HOMO SAPIENS (HUMAN)//P00973
 F-THYRO1001673//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.9e-08:49:65//HOMO SAPIENS (HUMAN)//
 P39194
 40 F-THYRO1001703//HYPOTHETICAL 69.8 KD PROTEIN IN BDF1-SFP1 INTERGENIC REGION//6.4e-16:134:
 35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q06053
 F-THYRO1001706
 F-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN)//2.7e-27:191:36//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q04652
 45 F-THYRO1001738//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE
 A INTERFERENCE PROTEIN)//0.0032:105:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36027
 F-THYRO1001745
 F-THYRO1001746//GENE 10 PROTEIN//1.0:55:30//SPIROPLASMA VIRUS SPV1-R8A2 B//P15901
 F-THYRO1001772//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.2e-05:41:63//HOMO SAPIENS (HUMAN)//
 50 P39188
 F-THYRO1001793//HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III//1.5e-26:161:42//
 CAENORHABDITIS ELEGANS//P41880
 F-THYRO1001809//LATENCY-RELATED PROTEIN 2//0.49:74:27//HERPES SIMPLEX VIRUS (TYPE 1 /
 STRAIN F)//P17589
 55 F-THYRO1001828//PROTEINASE INHIBITOR//0.11:34:50//SOLANUM MELONGENA (EGGPLANT) (AUBER-
 GINE)//P01078
 F-THYRO1001854//ACYL-COA-BINDING PROTEIN HOMOLOG (ACBP) (DIAZEPAM BINDING INHIBITOR HO-
 MOLOG) (DBI)//0.63:50:38//RANA RIDIBUNDA (LAUGHING FROG) (MARSH FROG)//P45883

F-THYRO1001895//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.1e-09:72:47//HOMO SAPIENS (HUMAN)//
 P39188
 F-THYRO1001907//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT)//0.79:36:
 44//TRYPANOSOMA CRUZI//Q26327
 5 F-VESEN1000122//HOMEOBOX PROTEIN HB9//0.57:64:32//HOMO SAPIENS (HUMAN)//P50219
 F-Y79AA1000013//METALLOTHIONEIN B (MT-B)//0.034:35:48//SALMO SALAR (ATLANTIC SALMON)//
 P52720
 F-Y79AA1000033//CHOLECYSTOKININ//0.97:49:30//PSEUDEMY'S SCRIPTA (SLIDER TURTLE)//P80345
 F-Y79AA1000037//DNA-BINDING PROTEIN BMI-1//1.4e-23:80:60//HOMO SAPIENS (HUMAN)//P35226
 10 F-Y79AA1000059//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.0075:127:36//STREPTO-
 MYCES FRADIAE//P20186
 F-Y79AA1000065//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-
 MENT)//0.022:135:29//HOMO SAPIENS (HUMAN)//P10162
 F-Y79AA1000131//REGULATORY PROTEIN E2//1.1e-05:175:26//HUMAN PAPILLOMAVIRUS TYPE 24//
 15 P50770
 F-Y79AA1000181//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.4e-06:187:29//MUS MUSCULUS
 (MOUSE)//P05143
 F-Y79AA1000202//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//6.2e-09:47:53//OWENIA FUSI-
 FORMIS//P21260
 20 F-Y79AA1000214//HISTONE H2A VARIANT//1.7e-50:107:100//GALLUS GALLUS (CHICKEN)//P02272
 F-Y79AA1000230//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HOR-
 MONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I)//0.27:64:34//HOMO SAPIENS
 (HUMAN)//P01148
 F-Y79AA1000231//HYPOTHETICAL 47.9 KD PROTEIN M021B04.12//2.5e-72:277:53//ARABIDOPSIS THAL-
 25 IANA (MOUSE-EAR CRESS)//O04658
 F-Y79AA1000258//PROLINE-RICH PROTEIN MP-2 PRECURSOR//2.8e-08:174:35//MUS MUSCULUS
 (MOUSE)//P05142
 F-Y79AA1000268//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT)//0.00020:176:33//RATTUS NORVEGICUS
 (RAT)//P13941
 30 F-Y79AA1000313//HYPOTHETICAL 54.0 KD PROTEIN C32A3.1 IN CHROMOSOME III//0.092:127:21//
 CAENORHABDITIS ELEGANS//Q09260
 F-Y79AA1000328//SEL-10 PROTEIN//5.3e-05:129:28//CAENORHABDITIS ELEGANS//Q93794
 F-Y79AA1000342//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN)//1.0:73:30//OVIS AR-
 IES (SHEEP)//P26372
 35 F-Y79AA1000346//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//1.8e-95:205:
 83//BOS TAURUS (BOVINE)//P53620
 F-Y79AA1000349//ANTIFREEZE PEPTIDE 4 PRECURSOR//0.036:37:54//PSEUDOPLEURONECTA AMERI-
 CANUS (WINTER FLOUNDER)//P02734
 F-Y79AA1000355//HYPOTHETICAL 18.2 KD PROTEIN ZK632.13 IN CHROMOSOME III//0.0031:106:28//
 40 CAENORHABDITIS ELEGANS//Q10120
 F-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161//1.4e-16:208:28//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P25343
 F-Y79AA1000405//LIGHT-HARVESTING PROTEIN B-800-850, ALPHA CHAIN C (ANTENNA PIGMENT PRO-
 TEIN, ALPHA CHAIN C) (LH II-C ALPHA)//0.98:50:30//RHODOPSEUDOMONAS PALUSTRIS//P35103
 45 F-Y79AA1000410//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.9e-20:62:79//HOMO SAPIENS (HUMAN)//
 P39194
 F-Y79AA1000420//HYPOTHETICAL 27.7 KD PROTEIN IN UME3-HDA1 INTERGENIC REGION//1.4e-06:86:38//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53970
 F-Y79AA1000469//HYPOTHETICAL 48.4 KD PROTEIN F44B9.5 IN CHROMOSOME III//2.8e-34:211:40//
 50 CAENORHABDITIS ELEGANS//P34426
 F-Y79AA1000480//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I//3.9e-15:90:32//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10414
 F-Y79AA1000538//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.37:41:48//HOMO SAPIENS (HUMAN)//
 P39195
 55 F-Y79AA1000539//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75)//
 1.8e-21:190:37//HOMO SAPIENS (HUMAN)//Q08170
 F-Y79AA1000540//SPERM PROTAMINE P1//0.00045:66:45//DASYURUS VIVERRINUS (SOUTHEASTERN
 QUOLL), AND DASYURUS HALLUCATUS//P42135

F-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT)//1.6e-79:186:87//MUS MUSCULUS (MOUSE)//P17427
 F-Y79AA1000574//AKLAVINONE C-11 HYDROXYLASE (EC 1.-.-.) (FRAGMENT)//0.010:35:60//STREPTOMY-
 5 CES PEUCETIUS//P32009
 F-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION//4.5e-27:197:36//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P28320
 F-Y79AA1000627//ZINC FINGER PROTEIN 134//1.6e-34:191:35//HOMO SAPIENS (HUMAN)//P52741
 F-Y79AA1000705//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION//8.7e-36:250:
 10 40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P31380
 F-Y79AA1000734//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A)//0.00037:108:
 27//CANDIDA BOIDINII (YEAST)//Q00316
 F-Y79AA1000748//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III//1.0e-23:210:34//
 CAENORHABDITIS ELEGANS//Q09316
 15 F-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP)//
 1.4e-53:156:68//MUS MUSCULUS (MOUSE)//Q61990
 F-Y79AA1000774//HYPOTHETICAL 77.9 KD PROTEIN IN RRN10-MCM2 INTERGENIC REGION//1.2e-11:231:
 26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38205
 F-Y79AA1000782//CUTICLE COLLAGEN 2//0.012:56:35//CAENORHABDITIS ELEGANS//P17656
 20 F-Y79AA1000784//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR//1.3e-08:82:39//PLASMODIUM LOPHU-
 RAE//P04929
 F-Y79AA1000794//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.043:13:53//HO-
 MO SAPIENS (HUMAN)//P30808
 F-Y79AA1000800//PRIA PROTEIN PRECURSOR//0.031:94:34//LENTINULA EDODES (SHIITAKE MUSH-
 25 ROOM) (LENTINUS EDODES)//Q01200
 F-Y79AA1000802//HYPOTHETICAL 67.4 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION//0.26:186:23//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53882
 F-Y79AA1000805//AMP DEAMINASE (EC 3.5.4.6) (MYOADENYLATE DEAMINASE)//0.99:78:35//SCHIZOSAC-
 CHAROMYCES POMBE (FISSION YEAST)//P50998
 30 F-Y79AA1000824//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION//3.4e-44:111:
 49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48234
 F-Y79AA1000827//HYPOTHETICAL BHLF1 PROTEIN//0.0046:187:33//EPSTEIN-BARR VIRUS (STRAIN
 B95-8) (HUMAN HERPESVIRUS 4)//P03181
 F-Y79AA1000833//TUBULIN ALPHA-1 CHAIN//1.0e-75:239:66//CRICETULUS GRISEUS (CHINESE HAM-
 35 STER)//P05209
 F-Y79AA1000850//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//0.0078:57:31//HOMO SAPI-
 ENS (HUMAN)//P22532
 F-Y79AA1000962//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE//8.5e-11:241:26//GALLUS GALLUS
 (CHICKEN)//P10587
 40 F-Y79AA1000966//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.69:122:31//TRYPANOSOMA BRU-
 CEI BRUCEI//P24499
 F-Y79AA1000968//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EX-
 CHANGE FACTOR)//3.3e-102:211:93//RATTUS NORVEGICUS (RAT)//P70541
 F-Y79AA1000969//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//1.0:67:38//GALLUS GALLUS (CHICK-
 45 EN)//P02457
 F-Y79AA1000976//INVOLUCRIN//0.99:66:31//CEBUS ALBIFRONS (WHITE-FRONTED CAPUCHIN)//P24709
 F-Y79AA1000985//PERICENTRIN//1.1e-24:116:59//MUS MUSCULUS (MOUSE)//P48725
 F-Y79AA1001023//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION//0.37:79:27//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38250
 50 F-Y79AA1001041//SPERMATID-SPECIFIC PROTEIN T1 [CONTAINS: SPERM PROTAMINE SP1]//0.93:43:39//
 SEPIA OFFICINALIS (COMMON CUTTLEFISH)//P80001
 F-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC
 1.3.99.-) (VLCAD)//1.5e-51:211:52//BOS TAURUS (BOVINE)//P48818
 F-Y79AA1001061//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.8e-25:85:69//HOMO SAPIENS (HUMAN)//
 55 P39194
 F-Y79AA1001068//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN]//
 0.0015:207:33//MUS MUSCULUS (MOUSE)//P28481
 F-Y79AA1001077//ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 11.9 (ACP 11.9)//0.99:36:41//ARANEUS DI-

ADEMATUS (SPIDER)//P80515
 F-Y79AA1001078//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III//1.0e-06:197:23//
 CAENORHABDITIS ELEGANS //P34492
 F-Y79AA1001105//HOMEBOX PROTEIN OTX2 //2.9e-62:163:79//MUS MUSCULUS (MOUSE)//P80206
 5 F-Y79AA1001145//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.024:42:59//HOMO SAPIENS (HUMAN)//
 P39195
 F-Y79AA1001167//HYPOTHETICAL 7.1 KD PROTEIN IN IAP2-VLF1 INTERGENIC REGION//0.96:20:50//
 AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41471
 F-Y79AA1001177//HYPOTHETICAL BHLF1 PROTEIN//3.9e-05:135:34//EPSTEIN-BARR VIRUS (STRAIN
 10 B95-8) (HUMAN HERPESVIRUS 4)//P03181
 F-Y79AA1001185//PUTATIVE CUTICLE COLLAGEN C09G5.5//0.00017:93:38//CAENORHABDITIS ELE-
 GANS//Q09456
 F-Y79AA1001211
 F-Y79AA1001216//TENSIN//0.012:134:32//GALLUS GALLUS (CHICKEN)//Q04205
 15 F-Y79AA1001228//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)//0.088:75:34//HOMO SAPIENS (HUMAN)//
 Q02817
 F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HY-
 DROXYSTEROID DEHYDROGENASE 1)//1.1e-40:139:51//RATTUS NORVEGICUS (RAT)//P51657
 F-Y79AA1001236//HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION//2.0e-22:108:53//
 20 SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38238
 F-Y79AA1001281
 F-Y79AA1001299//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.0022:49:44//MUS MUSCULUS
 (MOUSE)//P05143
 F-Y79AA1001312//50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR//0.98:117:25//ARABIDOP-
 25 SIS THALIANA (MOUSE-EAR CRESS)//P92959
 F-Y79AA1001323//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUA-
 MOUS CELL MARKER) (SPRP)//0.082:44:40//SUS SCROFA (PIG)//P35323
 F-Y79AA1001384//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII)//0.99:47:40//MUS MUSCULUS
 (MOUSE)//P33622
 30 F-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-1J)//9.8e-58:157:62//HOMO SAPIENS (HUMAN)//
 P31271
 F-Y79AA1001394//TRICHOHYALIN//4.7e-08:121:36//HOMO SAPIENS (HUMAN)//Q07283
 F-Y79AA1001402//ETS-DOMAIN TRANSCRIPTION FACTOR ERF//0.0087:81:33//MUS MUSCULUS
 (MOUSE)//P70459
 35 F-Y79AA1001493//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X//4.5e-21:125:44//
 CAENORHABDITIS ELEGANS//Q11076
 F-Y79AA1001511//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION//2.3e-17:249:
 31//SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53313
 F-Y79AA1001533//DNA-DIRECTED RNA POLYMERASE I49 KD POLYPEPTIDE (EC 2.7.7.6) (A49)//0.0099:
 40 155:23//SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q01080
 F-Y79AA1001541
 F-Y79AA1001548//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-17:53:83//HOMO SAPIENS (HUMAN)//
 P39192
 F-Y79AA1001555//MAJOR SURFACE ANTIGEN//0.046:62:29//HEPATITIS B VIRUS//P31873
 45 F-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-
 TIVATING ENZYME)//8.6e-11:144:31//ESCHERICHIA COLI//P27550
 F-Y79AA1001585//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.012:64:40//MUS MUS-
 CULUS (MOUSE)//P15265
 F-Y79AA1001594//CORNIFIN BETA//0.61:88:31//MUS MUSCULUS (MOUSE)//O09116
 50 F-Y79AA1001603//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)
 (TAFII-130) (TAFII130)//0.024:170:30//HOMO SAPIENS (HUMAN)//O00268
 F-Y79AA1001613//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1)//4.5e-09:136:27//HOMO
 SAPIENS (HUMAN)//P28698
 F-Y79AA1001647//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C//0.093:94:26//MYCOBACTERIUM TUBER-
 55 CULOSIS//P71779
 F-Y79AA1001665//HOMEBOX PROTEIN DLX-2 (HOMEBOX PROTEIN TES-1)//0.79:90:26//MUS MUSCU-
 LUS (MOUSE)//P40764
 F-Y79AA1001679//LAMBDA-CRYSTALLIN//1.6e-95:224:81//ORYCTOLAGUS CUNICULUS (RABBIT)//P14755

EP 1 074 617 A2

F-Y79AA1001692//GERM CELL-LESS PROTEIN//3.5e-08:78:38//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01820
 F-Y79AA1001696//INSULIN//1.0:33:27//ANGUILLA ROSTRATA (AMERICAN EEL)//P42633
 F-Y79AA1001705//HYPOTHETICAL BHLF1 PROTEIN//0.0013:192:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181
 F-Y79AA1001711//PARATHYMOSIN (ZINC-BINDING 11.5 KD PROTEIN)//0.032:38:34//RATTUS NORVEGICUS (RAT)//P04550
 F-Y79AA1001781
 F-Y79AA1001805//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP)//0.0063:128:30//HOMO SAPIENS (HUMAN)//P50552
 F-Y79AA1001827//SPERM PROTAMINE P1//0.015:45:40//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM)//P35305
 F-Y79AA1001846//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//2.4e-09:42:73//HOMO SAPIENS (HUMAN)//P39188
 F-Y79AA1001848//KRUEPPEL PROTEIN (FRAGMENT)//1.8e-10:63:44//PSYCHODA CINEREA//Q02035
 F-Y79AA1001866//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10)//0.00036:108:37//MUS MUSCULUS (MOUSE)//Q61967
 F-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN-1 RECEPTOR) (CD134 ANTIGEN)//3.2e-07:100:35//HOMO SAPIENS (HUMAN)//P43489
 F-Y79AA1001875//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD)//0.020:25:64//HOMO SAPIENS (HUMAN)//P20931
 F-Y79AA1001923//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.016:83:36//HOMO SAPIENS (HUMAN)//P10162
 F-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C//8.1e-13:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O42643
 F-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2:18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)//9.8e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P42743
 F-Y79AA1002083//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.036:53:45//HOMO SAPIENS (HUMAN)//P30808
 F-Y79AA1002089//HYPOTHETICAL 49.1 KD PROTEIN F02A9.4 IN CHROMOSOME III//0.12:171:22//CAENORHABDITIS ELEGANS//P34384
 F-Y79AA1002093//MAX PROTEIN//3.1e-07:111:29//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO)//P52161
 F-Y79AA1002103//SHORT NEUROTOXIN C//0.040:21:47//AIPYSURUS LAEVIS (OLIVE SEA SNAKE)//P19958
 F-Y79AA1002115//HYPOTHETICAL PROTEIN MJ0827//0.84:68:30//METHANOCOCCUS JANNASCHII//Q58237
 F-Y79AA1002125//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC REGION//3.4e-29:197:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40206
 F-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1)//1.9e-19:120:45//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24133
 F-Y79AA1002204//TBX6 PROTEIN (T-BOX PROTEIN 6)//0.0011:162:32//MUS MUSCULUS (MOUSE)//P70327
 F-Y79AA1002208//ANKYRIN//2.9e-08:231:29//MUS MUSCULUS (MOUSE)//Q02357
 F-Y79AA1002209//TYROSYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS)//3.7e-23:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48527
 F-Y79AA1002210//CORNIFIN A (SMALL PROLINE-RICH PROTEIN 1A) (SPR-1A) (SPRK)//0.0061:69:31//HOMO SAPIENS (HUMAN)//P35321
 F-Y79AA1002211//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//9.2e-10:43:62//HOMO SAPIENS (HUMAN)//P39193
 F-Y79AA1002220
 F-Y79AA1002229//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I//1.9e-21:147:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10264
 F-Y79AA1002234
 F-Y79AA1002246//MYOSIN IC HEAVY CHAIN//0.00066:131:34//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569

EP 1 074 617 A2

F-Y79AA1002258//HYPOTHETICAL 103.9 KD PROTEIN ZK370.3 IN CHROMOSOME III.//4.3e-45:164:48//
CAENORHABDITIS ELEGANS//Q02328
F-Y79AA1002298//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAG-
MENT).//0.0063:99:31//HOMO SAPIENS (HUMAN).//P10161
5 F-Y79AA1002307
F-Y79AA1002311//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III.//0.75:198:24//
CAENORHABDITIS ELEGANS//P46012
F-Y79AA1002351//CUTICLE COLLAGEN 34.//0.74:128:35//CAENORHABDITIS ELEGANS//P34687
F-Y79AA1002361//GLC7-INTERACTING PROTEIN 2.//0.050:71:29//SACCHAROMYCES CEREVISIAE (BAK-
ER'S YEAST).//P40036
10 F-Y79AA1002399//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1)
(CALMODULIN-BINDING PROTEIN P-57).//1.0:89:30//CARASSIUS AURATUS (GOLDFISH).//P17691
F-Y79AA1002407//HYPOTHETICAL 31.5 KD PROTEIN IN YGP1-YCK2 INTERGENIC REGION.//3.7e-16:232:
28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53899
15 F-Y79AA1002416//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//6.7e-72:
162:84//HOMO SAPIENS (HUMAN).//P17812
F-Y79AA1002431//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.81:34:41//HOMO SAPIENS
(HUMAN).//P22531
F-Y79AA1002433//CELL DIVISION CONTROL PROTEIN 68.//0.00024:85:27//SACCHAROMYCES CEREVI-
SIAE (BAKER'S YEAST).//P32558
20 F-Y79AA1002472//ZINC FINGER PROTEIN 35 (ZFP-35).//2.3e-60:217:44//MUS MUSCULUS (MOUSE).//
P15620
F-Y79AA1002482//ZINC FINGER PROTEIN 141.//2.0e-31:90:55//HOMO SAPIENS (HUMAN).//Q15928
F-Y79AA1002487//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN
25 CHROMOSOME I.//0.18:41:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

Homology Search Result Data 2.

[0300] The result of the homology search of the GenBank using the clone sequence of 5'-end except EST and STS.
30 [0301] Data include

the name of clone,
definition of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
35 the Accession No. of the top hit data, as in the order separated by //.
[0302] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.4e-106:695:86//L16953
F-HEMBA1000012//Caenorhabditis-elegans cosmid C16C10, complete sequence.//1.5e-24:374:66//Z46787
40 F-HEMBA1000020//Homo sapiens beta 2 gene.//3.5e-112:529:90//X02344
F-HEMBA1000030//Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GT-
Pase-activating protein (GIT1) mRNA, complete cds.//5.6e-124:743:88//AF085693
F-HEMBA1000042//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3
unordered pieces.//1.1e-25:529:65//AC004581
45 F-HEMBA1000046//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 125I3, WORKING
DRAFT SEQUENCE.//3.2e-11:330:63//AL033528
F-HEMBA1000050//Homo sapiens DNA sequence from PAC 172K10 on chromosome 6q24. Contains STS, GSS
and chromosome 6 fragment, complete sequence.//0.32:407:59//AL022477
F-HEMBA1000076//Homo sapiens full-length insert cDNA clone ZB97G06.//6.2e-135:594:98//AF086182
50 F-HEMBA1000111//CIT-HSP-2291M18.TF CIT-HSP Homo sapiens genomic clone 2291M18 genomic survey se-
quence.//2.8e-16:132:79//AQ004134
F-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//8.6e-98:230:93//
AC003104
F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.1e-167:791:98//AB018340
55 F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds.//2.2e-44:242:96//AB018331
F-HEMBA1000156//Rattus norvegicus scaffold attachment factor, B mRNA, complete cds.//1.1e-10:409:60//
AF056324
F-HEMBA1000158//Homo sapiens CAGH44 mRNA, partial cds.//1.6e-35:365:73//U80741

- F-HEMBA1000168//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING DRAFT SEQUENCE //0.99:290:61//AL031033
- F-HEMBA1000180//rat u2 small nuclear rna gene and flanks //3.7e-18:112:98//K00034
- F-HEMBA1000185
- 5 F-HEMBA1000193//Human FMR1 gene, 5' end //0.0012:191:67//L19476
- F-HEMBA1000201//Human Ini1 mRNA, complete cds //2.0e-73:440:92//U04847
- F-HEMBA1000213//Plasmodium falciparum MAL3P7, complete sequence //0.90:332:59//AL034559
- F-HEMBA1000216//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds //4.8e-117:585:83//AF060194
- 10 F-HEMBA1000227//H.sapiens CpG island DNA genomic Mse1 fragment, clone 179h6, reverse read cpg179h6.rt1a //1.9e-14:95:98//Z64921
- F-HEMBA1000231//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cpg90a5.rt1a //5.1e-34:186:97//Z56144
- F-HEMBA1000243//Human DNA sequence from PAC 440O21 on chromosome X contains ESTs and STS //4.1e-67:291:82//Z84481
- 15 F-HEMBA1000244//M.musculus Ank-1 mRNA for erythroid ankydn //0.029:316:59//X69065
- F-HEMBA1000251//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence //0.35:467:60//AC004454
- F-HEMBA1000264
- 20 F-HEMBA1000280//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces //8.9e-20:218:78//AC004825
- F-HEMBA1000282//Homo sapiens chromosome Y, clone 264.M.20, complete sequence //4.2e-08:134:77//AC004617
- F-HEMBA1000288//345L5.TPB CIT978SKA1 Homo sapiens genomic clone A-345L05, genomic survey sequence //1.1e-06:152:73//B17459
- 25 F-HEMBA1000290//Human ornithine decarboxylase gene, complete cds //3.2e-11:507:62//M33764
- F-HEMBA1000302//CIT-HSP-2169N13.TF CIT-HSP Homo sapiens genomic clone 2169N13, genomic survey sequence //5.4e-06:86:88//B90730
- F-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds //7.9e-111:701:86//AF030131
- 30 F-HEMBA1000304//HS_3006_A1_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=17 Row=A, genomic survey sequence //5.2e-40:240:92//AQ118226
- F-HEMBA1000307//Mus musculus mRNA for CDV-1R protein //7.9e-127:815:84//Y10495
- F-HEMBA1000327//HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence //1.4e-11:87:96//AQ187492
- 35 F-HEMBA1000333
- F-HEMBA1000338//Homo sapiens chromosome X, PAC 671D9, complete sequence //4.0e-66:271:84//AF031078
- F-HEMBA1000351//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence //0.64:334:60//AC004848
- F-HEMBA1000355//Pseudorabies virus serine/threonine kinase (ULPK) gene, partial cds and alkaline nuclease (AN) gene, complete cds //0.017:313:63//U25056
- 40 F-HEMBA1000356//Oryctolagus cuniculus Troponin T cardiac isoform mRNA, 3' end of cds //0.87:198:61//L40178
- F-HEMBA1000357//HS_3194_A1_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence //6.5e-90:436:98//AQ173748
- F-HEMBA1000366//HS_3027_B2_G06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=12 Row=N, genomic survey sequence //0.0074:192:64//AQ128843
- 45 F-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence //4.2e-106:133:99//AL031587
- F-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence //1.6e-22:659:63//AC006116
- 50 F-HEMBA1000387//Homo sapiens chromosome 12p13.3 clone RPC11-264F23, WORKING DRAFT SEQUENCE, 90 unordered pieces //3.2e-06:136:75//AC006122
- F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15, complete sequence //3.5e-111:284:95//AC004520
- 55 F-HEMBA1000392//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE //1.8e-39:332:80//AL031984
- F-HEMBA1000396//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, complete sequence //9.5e-35:364:73//U80460

- F-HEMBA1000411//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//8.1e-18:424:64//U96409
- F-HEMBA1000418//Drosophila melanogaster Oregon-R mitochondrial A+T region.//0.0026:564:59//U11584
- 5 F-HEMBA1000422//Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence.//9.2e-14:232:70//AC003112
- F-HEMBA1000428//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//3.8e-37:408:69//AC004554
- F-HEMBA1000434//Caenorhabditis elegans cosmid Y48E1B, complete sequence.//0.73:454:57//Z93393
- F-HEMBA1000442
- 10 F-HEMBA1000456//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//6.3e-06:62:96//B85188
- F-HEMBA1000459//Mus musculus hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds.//6.8e-70:580:79//AF028808
- F-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//2.8e-154:746:98//AC004839
- 15 F-HEMBA1000464//Homo sapiens, clone hRPK.15_A_1, complete sequence.//4.8e-25:397:72//AC006213
- F-HEMBA1000469//CIT-HSP-2167P21.TF CIT-HSP Homo sapiens genomic clone 2167P21, genomic survey sequence.//4.0e-83:406:99//B94160
- F-HEMBA1000488//Homo sapiens Chromosome 22q11.2 PAC Clone p_m11 In BCRL2-GGT Region, complete sequence.//4.2e-53:312:93//AC004033
- 20 F-HEMBA1000490//Campylobacter jejuni groES, groEL genes.//0.59:451:62//Y13334
- F-HEMBA1000491//Murine sarcoma virus (Harvey-strain) H-ras transforming p21 gene.//8.6e-06:338:58//X00740
- F-HEMBA1000501//Homo sapiens chromosome 17, clone hRPK.264_B_14, complete sequence.//9.4e-41:591:69//AC005884
- 25 F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os).//4.0e-07:57:100//D13666
- F-HEMBA1000505
- F-HEMBA1000508//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.035:329:61//AC004661
- F-HEMBA1000518//Caenorhabditis elegans cosmid C17H12.//0.96:425:58//AF045642
- 30 F-HEMBA1000519//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//1.6e-53:300:89//AC004616
- F-HEMBA1000520//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.7e-10:117:86//AC006006
- F-HEMBA1000523
- 35 F-HEMBA1000531//Mus musculus Hsp70-related NST-1 (hsr.1) mRNA, complete cds.//3.9e-35:290:80//U08215
- F-HEMBA1000534//Homo sapiens chromosome 17, clone hRPK.177_H_5, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.7e-36:328:77//AC005973
- F-HEMBA1000540//Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAI project).//0.057:265:63//AL033545
- 40 F-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//1.2e-110:572:88//D89340
- F-HEMBA1000545//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//7.5e-130:780:89//Z49237
- F-HEMBA1000555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134O19, WORKING DRAFT SEQUENCE.//3.2e-175:838:98//AL034555
- 45 F-HEMBA1000557//CIT-HSP-2369F15.TF CIT-HSP Homo sapiens genomic clone 2369F15, genomic survey sequence.//2.8e-32:315:78//AQ074611
- F-HEMBA1000561//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//3.4e-69:665:72//U92564
- F-HEMBA1000563//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.59:261:61//AC005504
- 50 F-HEMBA1000568//HS_3243_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3243 Col=24 Row=B, genomic survey sequence.//3.1e-54:323:91//AQ219628
- F-HEMBA1000569//M.musculus mRNA for GPI-anchored protein.//1.4e-19:440:61//X89571
- F-HEMBA1000575//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0016:557:57//AC005506
- 55 F-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//1.7e-11:132:79//AF045573
- F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.3e-43:228:97//AJ007509

F-HEMBA1000592//Mus musculus clone OST7314, genomic survey sequence//7.3e-07:68:94//AF046733
 F-HEMBA1000594//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs//8.7e-71:553:79//Z83822
 F-HEMBA1000604//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 237J2, WORKING
 5 DRAFT SEQUENCE//2.9e-21:158:75//AL021394
 F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds//1.1e-118:561:99//AB007925
 F-HEMBA1000622//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence//2.2e-28:426:70//AC004382
 F-HEMBA1000636//Human CpG island sequence, clone Q28B8//1.0e-15:274:68//D85773
 10 F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//6.7e-137:639:99//AB014590
 F-HEMBA1000655//, complete sequence//5.1e-83:685:80//AC005815
 F-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds//1.1e-91:597:84//U35776
 F-HEMBA1000662//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces//
 15 0.019:695:57//AC004907
 F-HEMBA1000673//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE//1.5e-48:325:85//Z86090
 F-HEMBA1000682//Homo sapiens (subclone 5_g5 from P1 H25) DNA sequence//7.7e-61:615:74//L43411
 F-HEMBA1000686
 20 F-HEMBA1000702
 F-HEMBA1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces//0.0037:569:57//AC005507
 F-HEMBA1000719//Streptomyces coelicolor cosmid 1C2//2.0e-09:483:62//AL031124
 F-HEMBA1000722//Toxoplasma gondii chloroplast, complete genome//0.00058:762:57//U87145
 25 F-HEMBA1000726//H.sapiens HLA-DRB1*15 gene//9.8e-49:189:89//X88791
 F-HEMBA1000727//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence//0.0054:206:67//B60158
 F-HEMBA1000747
 F-HEMBA1000749//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence//3.3e-05:124:75//AL024509
 30 F-HEMBA1000752//Human Chromosome X, complete sequence//5.9e-48:502:75//AC004073
 F-HEMBA1000769//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.011:179:67//AC005043
 35 F-HEMBA1000773//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y59A8, WORKING DRAFT SEQUENCE//0.070:231:63//Z98870
 F-HEMBA1000774//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence//6.2e-40:385:75//AC004953
 F-HEMBA1000791
 40 F-HEMBA1000817//Myrmecia pilosula HI87-135 mitochondrion cytochrome b gene, partial cds//0.99:244:58//U15678
 F-HEMBA1000822//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island//0.033:294:62//Z81370
 F-HEMBA1000827//Borrelia burgdorferi (section 50 of 70) of the complete genome//9.7e-05:463:58//AE001164
 45 F-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1-PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence//3.0e-153:732:98//AL022394
 50 F-HEMBA1000851//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds//1.6e-31:386:72//AF059273
 F-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPC14-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence//8.5e-115:455:98//AC005295
 F-HEMBA1000867
 55 F-HEMBA1000869//Human DNA sequence from cosmid J138O17, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element//6.6e-41:424:75//Z72519
 F-HEMBA1000870//Gnaptodon pumilio cytochrome oxidase II gene, partial cds; and tRNA-Asp, tRNA-His, and tRNA-Lys genes, complete sequence, mitochondrial genes for mitochondrial products//0.0049:211:66//AF034598

F-HEMBA1000872//CIT-HSP-2355D20.TF CIT-HSP Homo sapiens genomic clone 2355D20, genomic survey sequence.//3.7e-33:180:98//AQ059583
 F-HEMBA1000876//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//5.6e-37:262:72//Z83826
 5 F-HEMBA1000908//Triticum aestivum low-affinity cation transporter (LCT1) mRNA, complete cds//1.0:304:59//AF015523
 F-HEMBA1000910//M.musculus necdin mRNA, complete cds.//6.1e-08:256:61//M80840
 F-HEMBA1000918//Tetrahymena thermophila micronuclear developmentally eliminated sequence region.//0.13:232:63//U88158
 10 F-HEMBA1000919//Gallus domesticus filamin mRNA, complete cds.//1.0:213:65//U00147
 F-HEMBA1000934//CIT-HSP-2053H24.TR CIT-HSP Homo sapiens genomic clone 2053H24, genomic survey sequence.//5.5e-11:275:64//B69224
 F-HEMBA1000942//Homo sapiens clone DJ0754G14, WORKING DRAFT SEQUENCE, 15 unordered pieces.//9.7e-05:78:83//AC004878
 15 F-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//5.8e-140:661:99//AC005324
 F-HEMBA1000946
 F-HEMBA1000960//Homo sapiens clone DJ1111F22, WORKING DRAFT SEQUENCE, 12 unordered pieces.//8.3e-16:181:75//AC004967
 20 F-HEMBA1000968//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 69M21, WORKING DRAFT SEQUENCE.//4.4e-117:398:86//AL031735
 F-HEMBA1000971//H.sapiens CpG island DNA genomic MseI fragment, clone 182f4, forward read cpg182f4 fl1a.//1.5e-20:126:96//Z57528
 F-HEMBA1000972//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11.//0.34:642:59//AB020858
 25 F-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//5.1e-183:865:98//AC004817
 F-HEMBA1000975//Orf virus homologue of retroviral pseudoprotease gene, complete cds.//0.00065:391:62//M30023
 F-HEMBA10009851//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//3.4e-05:243:65//Z93929
 30 F-HEMBA1000986//Homo sapiens DNA from chromosome 19-cosmid R31491, genomic sequence.//6.6e-06:508:61//AD000813
 F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds.//1.2e-22:193:84//D84064 F-HEMBA1001007
 35 F-HEMBA1001008//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//7.8e-46:532:73//AL031577
 F-HEMBA1001009//Human mRNA for IgM heavy chain complete sequence.//0.97:369:59//X17115
 F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//4.4e-139:661:98//AB007937
 F-HEMBA1001019//Homo sapiens, clone hRPK.15_A_1, complete sequence.//1.6e-16:521:64//AC006213
 40 F-HEMBA1001020//Homo sapiens chromosome 17, clone hRPK.178_C_3, complete sequence.//3.8e-50:367:72//AC005702
 F-HEMBA1001022
 F-HEMBA1001024//Homo sapiens T-cell receptor alpha delta locus from bases 1 to 250529 (section 1 of 5) of the Complete Nucleotide Sequence.//5.0e-23:378:69//AE000658
 45 F-HEMBA1001026//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and STS.//7.6e-19:867:60//Z86064
 F-HEMBA1001043//HS_2219_B1_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=19 Row=B, genomic survey sequence.//3.0e-15:124:88//AQ301521
 F-HEMBA1001051//Human Chromosome X clone bWDX342, complete sequence.//4.8e-79:308:84//AC004072
 50 F-HEMBA1001052//Homo sapiens chromosome 17, clone hRPK.146_P_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.53:384:61//AC005341
 F-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 10.//2.8e-26:397:71//U06084
 F-HEMBA1001060//Homo sapiens chromosome 17, clone hRPK.855_D_21 complete sequence.//0.98:280:62//AC006079
 55 F-HEMBA1001071//Human mRNA for pro alpha 1 (III) collagen C-terminal propeptide.//1.1e-31:181:96//X01742
 F-HEMBA1001077//nuclear protein TIF1 [mice, mRNA, 3951 nt].//3.6e-13:338:65//S78219
 F-HEMBA1001080//Streptomyces coelicolor cosmid 1A9.//0.00012:364:63//AL034446

- F-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase Ix genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.5e-134:476:96//AC004586
 F-HEMBA1001088//Sequence 1 from patent US 5552529.//2.2e-71:303:78//I25863
 F-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//8.9e-119:609:96//AC005105
 5 F-HEMBA1001099
 F-HEMBA1001109//Homo sapiens BAC clone RG318M05 from 7q22-q31.1, complete sequence.//2.4e-58:347:87//AC005250
 F-HEMBA1001121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90G24, WORKING DRAFT SEQUENCE.//3.4e-21:226:65//AL008723
 10 F-HEMBA1001122//Plasmodium falciparum chromosome 2, section 20 of 73 of the complete sequence.//9.2e-07:732:57//AE001383
 F-HEMBA1001123//Homo sapiens full-length insert cDNA clone ZD38E12.//1.1e-11:231:68//AF086247
 F-HEMBA1001133//Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.011:163:69//AC004909
 15 F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds.//6.9e-72:527:77//AB018341
 F-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.3e-120:578:98//AC005077
 F-HEMBA1001172//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.010:520:59//AC005507
 20 F-HEMBA1001174//R.norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5.//1.0e-59:565:73//X78604
 F-HEMBA1001197//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0037:151:70//AC004815
 F-HEMBA1001208//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//7.4e-35:195:81//AC002410
 25 F-HEMBA1001213//Homo sapiens clone DJ0892G19, complete sequence.//1.9e-171:826:98//AC004917
 F-HEMBA1001226//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.00010:557:57//AC006009
 F-HEMBA1001235//Homo sapiens chromosome 17, clone hRPK.601_N_13, complete sequence.//0.0086:372:58//AC005389
 30 F-HEMBA1001247//H.sapiens CpG island DNA genomic MseI fragment, clone 11b11, reverse read cpg11b11.r1a.//2.0e-24:154:93//Z64441
 F-HEMBA1001257//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-88:659:81//AF047020
 F-HEMBA1001265//Human 18S ribosomal RNA.//1.0e-32:180:97//X03205
 35 F-HEMBA1001281
 F-HEMBA1001286//B.taurus mRNA for RF-36-DNA-binding protein.//7.7e-26:236:81//X15543
 F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.5e-28:530:64//AC004131
 F-HEMBA1001294//Yeast mitochondrial aapl gene for ATPase subunit 8.//2.8e-15:722:60//X00960
 40 F-HEMBA1001299//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//4.2e-24:288:76//AL031003
 F-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//7.2e-121:439:96//E12260
 F-HEMBA1001303//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.011:637:56//AC005505
 45 F-HEMBA1001310//HS_3252_B2_B12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=24 Row=D, genomic survey sequence.//1.2e-16:166:82//AQ217054
 F-HEMBA1001319//CIT-HSP-2034J6.TF CIT-HSP Homo sapiens genomic clone 2034J6, genomic survey sequence.//0.33:256:59//B79408
 50 F-HEMBA1001323//Homo sapiens proto-oncogene (Wnt-5a) mRNA, complete cds.//7.8e-30:165:99//L20861
 F-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs(BAC end sequences) and a CA repeat polymorphism, complete sequence.//5.4e-19:347:68//AL021368
 55 F-HEMBA1001327//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence.//0.012:152:65//AQ075713
 F-HEMBA1001330//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-103, com-

plete sequence.//0.0037:254:62//AL010208
 F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.1e-103:516:97//AF057358
 F-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//1.7e-150:706:99//AC006241
 F-HEMBA1001375//Streptomyces coelicolor cosmid 1E6.//1.0:375:59//AL033505
 F-HEMBA1001377//HS_3020_B1_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=23 Row=H, genomic survey sequence.//0.00022:63:77//AQ105297
 F-HEMBA1001383//Plasmodium falciparum chromosome 2, section 68 of 73 of the complete sequence.//0.00035:317:60//AE001431
 F-HEMBA1001387//HS_3039_B1_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//5.0e-90:437:98//AQ155035
 F-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//4.2e-47:159:89//AC005073
 F-HEMBA1001391//Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence.//2.0e-06:495:60//AL031256
 F-HEMBA1001398//H.sapiens CpG island DNA genomic MseI fragment, clone 70d11, forward read cpg70d11.ft1b.//0.018:46:97//Z62591
 F-HEMBA1001405//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//2.3e-74:623:71//AL034380
 F-HEMBA1001407//Mus musculus domesticus Torino (Sry) gene, complete cds.//0.36:363:57//U03645
 F-HEMBA1001411//Homo sapiens genomic DNA, 21q region, clone: S39BG29, genomic survey sequence.//8.4e-12:516:60//AG001050
 F-HEMBA1001413
 F-HEMBA1001415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 410I8, WORKING DRAFT SEQUENCE.//0.98:177:64//AL031732
 F-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.0e-177:859:97//AC006146
 F-HEMBA1001433//Homo sapiens clone DJ0892G19, complete sequence.//2.0e-35:376:64//AC004917
 F-HEMBA1001435//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//1.2e-74:284:84//AC005670
 F-HEMBA1001442//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-66, complete sequence.//0.056:194:63//AL010138
 F-HEMBA1001446//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//0.96:328:61//AC004047
 F-HEMBA1001450
 F-HEMBA1001454//Human DNA sequence from clone 598A24 on chromosome Xp11.1-11.23 Contains zinc finger X-linked proteins ZXDA, ZXDB, ESTs and STS, complete sequence.//2.0e-47:468:73//AL031115
 F-HEMBA1001455//CIT978SK-32J2.TV CIT978SK Homo sapiens genomic clone 32J2, genomic survey sequence.//1.5e-05:223:65//B78859
 F-HEMBA1001463//cSRL-69d1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-69d1, genomic survey sequence.//5.1e-66:564:77//B05652
 F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds.//1.9e-102:489:99//AB011144
 F-HEMBA1001478//HS_2228_A2_B03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=6 Row=C, genomic survey sequence.//4.5e-40:275:88//AQ032041
 F-HEMBA1001497//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//7.7e-47:311:85//AL031133
 F-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-IP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//2.0e-130:699:93//U89337
 F-HEMBA1001515//Homo sapiens chromosome 19, cosmid F24866, complete sequence.//4.1e-114:711:85//AC005794
 F-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//5.7e-162:769:98//AC004549
 F-HEMBA1001522//Caenorhabditis elegans cosmid ZK328.//8.6e-17:498:61//U50193
 F-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//0.31:120:69//Z98258

- F-HEMBA1001533
F-HEMBA1001557//*Chionoecetes opilio* (clone COP41) DNA microsatellite repeat regions.//7.0e-25:303:72//L49136
- 5 F-HEMBA1001566//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//7.2e-18:805:60//AL021026
- 10 F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2).//1.1e-64:338:95//AJ225044
- F-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.1e-148:698:99//AC004453
- F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.2e-173:678:99//AJ012449
- 15 F-HEMBA1001581//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.30:484:59//AC004980
- F-HEMBA1001585
F-HEMBA1001589//Human BAC clone RG317G18 from 7q31, complete sequence.//0.98:197:63//AC002432
- F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds.//8.2e-109:855:78//D50918
- 20 F-HEMBA1001608//RPC111-72E2.TJ RPC111 Homo sapiens genomic clone R-72E2, genomic survey sequence.//3.8e-05:235:64//AQ267131
- F-HEMBA1001620//*Oryza sativa* RINO1 mRNA for myo-inositol phosphate synthase, complete cds.//3.8e-40:719:64//AB012107
- F-HEMBA1001635//HS_3208_A1_D07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=13 Row=G, genomic survey sequence.//1.4e-15:120:90//AQ176944
- 25 F-HEMBA1001636//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.15:221:64//AC004216
- F-HEMBA1001640//HS_3253_B2_D03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=6 Row=H, genomic survey sequence.//9.1e-52:278:95//AQ216058
- F-HEMBA1001647//H.sapiens gene for plectin.//0.00052:629:61//Z54367
- 30 F-HEMBA1001651//*Salmo salar* DNA for a cryptic repeat.//7.9e-08:270:64//AJ012206
- F-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//5.9e-164:802:97//AC005368
- F-HEMBA1001658//*M.musculus* COL3A1 gene for collagen alpha-I.//2.4e-30:742:62//X52046
- 35 F-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.2e-144:682:99//AC005740
- F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//6.1e-152:725:98//AF072247
- F-HEMBA1001675//RPC111-54F8.TV RPC111 Homo sapiens genomic clone R-54F8, genomic survey sequence.//5.3e-75:341:85//AQ082126
- 40 F-HEMBA1001678//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//8.4e-54:551:74//AC002349
- F-HEMBA1001681
F-HEMBA1001702//*Plasmodium falciparum* chromosome 2, section 35 of 73 of the complete sequence.//0.94:676:54//AE001398
- 45 F-HEMBA1001709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//0.74:659:58//AL033531
- F-HEMBA1001711//*Lysiphlebus melandriicola* NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//3.0e-07:413:60//AF069178
- 50 F-HEMBA1001712//Homo sapiens BAC clone RG041H04 from 7q21-q22, complete sequence.//0.091:315:61//AC004519
- F-HEMBA1001714//*Rattus norvegicus* mitochondrial ATPase inhibitor gene, complete cds.//1.6e-28:218:75//U12250
- F-HEMBA1001718//HS_3056_A2_H08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=16 Row=O, genomic survey sequence.//2.0e-79:383:99//AQ106367
- 55 F-HEMBA1001723//HS_2188_A2_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//3.8e-28:174:94//AQ116793
- F-HEMBA1001731//HS_3021_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=21 Row=A, genomic survey sequence.//2.5e-11:420:62//AQ154658

- F-HEMBA1001734//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.00060:392:60//AC004617
- F-HEMBA1001744//HS_3194_A1_D05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//5.8e-29:163:97//AQ252295
- 5 F-HEMBA1001745//Homo sapiens chromosome 9q34, clone 280C11, complete sequence.//0.66:627:59//AC002102
- F-HEMBA1001746//HS_2163_B1_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=7 Row=L, genomic survey sequence.//1.4e-16:238:70//AQ085995
- F-HEMBA1001761//Genomic sequence from Mouse 9, complete sequence.//3.5e-52:198:86//AC002109
- 10 F-HEMBA1001781
- F-HEMBA1001784//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered-pieces.//5.5e-13:296:65//AC002099
- F-HEMBA1001791//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//0.18:534:59//AF038458
- 15 F-HEMBA1001800//CrT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//2.2e-40:335:80//AQ009222
- F-HEMBA1001803//M.musculus (Ba1b/C) P/L01 mRNA.//1.7e-25:286:74//Z31360
- F-HEMBA1001804//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-58:358:89//M21977
- F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//7.8e-174:809:98//AB007969
- 20 F-HEMBA1001809//Bovine herpesvirus 1 complete genome.//9.0e-09:639:57//AJ004801
- F-HEMBA1001815
- F-HEMBA1001819//HS_3079_B1_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=J, genomic survey sequence.//1.4e-79:396:97//AQ186616
- 25 F-HEMBA1001820//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//0.00026:436:60//AC005013
- F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds.//1.2e-40:510:65//AF064243
- F-HEMBA1001824//Homo sapiens expanded SCA7 CAG repeat.//6.1e-20:344:68//AF020275
- F-HEMBA1001835//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.0094:553:58//AC005161
- 30 F-HEMBA1001844//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//1.2e-22:316:70//AC005867
- F-HEMBA1001847//M.musculus Zfp-29 gene for zinc finger protein.//5.3e-27:397:69//X55126
- F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//8.8e-184:865:98//AB014517
- 35 F-HEMBA1001864//Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence.//0.38:337:62//AC005395
- F-HEMBA1001866//Caenorhabditis elegans cosmid F48E3.//1.4e-10:224:63//U28735
- F-HEMBA1001869//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//6.7e-98:288:91//AC005065
- 40 F-HEMBA1001888//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//4.9e-114:476:84//AC003693
- F-HEMBA1001896//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete cds.//2.2e-137:839:86//AF026954
- F-HEMBA1001910//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//0.90:221:63//AC003065
- 45 F-HEMBA1001912//HS_2237_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//9.7e-76:364:100//AQ033732
- F-HEMBA1001913//Leishmania major chromosome 3 clone L4625 strain Friedlin, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00063:219:65//AC005766
- 50 F-HEMBA1001915//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 5/10.//0.00011:366:63//AB020873
- F-HEMBA1001918//Pneumocystis carinii gene for major surface glycoprotein MSG105, exon1-2, complete cds.//0.00024:562:58//D82031
- F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.1e-184:855:99//AF000145
- 55 F-HEMBA1001939//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2)

- pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.1e-42:380:80//AL022310
 F-HEMBA1001940//Homo sapiens clone DJ1093116, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-175:861:97//AC005629
 F-HEMBA1001942//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE,
 5 66 unordered pieces.//0.097:107:71//AC006057
 F-HEMBA1001945//Drosophila F family transposable element F12 3' region.//0.94:140:65//X01934
 F-HEMBA1001950//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15b5, forward read cpg15b5.ft1q.//
 1.4e-27:168:95//Z54728
 F-HEMBA1001960//Locusta migratoria mRNA for nAChR alpha1 subunit.//0.010:108:71//AJ000390
 10 F-HEMBA1001962//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING
 DRAFT SEQUENCE, 9 unordered pieces.//9.7e-05:494:60//AC005507
 F-HEMBA1001964
 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/
 Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains
 15 a putative CpG island, ESTs and GSSs, complete sequence.//9.6e-122:373:99//AL031178
 F-HEMBA1001979//HS_3067_B1_A06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3067 Col=11 Row=B, genomic survey sequence.//0.43:193:64//AQ143506
 F-HEMBA1001987//Plasmodium falciparum MAL3P6, complete sequence.//1.0:428:56//Z98551
 F-HEMBA1001991//HS_2237_A2_G09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 20 nomic clone Plate=2237 Col=18 Row=M, genomic survey sequence.//4.3e-05:240:64//AQ067283
 F-HEMBA1002003//protein phosphatase 2C isoform [rats, liver, mRNA, 1950, nt].//2.7e-33:364:74//S90449
 F-HEMBA1002008//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00032:214:68//AC005948
 F-HEMBA1002018
 F-HEMBA1002027//Human p37NB mRNA, complete cds.//0.014:58:96//U32907
 25 F-HEMBA1002035//Mouse transcriptional control element.//7.8e-07:200:69//M17284
 F-HEMBA1002039//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of
 the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//0.31:497:58//AL031053
 F-HEMBA1002049//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//4.5e-
 42:532:63//AC005216
 30 F-HEMBA1002084//Homo sapiens chromosome 19 cosmid F15386, genomic sequence, complete sequence.//
 0.81:435:59//AF025422
 F-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//7.2e-130:
 769:87//U92703
 F-HEMBA1002100//Homo sapiens PAC clone DJ0991G20, complete sequence.//1.3e-47:124:96//AC004943
 35 F-HEMBA1002102//Xenopus laevis mRNA for xSox7 protein, complete cds.//2.7e-13:132:71//D83649
 F-HEMBA1002113//F.rubripes GSS sequence, clone 063K10bB4, genomic survey sequence.//0.029:142:66//
 Z88840
 F-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.3e-14:515:62//AC000378
 F-HEMBA1002125//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds.//0.98:
 40 222:61//AF031815
 F-HEMBA1002139//Caenorhabditis elegans cosmid F55C9, complete sequence.//0.0081:371:60//Z81549
 F-HEMBA1002144//Saccharomyces cerevisiae mitochondrion transfer RNA-Met (tRNA-Met) gene, oxil gene, and
 ORF1.//4.9e-06:341:61//L36888
 F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds.//0.00017:353:62//AB018263
 45 F-HEMBA1002151
 F-HEMBA1002153//CITBI-E1-2519120.TR CITBI-E1 Homo sapiens genomic clone 2519120, genomic survey se-
 quence.//8.5e-61:334:94//AQ277613
 F-HEMBA1002160//Homo sapiens clone DJ1189D06, complete sequence.//8.5e-44:385:77//AC005232
 F-HEMBA1002161//Coturnix coturnix slow myosin heavy chain 2 (qmyhc2) mRNA, partial cds.//2.1e-59:571:74//
 50 AF006829
 F-HEMBA1002162//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-
 plete sequence.//5.3e-53:698:67//AC006210
 F-HEMBA1002166//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3
 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-50:319:78//AL008712
 55 F-HEMBA1002177//Homo sapiens BAC clone RG293F11 from 7q21-7q22, complete sequence.//2.5e-18:150:88//
 AC000066
 F-HEMBA1002185//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//
 0.00066:466:59//AC004825

F-HEMBA1002189//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces //3.3e-23:176:77//AC005015
 F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds //1.0:382:59//AB014589
 F-HEMBA1002199//Homo sapiens chromosome 4 clone B55B24 map 4q25, complete sequence //1.8e-20:368:66//AC005150
 5 F-HEMBA1002204//HS_2055_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=17 Row=O, genomic survey sequence //1.2e-06:178:65//AQ235350
 F-HEMBA1002212//S.cerevisiae chromosome IV reading frame ORF YDL101c //0.035:345:60//Z74149
 F-HEMBA1002215//M.musculus mRNA for testin //4.6e-80:504:87//X78989
 10 F-HEMBA1002226//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence //5.7e-63:336:74//AC003035
 F-HEMBA1002229//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence //2.6e-39:311:81//AC006044
 F-HEMBA1002237//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence //1.6e-12:397:64//AC004861
 15 F-HEMBA1002241
 F-HEMBA1002253
 F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds //3.5e-151:731:97//AF061936
 20 F-HEMBA1002265//Human DNA sequence from cosmid N28H9 on chromosome 22q11.2-qter contains ESTs, STS and endogenous retrovirus //1.3e-09:313:62//Z71183
 F-HEMBA1002267
 F-HEMBA1002270//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence //0.069:495:58//AC006210
 25 F-HEMBA1002321//Homo sapiens PAC clone DJ0991O23, complete sequence //0.019:564:58//AC004944
 F-HEMBA1002328//CIT-HSP-2387N15.TF.1 CIT-HSP Homo sapiens genomic clone 2387N15, genomic survey sequence //1.8e-71:346:99//AQ240836
 F-HEMBA1002337//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence //0.84:547:57//AB020754
 30 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds //2.4e-185:872:98//AB018314
 F-HEMBA1002348//CIT-HSP-2372K24.TR CIT-HSP Homo sapiens genomic clone 2372K24, genomic survey sequence //9.1e-33:230:75//AQ110676
 F-HEMBA1002349//Plasmodium falciparum histidine-rich protein II (HRP II) gene, complete cds //9.4e-06:504:57//U69551
 35 F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds //7.3e-188:872:99//AF092563
 F-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11 //2.1e-20:262:72//AB020868
 F-HEMBA1002389//D.discoideum spore coat 60 (sp60) gene, 5' flank //0.010:95:73//M34546
 40 F-HEMBA1002417//Canis familiaris ZO-3 (zo-3) mRNA, complete cds //6.2e-120:767:85//AF023617
 F-HEMBA1002419//HS-1047-A1-F01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=1 Row=K, genomic survey sequence //7.6e-06:111:76//B38165
 F-HEMBA1002430//HS_3137_B2_F10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=20 Row=L, genomic survey sequence //1.6e-56:367:88//AQ148697
 45 F-HEMBA1002439//Dictyostelium discoideum actin 8 gene, 3' UTR //0.67:129:64//M25216
 F-HEMBA1002458//Mus musculus REX-3 mRNA, complete cds //1.1e-30:274:72//AF051347
 F-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence //4.0e-173:822:98//AC005378
 F-HEMBA1002462//Sequence 41 from patent US 5708157 //9.8e-51:519:73//I80067
 F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds //4.0e-108:603:92//D50912
 50 F-HEMBA1002475//Streptomyces coelicolor cosmid 2H4 //0.0068:626:57//AL031514
 F-HEMBA1002477//Homo sapiens BAC clone NH0342K06 from 2, complete sequence //1.5e-40:349:78//AC005034
 F-HEMBA1002486
 F-HEMBA1002495//HS_3218_B1_A12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=23 Row=B, genomic survey sequence //1.0:179:67//AQ181410
 55 F-HEMBA1002498//Homo sapiens full-length insert cDNA clone ZD76B01 //1.4e-129:619:98//AF086404
 F-HEMBA1002503//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces //1.9e-24:306:68//AC004873

- F-HEMBA1002508//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.9e-76:464:83//AC004799
- F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//2.8e-157:738:98//AJ011972
- 5 F-HEMBA1002515//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 407F11, WORKING DRAFT SEQUENCE.//2.6e-07:307:64//AL022329
- F-HEMBA1002538//HS_2185_B2_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2185 Col=8 Row=D, genomic survey sequence.//4.7e-37:339:78//AQ298315
- 10 F-HEMBA1002542//HS_3197_B2_B10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//3.2e-70:372:95//AQ188792
- F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//3.5e-137:655:98//AF016903
- F-HEMBA1002552//Human Hep27 protein mRNA, complete cds.//8.8e-07:173:68//U31875
- F-HEMBA1002555//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.2e-15:628:60//AC004670
- 15 F-HEMBA1002558//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-41:353:76//AC002366
- F-HEMBA1002561//Homo sapiens chromosome 17, clone HRPC29G21, complete sequence.//1.1e-39:538:66//AC003687
- 20 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//1.3e-140:457:99//AF075587
- F-HEMBA1002583//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey sequence.//5.1e-79:385:99//AQ038102
- F-HEMBA1002590//Homo sapiens chromosome 17, clone hRPK.167_N_20, complete sequence.//1.9e-35:430:70//AC005940
- 25 F-HEMBA1002592//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//4Ae-19:303:71//Z93403
- F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//4.4e-175:820:99//AB011169
- F-HEMBA1002621//Homo sapiens PAC clone DJ0650P09 from 7q21, complete sequence.//0.14:353:58//AC004413
- 30 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//2.9e-187:632:97//AB018351
- F-HEMBA1002628//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-05:792:58//AC004153
- F-HEMBA1002629//Streptomyces coelicolor cosmid 1A9.//8.4e-08:576:58//AL034446
- 35 F-HEMBA1002645//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE.//5.6e-47:222:86//AL031118
- F-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//3.8e-182:859:99//AC004839
- F-HEMBA1002659//Z. mobilis alcohol dehydrogenase I (adhA) gene, complete cds.//0.97:144:66//M32100
- 40 F-HEMBA1002661//Homo sapiens PAC clone DJ0698G21 from 7p21-p22, complete sequence.//1.3e-116:774:84//AC004535
- F-HEMBA1002666
- F-HEMBA1002678//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1137F22, WORKING DRAFT SEQUENCE.//5.7e-156:750:98//AL034421
- 45 F-HEMBA1002679//nbxb0002cC12r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002F23r, genomic survey sequence.//4.3e-09:517:58//AQ051621
- F-HEMBA1002688//Herpes simplex virus type 2 (strain HG52), complete genome.//8.3e-20:651:61//Z86099
- F-HEMBA1002696//Mus musculus proteasome regulator PA28 beta subunit gene, complete cds.//7.6e-62:306:81//AF060195
- 50 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds.//1.9e-10:327:62//AB007924
- F-HEMBA1002712
- F-HEMBA1002716//HS_3064_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=19 Row=E, genomic survey sequence.//8.4e-97:491:96//AQ142980
- F-HEMBA1002728//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//6.1e-21:217:77//AC004782
- 55 F-HEMBA1002730//Human platelet glycoprotein IIIa (GPIIIa) gene, exon 1.//0.57:125:67//M57481
- F-HEMBA1002742//RPCI11-39J10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-39J10, genomic survey sequence.//1.1e-86:414:99//AQ029102

EP 1 074 617 A2

F-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence//7.1e-70:303:82//AC003694
F-HEMBA1002748//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41018, WORKING DRAFT SEQUENCE//0.096:212:62//AL031732
5 F-HEMBA1002750//Homo sapiens chromosome 5, PAC clone 170m10 (LBNL H89), complete sequence//6.7e-40:232:70//AC004622
F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.0e-177:834:98//AB011126
F-HEMBA1002770//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein)//1.3e-140:840:88//E12829
10 F-HEMBA1002777//F.rubripes GSS sequence, clone 189C06dB12, genomic survey sequence//1.1e-28:263:77//AL007965
F-HEMBA1002779//CIT-HSP-233311.TF CIT-HSP Homo sapiens genomic clone 233311, genomic survey sequence//1.8e-32:180:98//AQ036891
F-HEMBA1002780//Homo sapiens PAC clone DJ0244J05 from 5q31, complete sequence//7.0e-06:199:67//AC004592
15 F-HEMBA1002794//H.sapiens mRNA for protein kinase C mu//0.00015:244:67//X75756
F-HEMBA1002801//Plasmodium falciparum MAL3P2, complete sequence//0.0010:534:57//AL034558
F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//1.1e-167:820:97//AF071185
F-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces//3.1e-113:254:90//AC005043
20 F-HEMBA1002818//Cricetulus griseus H411 precursor (H411) mRNA, complete cds//1.2e-122:760:86//AF046870
F-HEMBA1002826//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence//0.0055:235:65//AL022153
F-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence//1.4e-170:744:99//AC004707
25 F-HEMBA1002850//Ephedrus persicae NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds//1.3e-05:334:59//AF069186
F-HEMBA1002863//CIT-HSP-2323A16.TF CIT-HSP Homo sapiens genomic clone 2323A16, genomic survey sequence//2.9e-140:750:93//AQ028419
30 F-HEMBA1002876//HS_2270_B1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=5 Row=P, genomic survey sequence//0.44:163:64//AQ164031
F-HEMBA1002886
F-HEMBA1002896//Homo sapiens chromosome 5, P1 clone 793C5 (LBNL H58), complete sequence//0.00015:277:61//AC005195
35 F-HEMBA1002921
F-HEMBA1002924//CIT-HSP-2171H4.TR CIT-HSP Homo sapiens genomic clone 2171H4, genomic survey sequence//0.0016:175:66//B89715
F-HEMBA1002934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE//1.2e-169:797:98//AL031681
40 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//4.9e-173:803:99//AB011148
F-HEMBA1002937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE//1.2e-163:411:99//AL033531
F-HEMBA1002939//RPCI11-74O14.TJ RPCI11 Homo sapiens genomic clone R-74O14, genomic survey sequence//1.7e-41:215:99//AQ266676
45 F-HEMBA1002944//RPCI11-55C2.TV RPCI11 Homo sapiens genomic clone R-55C2, genomic survey sequence//1.7e-37:375:74//AQ082240
F-HEMBA1002951//Homo sapiens chromosome 19, cosmid F20887, complete sequence//0.00074:683:58//AC005578
F-HEMBA1002954//RPCI11-79F7.TV RPCI11 Homo sapiens genomic clone R-79F7, genomic survey sequence//6.1e-24:250:78//AQ284146
50 F-HEMBA1002968//HS_2262_B2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=8 Row=N, genomic survey sequence//0.99:270:60//AQ217059
F-HEMBA1002970//RPCI11-5L24.TV RPCI11 Homo sapiens genomic clone RPCI11-5L24, genomic survey sequence//1.4e-10:189:71//B49289
55 F-HEMBA1002971//CIT-HSP-2363L16.TF CIT-HSP Homo sapiens genomic clone 2363L16, genomic survey sequence//4.3e-21:181:80//AQ080538
F-HEMBA1002973//Rattus norvegicus Wistar 3',5'-cyclic AMP phosphodiesterase (PDE4-10) gene, exon 10//2.5e-40:257:89//U01290

- F-HEMBA1002997//CIT-HSP-2387H15.TF.1 CIT-HSP Homo sapiens genomic clone 2387H15, genomic survey sequence.//9.5e-17:128:92//AQ240797
- F-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.1e-62:713:73//U20286
- 5 F-HEMBA1003021//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.5e-50:331:85//AC005484
- F-HEMBA1003033//Drosophila melanogaster, chromosome 3L, region 62A10-62B5, P1 clones DS02777, DS03222, DS02345, and DS04808, complete sequence.//2.6e-20:357:66//AC005557
- 10 F-HEMBA1003034//Human DNA sequence from 4PTCL, Huntington's Disease Region, chromosome 4p16.3.//4.5e-60:415:73//Z95704
- F-HEMBA1003035//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//2.3e-05:591:57//AC004617
- F-HEMBA1003037//RPC11-88F2.TJ RPC11 Homo sapiens genomic clone R-88F2, genomic survey sequence.//0.68:230:60//AQ286677
- 15 F-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//8.1e-128:550:94//AC004983
- F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//1.0e-164:777:98//AF054182
- 20 F-HEMBA1003064//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-07:744:59//AC005505
- F-HEMBA1003067//Rat dynorphin gene, exon 3.//1.0:140:63//M32783
- F-HEMBA1003071//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//1.5e-20:595:65//U72648
- F-HEMBA1003077//CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.//4.4e-33:176:99//AQ080257
- 25 F-HEMBA1003078//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//9.4e-43:478:70//Z99297
- F-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.96:57:85//AC004673
- 30 F-HEMBA1003083//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//8.0e-74:359:81//AC004548
- F-HEMBA1003086//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//3.6e-11:734:58//AF001550
- 35 F-HEMBA1003096//Sequence 4 from patent US 5440017.//5.7e-56:594:71//I13750
- F-HEMBA1003098//Human DNA sequence from cosmid SRL11M20, chromosome region 11p13. Contains EST and STS.//1.9e-09:230:69//Z83308
- F-HEMBA1003117//Mouse TIS11 primary response gene, complete cds.//0.00054:480:60//M58564
- 40 F-HEMBA1003129//HS_3139_B2_F05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=10 Row=L, genomic survey sequence.//2.3e-100:510:97//AQ187635
- F-HEMBA1003133//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//1.3e-78:370:90//AC005259
- F-HEMBA1003136
- F-HEMBA1003142//Homo sapiens full-length insert cDNA clone ZC39B06.//6.9e-121:563:100//AF086197
- 45 F-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//6.7e-183:850:99//AJ005670
- F-HEMBA1003166//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence, complete sequence.//3.8e-27:229:76//AC002302
- F-HEMBA1003175//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, WORKING DRAFT SEQUENCE.//9.4e-09:837:58//AB000882
- 50 F-HEMBA1003179//Homo sapiens DNA sequence from Fosmid 27C3 on chromosome 22q11.2-qter. Contains two possibly alternatively spliced unknown genes, one with homology to a worm protein. Contains ESTs, complete sequence.//5.4e-115:174:98//AL022325
- F-HEMBA1003197//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//1.1e-05:473:59//AC005824
- 55 F-HEMBA1003199//Rattus norvegicus Sprague-Dawley thyroid hormone receptor alpha gene, exon 1.//1.6e-05:367:61//U09302
- F-HEMBA1003202//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//9.0e-23:247:73//AC004003

F-HEMBA1003204//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//4.7e-26:141:83//Z83824

F-HEMBA1003212//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.9e-31:158:86//AC002037

5 F-HEMBA1003220//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.4e-24:284:75//AC004150

F-HEMBA1003222//RPC11-47P17.TJ RPC11 Homo sapiens genomic clone R-47P17, genomic survey sequence.//8.7e-39:202:99//AQ202885

F-HEMBA1003229//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence.//0.86:227:62//AB019230

10 F-HEMBA1003235//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.6e-05:372:61//AE001373

F-HEMBA1003250//HS-1063-A1-H02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 796 Col=3 Row=O, genomic survey sequence.//0.00032:57:96//B46142

15 F-HEMBA1003257//H.sapiens mRNA for RDC-1 POU domain containing protein.//2.2e-08:531:59//X64624

F-HEMBA1003273//H.sapiens flow-sorted chromosome 6 HindIII-fragment, SC6pA19H4.//0.070:267:64//Z78949

F-HEMBA1003276//CIT-HSP-2301B4.TF CIT-HSP Homo sapiens genomic clone 2301B4, genomic survey sequence.//5.2e-08:295:63//AQ015073

F-HEMBA1003278//HS_3075_A1_G09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=M, genomic survey sequence.//0.98:399:58//AQ120599

20 F-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.8e-101:277:97//AC005840

F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds.//9.0e-145:539:97//AF038662

25 F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//5.0e-166:799:98//AB011109

F-HEMBA1003296//CITBI-E1-2507M8.TR CITBI-E1 Homo sapiens genomic clone 2507M8, genomic survey sequence.//1.9e-05:388:63//AQ262551

F-HEMBA1003304//Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene.//8.0e-05:388:62//L17343

30 F-HEMBA1003309//Crassostrea gigas clone CN20 microsatellite sequence.//0.0017:210:64//AF051177

F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//4.6e-188:865:99//AB001872

F-HEMBA1003322//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//2.4e-54:316:87//Z93015

35 F-HEMBA1003327//CIT-HSP-2024C24.TRB CIT-HSP Homo sapiens genomic clone 2024C24, genomic survey sequence.//8.4e-12:166:76//B67147

F-HEMBA1003328//HS_2230_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=16 Row=P, genomic survey sequence.//0.026:128:71//AQ153313

F-HEMBA1003330//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.0e-160:745:99//AF045555

40 F-HEMBA1003348//HS_3194_A1_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=M, genomic survey sequence.//5.0e-79:381:99//AQ173779

F-HEMBA1003369//H.vulgare GAA-satellite DNA.//0.12:89:71//Z50100

F-HEMBA1003370//Homo sapiens cosmid 123E15, complete sequence.//3.5e-32:199:80//AF024533

45 F-HEMBA1003373//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//0.019:117:71//AL034405

F-HEMBA1003376//Human clone HS4.66 Alu-Ya5 sequence.//4.2e-30:196:85//U67229

F-HEMBA1003380//Homo sapiens DNA sequence from clone 394P21 on chromosome 1p36.12-36.13. Contains the PAX7 gene, locus D1S2644, ESTs and STSs, complete sequence.//4.6e-22:206:81//AL021528

50 F-HEMBA1003384//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00094:72:90//AC006026

F-HEMBA1003395//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.00041:826:57//AL031744

F-HEMBA1003402//CIT-HSP-2339K16.TR CIT-HSP Homo sapiens genomic clone 2339K16, genomic survey sequence.//2.4e-05:265:64//AQ056234

55 F-HEMBA1003403//Homo sapiens chromosome 4 clone B353C18.map 4q25, complete sequence.//4.3e-135:780:90//AC004066

F-HEMBA1003408

- F-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence//1.9e-41:239:95//AL031321
- F-HEMBA1003418//Rattus norvegicus Wistar polymeric immunoglobulin receptor (PIGR) gene, 3'UTR and trinucleotide repeat microsatellites//2.2e-06:247:64//J08273
- 5 F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//1.4e-149:697:99//AF051334
- F-HEMBA1003447//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence//1.7e-77:461:90//AC004066
- F-HEMBA1003461//Rhodobacter sphaeroides FliH (fliH) gene, partial cds, FliI (fliI) and FliJ (fliJ) genes, complete cds//8.6e-08:752:58//J31090
- 10 F-HEMBA1003463//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence//0.089:172:68//AC004098
- F-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence//4.5e-150:562:97//AC005041
- F-HEMBA1003528//Streptomyces fradiae gene for trypsinogen precursor, complete cds//4.7e-09:433:60//D16687
- F-HEMBA1003531//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence//2.3e-48:297:90//AC004990
- 15 F-HEMBA1003538//Human complement C1r mRNA, complete cds//4.3e-22:474:63//M14058
- F-HEMBA1003545//Rattus norvegicus (clone 1.6kb) islet-2 mRNA, complete cds//3.5e-143:805:91//L35571
- F-HEMBA1003548
- F-HEMBA1003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447E6, WORKING DRAFT SEQUENCE//3.4e-58:331:83//AL031724
- 20 F-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence//6.0e-99:703:84//AC005913
- F-HEMBA1003560//Bovine GTP-binding regulatory protein gamma-6 subunit mRNA, complete cds//1.3e-99:587:89//J05071
- 25 F-HEMBA1003568//HS_3149_A1_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3149 Col=7 Row=E, genomic survey sequence//4.1e-05:389:57//AQ166810
- F-HEMBA1003569//Homo sapiens BAC clone NH0335J18 from 2, complete sequence//1.6e-102:669:85//AC005539
- F-HEMBA1003571//Dictyostelium discoideum RegA (regA) gene, complete cds//0.00033:649:58//U60170
- 30 F-HEMBA1003579//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE//0.00034:623:56//AL031744
- F-HEMBA1003581//Mouse mRNA for talin//3.3e-41:181:86//X56123
- F-HEMBA1003591//Homo sapiens chromosome 16, BAC clone RPCI-11_192K18, complete sequence//4.4e-70:273:94//AC006075
- 35 F-HEMBA1003595//Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence//6.0e-17:768:58//AE001395
- F-HEMBA1003597//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence//4.0e-09:777:56//AE001398
- F-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence//1.3e-146:692:98//AC005153
- 40 F-HEMBA1003615//HS_2010_A2_A07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=14 Row=A, genomic survey sequence//1.1e-22:137:97//AQ226592
- F-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds//2.4e-169:501:97//AB015344
- F-HEMBA1003621//Mus musculus PIAS3 mRNA, complete cds//4.7e-37:165:92//AF034080
- 45 F-HEMBA1003622//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.0024:514:58//AC005139
- F-HEMBA1003630//CIT-HSP-2168N15.TR CIT-HSP Homo sapiens genomic clone 2168N15, genomic survey sequence//6.5e-15:358:63//B92984
- F-HEMBA1003637//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces//5.0e-21:238:76//AC005077
- 50 F-HEMBA1003640//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 112K5, WORKING DRAFT SEQUENCE//2.3e-15:371:63//Z85987
- F-HEMBA1003645//A.thaliana 81kb genomic sequence//1.0:529:57//X98130
- F-HEMBA1003646
- 55 F-HEMBA1003656
- F-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence//1.6e-175:824:98//AC005746
- F-HEMBA1003667//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces

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es.//1.1e-24:190:87//AC004765
F-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.7e-162:579:99//
AC005065
F-HEMBA1003680//H.sapiens DNA sequence.//7.3e-22:172:87//Z22322
5 F-HEMBA1003684//H.sapiens mRNA for Miz-1 protein.//0.0054:146:70//Y09723
F-HEMBA1003690//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//2.9e-72:606:77//AF039691
F-HEMBA1003692
F-HEMBA1003711//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//0.55:450:60//
AC003101
10 F-HEMBA1003714
F-HEMBA1003715//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and
genomic marker DXS8098, complete sequence.//3.0e-16:316:68//AL023575
F-HEMBA1003720//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//1.3e-41:483:
73//AC004056
15 F-HEMBA1003725//CIT-HSP-2351H9.TF CIT-HSP Homo sapiens genomic clone 2351H9, genomic survey se-
quence.//1.1e-112:532:99//AQ079348
F-HEMBA1003729//HS_3043_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3043 Col=13 Row=I, genomic survey sequence.//1.6e-12:87:98//AQ129345
F-HEMBA1003733//Homo sapiens, clone hRPK.15_A_1, complete sequence.//4.7e-104:761:82//AC006213
20 F-HEMBA1003742//HS_3027_A2_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3027 Col=4 Row=C, genomic survey sequence.//3.4e-08:67:97//AQ154731
F-HEMBA1003758//CIT-HSP-2379D18.TR CIT-HSP Homo sapiens genomic clone 2379D18, genomic survey se-
quence.//2.9e-10:310:63//AQ113513
F-HEMBA1003760//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//6.4e-114:714:86//
25 AF060194
F-HEMBA1003773//Plasmodium falciparum 3D7 chromosome 12.PFYAC336 genomic sequence, WORKING
DRAFT SEQUENCE, 5 unordered pieces.//0.078:378:58//AC005139
F-HEMBA1003783//Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3
like pseudogene, EST, STS.//9.0e-135:804:89//Z99496
30 F-HEMBA1003784//Caenorhabditis elegans cosmid C55B6.//0.054:463:58//U88181
F-HEMBA1003799//Homo sapiens Chromosome 22q11.2 Cosmid Clone 105a In DGCR Region, complete se-
quence.//1.9e-44:425:76//AC000070
F-HEMBA1003803//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.95:198:62//L40178
F-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//1.2e-138:275:99//
35 AC004596
F-HEMBA1003805//Mus musculus quaking type I (QKI) mRNA, complete cds.//6.6e-148:753:95//U44940
F-HEMBA1003807//HS-1068-B1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic
clone Plate=CT 278 Col=11 Row=N, genomic survey sequence.//6.7e-07:241:67//B47212
F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds.//1.0e-83:586:87//AB014516
40 F-HEMBA1003836//S.cerevisiae chromosome IX cosmid 9150.//5.1e-16:368:63//Z38125
F-HEMBA1003838//CIT-HSP-384J15.TR CIT-HSP Homo sapiens genomic clone 384J15, genomic survey se-
quence.//1.4e-45:180:90//B54810
F-HEMBA1003856//Homo sapiens chromosome 10 clone CIT9875K-1188B12 map 10p12.1, complete se-
quence.//0.0014:574:58//AC005875
45 F-HEMBA1003864//, complete sequence.//2.1e-91:234:95//AC005300
F-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//5.9e-81:853:71//AF030430
F-HEMBA1003879//H.sapiens CBP80 mRNA.//2.0e-08:87:95//X80030
F-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SE-
QUENCE.//1.7e-180:853:98//AP000036
50 F-HEMBA1003885//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.5e-39:376:67//
AC004079
F-HEMBA1003893//H.sapiens CpG island DNA genomic MseI fragment, clone 11b6, forward read cpg11b6.ft1a.//
3.6e-32:173:99//Z59012
F-HEMBA1003902//RPCI11-26M20.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-26M20, genomic survey
sequence.//8.2e-12:422:61//AQ003455
55 F-HEMBA1003908//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.0063:
468:58//AE001401
F-HEMBA1003926//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310O13, WORKING

DRAFT SEQUENCE.//3.6e-27:278:76//AL031658
 F-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//1.4e-55:315:81//AF109718
 F-HEMBA1003939//HS-1047-A1-G04-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone
 Plate=CT 830 Col=7 Row=M, genomic survey sequence.//6.1e-09:413:63//B38195
 5 F-HEMBA1003942//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING
 DRAFT SEQUENCE, 14 unordered pieces.//0.42:205:65//AC005140
 F-HEMBA1003950//M.capricolum DNA for CONTIG MC072.//0.029:458:58//Z33058
 F-HEMBA1003953//HS_2268_A1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2268 Col=7 Row=C, genomic survey sequence.//9.0e-07:239:64//AQ085098
 10 F-HEMBA1003958//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.8e-57:424:
 74//AC004894
 F-HEMBA1003959//RPC111-78E8.TV RPC111 Homo sapiens genomic clone R-78E8, genomic survey sequence.//
 4.3e-86:441:9611AQ285498
 F-HEMBA1003976//HS_3146_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3146 Col=17 Row=O, genomic survey sequence.//6.3e-10:129:80//AQ141146
 15 F-HEMBA1003978
 F-HEMBA1003985//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105C5,
 WORKING DRAFT SEQUENCE.//1.0:258:60//Z98855
 F-HEMBA1003987
 20 F-HEMBA1003989//Streptomyces coelicolor cosmid 1A9.//0.40:238:61//AL034446
 F-HEMBA1004000//Rattus norvegicus satellite sequence d0Mco2.//2.0e-07:116:70//U19354
 F-HEMBA1004011//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING
 DRAFT SEQUENCE, 2 unordered pieces.//0.098:286:60//AC004710
 F-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//2.8e-185:896:97//
 25 AC005670
 F-HEMBA1004015//Homo sapiens chromosome 17, clone hRPK.721_K_1, complete sequence.//6.3e-68:417:80//
 AC005411
 F-HEMBA1004024//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete
 sequence.//2.0e-47:418:77//AC005859
 30 F-HEMBA1004038//Homo sapiens genomic DNA, chromosome 21q11.1, segment 23/28, WORKING DRAFT SE-
 QUENCE.//1.6e-51:564:74//AP000052
 F-HEMBA1004042//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.2e-05:
 636:55//AE001398
 F-HEMBA1004045//Homo sapiens (subclone 1_g7 from BAC H76) DNA sequence, complete sequence.//1.9e-31:
 35 373:76//AC002252
 F-HEMBA1004048//Homo sapiens DNA for P35-related protein, exon 2.//0.039:234:63//D63393
 F-HEMBA1004049//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//
 4.8e-135:780:89//AC003106
 F-HEMBA1004055//Human chromosome 3p21.1 gene sequence.//4.7e-09:457:58//L13435
 40 F-HEMBA1004056//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING
 DRAFT SEQUENCE.//3.3e-25:246:77//AL021977
 F-HEMBA1004074//CIT-HSP-2053J5.TF CIT-HSP Homo sapiens genomic clone 2053J5, genomic survey se-
 quence.//7.8e-24:233:76//B68555
 F-HEMBA1004086//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence,
 45 and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//4.5e-08:614:59//
 U49822
 F-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//5.9e-121:502:85//
 AF091234
 F-HEMBA1004111//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14;
 50 HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.0e-36:317:80//AC006160
 F-HEMBA1004131//Mus musculus clone OST2067, genomic survey sequence.//8.7e-24:320:71//AF046393
 F-HEMBA1004132//HS_3226_B1_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3226 Col=19 Row=H, genomic survey sequence.//9.7e-13:232:71//AQ182017
 F-HEMBA1004133
 55 F-HEMBA1004138//HS_3036_B1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3036 Col=21 Row=N, genomic survey sequence.//0.0035:165:64//AQ294763
 F-HEMBA1004143
 F-HEMBA1004146

- F-HEMBA1004150//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.00011:618:60//Z96811
- F-HEMBA1004164//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.9e-30:454:68//AC005913
- 5 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//4.5e-133:649:97//AF067855
- F-HEMBA1004199
- F-HEMBA1004200//HS_2015_A1_B05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=9 Row=C, genomic survey sequence.//8.5e-34:236:87//AQ247957
- F-HEMBA1004202//Mus musculus chromosome 11, clone mCIT.268_P_23, complete sequence.//7.8e-59:216:83//AC004807
- 10 F-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//6.3e-98:173:98//AC005488
- F-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.2e-166:791:98//U50748
- 15 F-HEMBA1004225//Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence.//6.5e-08:584:60//AE001424
- F-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//8.0e-115:713:86//AF095927
- F-HEMBA1004238
- 20 F-HEMBA1004241//CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence.//0.57:552:58//AC004708
- F-HEMBA1004246//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//6.1e-21:254:77//AL031010
- F-HEMBA1004248//Rattus rattus insulin-induced growth-response protein (CL-6) mRNA, complete cds.//1.7e-30:315:74//L13619
- 25 F-HEMBA1004264//Homo sapiens cosmid clone LUCA20 from 3p21.3, complete sequence.//4.4e-07:674:60//AC004693
- F-HEMBA1004267//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//3.1e-78:335:87//AC004707
- 30 F-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.4e-176:856:97//AC005831
- F-HEMBA1004274//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993
- F-HEMBA1004275//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4, WORKING DRAFT SEQUENCE.//5.2e-17:109:99//Z98051
- 35 F-HEMBA1004276//CIT-HSP-2387K6.TF.1 CIT-HSP Homo sapiens genomic clone 2387K6, genomic survey sequence.//5.0e-07:63:98//AQ240477
- F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//2.1e-185:868:99//AF022795
- 40 F-HEMBA1004289//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence.//1.0:387:59//AB013395
- F-HEMBA1004295//Homo sapiens DNA, anonymous heat-stable fragment RP11-3A.//7.8e-06:92:89//AB012254
- F-HEMBA1004306//Homo sapiens clone DJ0811N16, complete sequence.//0.00037:413:59//AC004897
- F-HEMBA1004312//Rickettsia prowazekii strain Madrid E, complete genome; segment 2/4.//0.28:522:57//AJ235271
- 45 F-HEMBA1004321//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-136:548:92//AC006130
- F-HEMBA1004323//Human DNA sequence from PAC 450C20 on chromosome X.//1.3e-32:320:65//Z84720
- F-HEMBA1004327//Homo sapiens mRNA for KIAA0522 protein, partial cds.//0.93:222:62//AB011094
- 50 F-HEMBA1004330//Homo sapiens clone DJ1196H06, WORKING DRAFT SEQUENCE, 4 unordered pieces.//7.0e-168:895:93//AC004995
- F-HEMBA1004334//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//4.6e-73:713:75//AC002980
- F-HEMBA1004335//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE.//1.3e-25:121:85//AL024498
- 55 F-HEMBA1004341
- F-HEMBA1004353//*** ALU WARNING: Human Alu-Sc subfamily consensus sequence.//6.4e-38:278:85//U14571
- F-HEMBA1004354//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.1e-45:

- F-HEMBA1004150//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//
0.00011:618:60//Z96811
- F-HEMBA1004164//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library)
complete sequence.//2.9e-30:454:68//AC005913
- 5 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//4.5e-133:649:97//AF067855
- F-HEMBA1004199
- F-HEMBA1004200//HS_2015_A1_B05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=2015 Col=9 Row=C, genomic survey sequence.//8.5e-34:236:87//AQ247957
- F-HEMBA1004202//Mus musculus chromosome 11, clone mCIT.268_P_23, complete sequence.//7.8e-59:216:
10 83//AC004807
- F-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//
6.3e-98:173:98//AC005488
- F-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.2e-166:791:98//
U50748
- 15 F-HEMBA1004225//Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence.//6.5e-08:
584:60//AE001424
- F-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//8.0e-115:713:86//
AF095927
- F-HEMBA1004238
- 20 F-HEMBA1004241//CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence.//0.57:552:58//AC004708
- F-HEMBA1004246//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel
gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//6.1e-21:254:77//
AL031010
- F-HEMBA1004248//Rattus rattus insulin-induced growth-respons protein (CL-6) mRNA, complete cds.//1.7e-30:
25 315 :74//L13619
- F-HEMBA1004264//Homo sapiens cosmid clone LUCA20 from 3p21.3, complete sequence.//4.4e-07:674:60//
AC004693
- F-HEMBA1004267//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//3.1e-78:335:
30 87//AC004707
- F-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC
Library) complete sequence.//1.4e-176:856:97//AC005831
- F-HEMBA1004274//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993
- F-HEMBA1004275//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4, WORKING
35 DRAFT SEQUENCE.//5.2e-17:109:99//Z98051
- F-HEMBA1004276//CIT-HSP-2387K6.TF.1 CIT-HSP Homo sapiens genomic clone 2387K6, genomic survey se-
quence.//5.0e-07:63:98//AQ240477
- F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//2.1e-185:868:
40 99//AF022795
- F-HEMBA1004289//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence.//
1.0:387:59//AB013395
- F-HEMBA1004295//Homo sapiens DNA, anonymous heat-stable fragment RP11-3A.//7.8e-06:92:89//AB012254
- F-HEMBA1004306//Homo sapiens clone DJ0811N16, complete sequence.//0.00037:413:59//AC004897
- F-HEMBA1004312//Rickettsia prowazekii strain Madrid E, complete genome; segment 2/4.//0.28:522:57//
45 AJ235271
- F-HEMBA1004321//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-136:548:92//
AC006130
- F-HEMBA1004323//Human DNA sequence from PAC 450C20 on chromosome X.//1.3e-32:320:65//Z84720
- F-HEMBA1004327//Homo sapiens mRNA for KIAA0522 protein, partial cds.//0.93:222:62//AB011094
- 50 F-HEMBA1004330//Homo sapiens clone DJ1196H06, WORKING DRAFT SEQUENCE, 4 unordered pieces.//
7.0e-168:895:93//AC004995
- F-HEMBA1004334//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//4.6e-
73:713:75//AC002980
- F-HEMBA1004335//Human DNA-sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING
55 DRAFT SEQUENCE.//1.3e-25:121:85//AL024498
- F-HEMBA1004341
- F-HEMBA1004353//***ALU WARNING: Human Alu-Sc subfamily consensus sequence.//6.4e-38:278:85//U14571
- F-HEMBA1004354//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.1e-45:

190:92//U75968
 F-HEMBA1004356
 F-HEMBA1004366//P.falciparum complete gene map of plastid-like DNA (IR-A)//2.2e-07:736:57//X95275
 F-HEMBA1004372//H.sapiens dystrophin gene intron 44//1.0:129:62//X77644
 5 F-HEMBA1004389//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end//4.7e-42:237:94//M21977
 F-HEMBA1004394//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence//5.2e-05:
 519:59//AE001402
 F-HEMBA1004396//Human BAC clone RG302F04 from 7q31, complete sequence//4.0e-32:261:76//AC002463
 F-HEMBA1004405//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING
 10 DRAFT SEQUENCE, 9 unordered pieces//1.4e-07:693:58//AC005507
 F-HEMBA1004408//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces//
 1.2e-69:195:100//AC005037
 F-HEMBA1004429//HS_3193_A1_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3193 Col=11 Row=C, genomic survey sequence//5.1e-67:386:91//AQ172942
 15 F-HEMBA1004433//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence//3.2e-27:242:82//
 AC002554
 F-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces//
 1.7e-75:590:81//AC004846
 F-HEMBA1004461//Human DNA sequence from clone 657J8 on chromosome Xq26.1-26.3 Contains GSS, com-
 20 plete sequence//0.045:215:66//AL034407
 F-HEMBA1004479//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds//5.2e-43:364:79//
 AF060194
 F-HEMBA1004482//Plasmodium falciparum 3D7 chromosome 12. PFYAC181 genomic sequence, WORKING
 DRAFT SEQUENCE, 8 unordered pieces//6.8e-17:791:59//AC005505
 25 F-HEMBA1004499//Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence//4.4e-125:251:
 94//AC004686
 F-HEMBA1004502//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING
 DRAFT SEQUENCE, 3 unordered pieces//0.012:635:57//AC004709
 F-HEMBA1004506//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence//2.8e-127:766:
 30 88//AC004453
 F-HEMBA1004507
 F-HEMBA1004509//Arabidopsis thaliana DNA chromosome 4, BAC clone T10114 (ESSAll project)//1.0e-13:244:
 67//AL021712
 F-HEMBA1004534//Human mRNA for actin-binding protein (filamin) (ABP-280)//1.6e-72:678:74//X53416
 35 F-HEMBA1004538//Sequence 1 from patent US 5612190//0.00015:416:59//I36871
 F-HEMBA1004542//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.95:
 202:64//AC005038
 F-HEMBA1004554//Arabidopsis thaliana BAC T26D22//0.45:624:56//AFO58826
 F-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds//9.1e-10:173:70//D87457
 40 F-HEMBA1004573//Human BAC clone RG114A06 from 7q31, complete sequence//6.1e-23:134:73//AC002542
 F-HEMBA1004577//Homo sapiens Chromosome 16 BAC clone CIT987SK-582J2, complete sequence//1.6e-15:
 190:77//AC004525
 F-HEMBA1004586//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces//
 3.1e-31:388:76//AC004895
 45 F-HEMBA1004596//RPC111-81O21.TJ RPC111 Homo sapiens genomic clone R-81O21, genomic survey se-
 quence//2.2e-90:458:90//AQ285136
 F-HEMBA1004604//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds//8.6e-105:699:
 84//AF071316
 F-HEMBA1004610//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence//5.4e-20:267:
 50 72//AC004983
 F-HEMBA1004617//CIT-HSP-2319H15.TF CIT-HSP Homo sapiens genomic clone 2319H15, genomic survey se-
 quence//6.2e-26:147:99//AQ034944
 F-HEMBA1004629//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING
 DRAFT SEQUENCE, 3 unordered pieces//5.6e-06:766:56//AC005504
 55 F-HEMBA1004631//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NU-
 CLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs//4.7e-73:412:92//Z83843
 F-HEMBA1004632//Canine herpesvirus DNA for gene homolog of HSV1 UL16, EHV1 ORF 46, VZV ORF 44//
 0.92:181:61//X90418

- F-HEMBA1004637//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor//7.8e-47:784:65//X74904
 F-HEMBA1004638//Rattus norvegicus homeodomain protein Nkx6.1 (nkx6.1) mRNA, complete cds//6.4e-06:458:61//AF004431
 F-HEMBA1004666//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y47D3,
 5 WORKING DRAFT SEQUENCE//0.30:733:55//Z98865
 F-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence//7.5e-136:521:98//AL031432
 F-HEMBA1004670//Homo sapiens Chromosome 22q12 Cosmid Clone p90g5, complete sequence//0.43:365:59//AC000045
 10 F-HEMBA1004672
 F-HEMBA1004693//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.096:651:54//AC005308
 F-HEMBA1004697//CIT-HSP-2326C13.TR CIT-HSP Homo sapiens genomic clone 2326C13, genomic survey sequence//0.23:238:65//AQ040642
 15 F-HEMBA1004705//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPC11-93D11 (from Roswell Park Cancer Center) complete sequence//2.1e-27:375:72//AC002357
 F-HEMBA1004709//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence//1.6e-36:191:91//AC006210
 F-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence//1.1e-133:639:99//AC005562
 20 F-HEMBA1004725//RPC111-75013.TJ RPC111 Homo sapiens genomic clone R-75013, genomic survey sequence//6.2e-32:169:100//AQ266512
 F-HEMBA1004730//Human BAC clone RG035E18 from 7q31, complete sequence//8.0e-68:732:72//AC004029
 F-HEMBA1004733//CIT-HSP-2305M23.TF CIT-HSP Homo sapiens genomic clone 2305M23, genomic survey sequence//4.9e-18:209:69//AQ017556
 25 F-HEMBA1004734//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds//1.8e-13:451:62//AF028340
 F-HEMBA1004736//Human DNA Sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR1). Contains ESTs, an STS and GSSs, complete sequence//5.0e-87:646:78//Z94056
 30 F-HEMBA1004748//Human BAC clone RG204116 from 7q31, complete sequence//0.24:526:57//AC002461
 F-HEMBA1004751//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces//1.4e-25:268:76//AC004913
 F-HEMBA1004752//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp)//1.1e-07:503:61//X83546
 35 F-HEMBA1004753//Homo sapiens Chromosome 12 Cosmid Clone 6e5, complete sequence//4.5e-38:314:81//AC000028
 F-HEMBA1004756//Homo sapiens, complete sequence//1.4e-111:326:84//AC005854
 F-HEMBA1004758//Sequence 29 from patent US 5534410//3.9e-135:769:91//I23472
 40 F-HEMBA1004763//Homo sapiens apoptosis inhibitor survivin gene, complete cds//3.6e-47:404:79//U75285
 F-HEMBA1004768//Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence//6.7e-107:890:78//AC004941
 F-HEMBA1004770//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces//7.9e-09:806:59//AC004709
 45 F-HEMBA1004771//G.muris ribosomal RNA operon DNA encoding 16S, 23S and 5.8S ribosomal RNA//0.69:239:61//X65063
 F-HEMBA1004776
 F-HEMBA1004778
 F-HEMBA1004795//Drosophila melanogaster A-kinase anchor protein DAKAP550 mRNA, partial cds//3.4e-46:778:64//AF003622
 50 F-HEMBA1004803//Homo sapiens chromosome Y, clone 264,M,20, complete sequence//4.3e-82:580:82//AC004617
 F-HEMBA1004806//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence//5.4e-07:642:59//AC005083
 55 F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//1.4e-46:171:92//L01042
 F-HEMBA1004816//Homo sapiens calpastatin (CAST) gene, exons 10-14//3.5e-31:546:66//M86257
 F-HEMBA1004820//C.botulinum progenitor toxin complex genes//0.0014:343:62//X87972

- F-HEMBA1004847//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68)//1.5e-85:512:88//X53744
- F-HEMBA1004850//Homo sapiens TGF-beta type I receptor (TGFBRI) gene, exon 1//0.0065:284:61//AF054590
- F-HEMBA1004863//Genomic sequence from Mouse 11, complete sequence//0.92:250:59//AC000400
- 5 F-HEMBA1004864
- F-HEMBA1004865//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence//3.6e-12:214:72//AL031120
- F-HEMBA1004880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence//1.1e-08:255:69//AC004020
- 10 F-HEMBA1004889//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds//0.062:155:69//U32943
- F-HEMBA1004900//Plasmodium falciparum unidentified mRNA sequence//0.00055:323:60//L12043
- F-HEMBA1004909//Homo sapiens chromosome 17, clone 289A8, complete sequence//9.6e-16:166:80//AC003051
- 15 F-HEMBA1004918//Turritella communis mitochondrial 16S ribosomal RNA gene, partial//0.81:146:65//M94003
- F-HEMBA1004923//Human DNA from overlapping chromosome 19-specific cosmids R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence//1.4e-36:338:78//AC003006
- F-HEMBA1004929//CIT-HSP-2373I16.TR CIT-HSP Homo sapiens genomic clone 2373I16, genomic survey sequence//2.4e-86:443:96//AQ108676
- 20 F-HEMBA1004930//Homo sapiens PAC clone DJ0608H12 from 7q21, complete sequence//4.6e-20:219:73//AC004109
- F-HEMBA1004933//HS-1003-A1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 497 Col=19 Row=I, genomic survey sequence//1.4e-28:216:85//B30726
- F-HEMBA1004934//Homo sapiens chromosome 21q22.3 PAC 267O10, complete sequence//0.53:222:61//AF042091
- 25 F-HEMBA1004944//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces//1.2e-58:509:78//AC005482
- F-HEMBA1004954//HS_2033_A2_A08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=16 Row=A, genomic survey sequence//3.7e-47:243:99//AQ229758
- 30 F-HEMBA1004956//P.falciparum complete gene map of plastid-like DNA (IR-B)//0.048:421:58//X95276
- F-HEMBA1004960//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8//0.89:333:58//Z97343
- F-HEMBA1004972
- F-HEMBA1004973//RPC111-66P8.TK RPC111 Homo sapiens genomic clone R-66P8, genomic survey sequence//3.5e-22:245:77//AQ238471
- 35 F-HEMBA1004977//Homo sapiens full-length insert cDNA clone YZ83B08//9.0e-11:84:98//AF086080
- F-HEMBA1004978//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence//0.0021:152:66//AQ075713
- F-HEMBA1004980//HS_3018_A2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=8 Row=I, genomic survey sequence//1.9e-77:392:97//AQ071873
- 40 F-HEMBA1004983//Albinaria corrugata isolate cor. Prn1.1 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence//0.0030:276:61//AF031680
- F-HEMBA1004995//Homo sapiens chromosome 16, cosmid bridge clone 306E6 (LANL), complete sequence//4.2e-138:640:99//AC005590
- 45 F-HEMBA1005008//Human mariner1 transposase gene, complete consensus sequence//6.8e-20:160:88//U52077
- F-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds//2.0e-144:668:99//AF041474
- F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.4e-146:693:98//AB014548
- 50 F-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/I pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence//2.2e-115:668:90//AL009179
- F-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence//4.6e-138:591:98//AC004596
- 55 F-HEMBA1005039//CIT-HSP-2338L5.TR CIT-HSP Homo sapiens genomic clone 2338L5, genomic survey sequence//3.7e-61:271:88//AQ055486
- F-HEMBA1005047//Mus musculus mRNA for Rab24 protein//3.8e-17:218:73//Z22819
- F-HEMBA1005050//Human Tis11d gene, complete cds//0.079:251:63//U07802

EP 1 074 617 A2

- F-HEMBA1005062//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces //0.018:560:56//AC004688
- F-HEMBA1005066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE //3.4e-97:432:84//AL034410
- 5 F-HEMBA1005075//H.sapiens DNA 3' flanking simple sequence region clone wg2c3 //6.9e-07:176:68//X76589
- F-HEMBA1005079//CIT-HSP-2325M21.TRB CIT-HSP Homo sapiens genomic clone 2325M21, genomic survey sequence //2.1e-48:274:93//AQ038720
- F-HEMBA1005083//HS_2248_B1_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=9 Row=H, genomic survey sequence //3.4e-06:230:64//AQ129575
- 10 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds //1.3e-161:762:98//AF080561
- F-HEMBA1005113//L.esculentum microsatellite repeat DNA region //0.0038:742:57//X90770
- F-HEMBA1005123//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces //9.6e-83:479:78//AC004854
- 15 F-HEMBA1005133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE //3.9e-24:576:64//AL023808
- F-HEMBA1005149//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence //4.7e-36:283:80//AC004542
- F-HEMBA1005152//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces //5.0e-10:332:64//AC004469
- 20 F-HEMBA1005159//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE //4.0e-10:734:58//AP000023
- F-HEMBA1005185//H.sapiens CpG island DNA genomic MseI fragment, clone 91b2, forward read cpg91b2.ft1a./12.2e-14:93:100//Z63847
- 25 F-HEMBA1005201//Drosophila melanogaster cosmid 152A3 //4.7e-35:679:64//AL009194
- F-HEMBA1005202//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68) //6.7e-138:778:90//X53744
- F-HEMBA1005206//Drosophila melanogaster Su(P) and anon-73B1 genes and partial o25 gene and Pros26 gene //7.1e-12:376:62//AJ011320
- 30 F-HEMBA1005219//Homo sapiens mRNA for KIAA0445 protein, complete cds //7.1e-05:411:60//AB007914
- F-HEMBA1005223//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence //3.5e-06:212:66//AC004542
- F-HEMBA1005232//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces //3.7e-07:625:57//AC005308
- 35 F-HEMBA1005241//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence //8.7e-45:567:72//AC005154
- F-HEMBA1005244//Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 174A6, U172D6, and U186B3 from Xp22, complete sequence //0.96:298:62//AC002365
- F-HEMBA1005251
- 40 F-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence //4.5e-160:392:99//AC005837
- F-HEMBA1005274//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence //2.3e-05:496:60//AF069291
- F-HEMBA1005275//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence //5.7e-05:220:64//AL033521
- 45 F-HEMBA1005293//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds //2.4e-20:338:65//U97018
- F-HEMBA1005296
- F-HEMBA1005304//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence //1.6e-51:381:78//AL031012
- 50 F-HEMBA1005311
- F-HEMBA1005314//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE //0.94:226:63//AP000031
- F-HEMBA1005315//Homo sapiens BAC810, complete sequence //9.5e-15:684:62//U85198
- 55 F-HEMBA1005318//Human DNA sequence from PAC 394F12 on chromosome X contains EST, STS, CpG island clone //2.6e-05:472:59//Z83823
- F-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214_C_8, complete sequence //3.3e-90:300:90//AC005803

EP 1 074 617 A2

F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//1.4e-151:740:97//AJ007581
 F-HEMBA1005353//CIT-HSP-2310N10.TR CIT-HSP Homo sapiens genomic clone 2310N10, genomic survey se-
 quence//2.1e-86:438:97//AQ016145
 F-HEMBA1005359//Human zinc finger protein ZNF137 mRNA, complete cds//1.8e-98:500:88//U09414
 5 F-HEMBA1005367//Mus musculus melastatin mRNA, complete cds//8.3e-72:577:73//AF047714
 F-HEMBA1005372//Human DNA sequence from PAC 293E14 contains ESTs, STS//1.3e-07:274:66//Z82900
 F-HEMBA1005374//Homo sapiens clone 277F10, WORKING DRAFT SEQUENCE, 5 unordered pieces//1.9e-48:
 611:69//AC004813
 F-HEMBA1005382//HS_3063_B2_F11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 10 nomic clone Plate=3063 Col=22 Row=L, genomic survey sequence//1.6e-27:154:98//AQ103204
 F-HEMBA1005389//Plasmodium falciparum telomere nucleotide sequence//4.0e-07:443:61//M23175
 F-HEMBA1005394//CIT-HSP-2368B11.TR CIT-HSP Homo sapiens genomic clone 2368B11, genomic survey se-
 quence//7.6e-17:225:71//AQ076749
 F-HEMBA1005403//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING
 15 DRAFT SEQUENCE//4.5e-131:278:98//AL034379
 F-HEMBA1005408//HS_3007_B2_G04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3007 Col=8 Row=N, genomic survey sequence//8.0e-06:218:66//AQ294366
 F-HEMBA1005410//Human DNA sequence from cosmid cU120E2, on chromosome X contains Lowe oculocere-
 brorenal syndrome (OCRL) ESTs and STS//1.5e-41:432:76//Z73496
 20 F-HEMBA1005411
 F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.0e-169:
 537:99//AF041248
 F-HEMBA1005426
 F-HEMBA1005443//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence//7.1e-37:260:76//
 25 AC006130
 F-HEMBA1005447//CIT-HSP-2173N7.TR CIT-HSP Homo sapiens genomic clone 2173N7, genomic survey se-
 quence//5.0e-133:631:98//B93234
 F-HEMBA1005468//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related
 C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete
 30 sequence//1.5e-118:868:83//AL022576
 F-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence//1.2e-179:838:
 99//AC005212
 F-HEMBA1005472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING
 DRAFT SEQUENCE//3.4e-20:187:74//AL031985
 35 F-HEMBA1005474//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SE-
 QUENCE//4.1e-22:445:65//AP000041
 F-HEMBA1005475//CIT-HSP-2322D14.TR CIT-HSP Homo sapiens genomic clone 2322D14, genomic survey se-
 quence//6.7e-51:269:97//AQ026941
 F-HEMBA1005497//HS_3097_A2_G05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 40 nomic clone Plate=3097 Col=10 Row=M, genomic survey sequence//1.4e-66:345:96//AQ103810
 F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, complete sequence//5.4e-178:818:
 98//AC004957
 F-HEMBA1005506//Mus musculus (clone 0EBF17) early B-cell factor (EBF) mRNA, complete cds//2.6e-06:73:
 98//L12147
 45 F-HEMBA1005508//Homo sapiens clone hRPK.1_A_1, complete sequence//0.00012:455:60//AC006196
 F-HEMBA1005511//Homo sapiens MHC class 1 region//3.3e-43:421:77//AF055066
 F-HEMBA1005513//Drosophila melanogaster males-absent on the first (mol) gene, complete cds//2.3e-20:352:
 69//U71219
 F-HEMBA1005517//Homo sapiens DNA for (CGG)n trinucleotide repeat region, isolate E7//2.5e-08:431:62//
 50 AJ001216
 F-HEMBA1005518//M.musculus mRNA for paladin gene//8.2e-90:651:81//X99384
 F-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces//
 7.8e-167:755:99//AC004913
 F-HEMBA1005526//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence//2.4e-42:475:73//
 55 AC006241
 F-HEMBA1005528//Mus musculus mCAF1 protein mRNA, complete cds//1.2e-94:512:92//U21855
 F-HEMBA1005530
 F-HEMBA1005548//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 970A17, WORKING

DRAFT SEQUENCE.//9.4e-87:422:99//AL034431
 F-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//6.1e-41:486:68//AC004743
 F-HEMBA1005558//Drosophila melanogaster DNA sequence (P1 DS00837 (D87)), complete sequence.//2.9e-19:306:68//AC004377
 5 F-HEMBA1005568//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0093:345:60//AC004153
 F-HEMBA1005570//Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence.//4.2e-09:592:59//AE001407
 10 F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds.//5.9e-127:610:98//AB007932
 F-HEMBA1005577//HS-1004-A1-E11 -MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 498 Col=21 Row=I, genomic survey sequence.//0.00034:254:64//B30971
 F-HEMBA1005581//Rattus norvegicus mRNA for MEGF5, complete cds.//4.0e-57:826:65//AB011531
 F-HEMBA1005582//HS_3242_A1_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=13 Row=C, genomic survey sequence.//1.1e-13:91:98//AQ211275
 15 F-HEMBA1005583
 F-HEMBA1005588//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//8.7e-31:283:75//AC006025
 F-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//8.3e-158:748:99//AC005746
 20 F-HEMBA1005595//CIT-HSP-2309F14.TF CIT-HSP Homo sapiens genomic clone 2309F14, genomic survey sequence.//6.4e-30:194:91//AQ016527
 F-HEMBA1005606//CIT-HSP-2326I6.TR CIT-HSP Homo sapiens genomic clone 2326I6, genomic survey sequence.//0.0014:132:70//AQ041484
 25 F-HEMBA1005609//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-33:249:85//AC005089
 F-HEMBA1005616//Homo sapiens DNA sequence from PAC 43C13 on chromosome Xq21.1-Xq21.3. rab proteins geranylgeranyltransferase component A 1 (rab escort protein 1) (REP-1) (choroideraemia protein) (TCD protein).//6.5e-29:279:69//AL009175
 30 F-HEMBA1005621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//6.4e-90:158:87//AL031731
 F-HEMBA1005627//RPCI11-34P9 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-34P9, genomic survey sequence.//0.014:168:67//AQ045110
 F-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.0e-149:736:93//AC004460
 35 F-HEMBA1005632
 F-HEMBA1005634//Human DNA sequence from PAC 187N21 on chromosome 6p21.2-6p21.33. Contains ESTs.//6.6e-38:452:67//Z98036
 F-HEMBA1005666
 F-HEMBA1005670//Homo sapiens PAC clone DJ0665C04 from 7p14-p13, complete sequence.//5.1e-59:687:74//AC004850
 40 F-HEMBA1005679//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-47:357:85//AC005478
 F-HEMBA1005680
 F-HEMBA1005685//RPCI11-23D19.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23D19, genomic survey sequence.//0.99:228:63//AQ013742
 45 F-HEMBA1005699//Human ligand for eph-related receptor tyrosine kinases (EPLG8) mRNA, complete cds.//1.4e-72:406:92//U57001
 F-HEMBA1005705//Human (D21S172) DNA segment containing (CA) repeat.//0.00040:190:66//X56513
 F-HEMBA1005717//Plasmodium falciparum MAL3P1, complete sequence.//0.0099:260:63//Z97348
 50 F-HEMBA1005732//Human mRNA for KIAA0003 gene, complete cds.//8.1e-19:151:88//D14697
 F-HEMBA1005737//Homo sapiens PAC clone DJ1099C19 from 7q21-q22, complete sequence.//5.6e-15:157:79//AC005156
 F-HEMBA1005746//RPCI11-63N8.TK RPCI11 Homo sapiens genomic clone R-63N8, genomic survey sequence.//1.3e-18:113:100//AQ238535
 55 F-HEMBA1005755//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.6e-56:764:70//Z97181
 F-HEMBA1005765//Human DNA sequence from PAC 288L1 on chromosome 22q12-qter contains ESTs and polymorphic CA repeat (D22S1152).//1.1e-30:275:77//Z82196

EP 1 074 617 A2

- F-HEMBA1005780//RPC111-74E19.TJ RPC111 Homo sapiens genomic clone R-74E19, genomic survey sequence.//0.0011:283:62//AQ268432
- F-HEMBA1005813//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//0.14:326:61//AC004079
- 5 F-HEMBA1005815//M.musculus mRNA for skeletal muscle-specific calpain.//6.3e-10:706:59//X92523
- F-HEMBA1005822//Mouse Bac 291G16, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.87:417:56//AC003020
- F-HEMBA1005829//Homo sapiens Chromosome 22q11.2 Fosmid Clone f39e1 In DGCR Region, complete sequence.//8.8e-42:370:79//AC000094
- 10 F-HEMBA1005834//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-42:690:67//AL022577
- F-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aE9, genomic survey sequence.//4.3e-07:253:59//AL018749
- 15 F-HEMBA1005853//CIT-HSP-2289L23.TR CIT-HSP Homo sapiens genomic clone-2289L23, genomic survey sequence.//2.2e-68:333:99//B98952
- F-HEMBA1005884//Homo sapiens chromosome 5, BAC clone 78c6 (LBNL H191), complete sequence.//1.9e-57:331:87//AC005351
- 20 F-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//5.1e-182:864:98//AC004945
- F-HEMBA1005894//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//3.0e-44:340:80//AC004086
- F-HEMBA1005909//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethyl-aniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//8.3e-12:828:57//AL021026
- 25 F-HEMBA1005911//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//1.0e-44:328:77//AL031584
- 30 F-HEMBA1005921//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//1.3e-41:431:77//AC005666
- F-HEMBA1005931//Homo sapiens chromosome 12p13.3 clone RPC14-761J14, WORKING DRAFT SEQUENCE, 60 unordered pieces.//1.1e-29:394:70//AC006086
- 35 F-HEMBA1005934//Homo sapiens PAC clone DJ1140G11 from 14q24.3, complete sequence.//8.1e-06:115:80//AC004974
- F-HEMBA1005962//RPC111-17O15.TV RPC1-11 Homo sapiens genomic clone RPC1-11-17O15, genomic survey sequence.//9.5e-36:315:84//B82821
- 40 F-HEMBA1005963//HS_3055_A1_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//9.3e-73:372:97//AQ147357
- F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.3e-149:697:99//AF082516
- F-HEMBA1005991//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//6.3e-07:423:60//AE001408
- 45 F-HEMBA1005999//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//3.8e-09:360:64//AC005599
- F-HEMBA1006002
- F-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//4.5e-83:495:90//AF036405
- F-HEMBA1006031
- 50 F-HEMBA1006035
- F-HEMBA1006036//Human (lambda) DNA for immunoglobulin light chain.//2.4e-59:652:74//D87009
- F-HEMBA1006042//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.1e-43:330:7011AC005386
- F-HEMBA1006067//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.11:433:59//AC004153
- 55 F-HEMBA1006081
- F-HEMBA1006090//, complete sequence.//4.5e-139:748:92//AC005500
- F-HEMBA1006091//Homo sapiens gene encoding telethonin, exons 1 to 2, partial.//0.0091:346:62//AJ011098

- F-HEMBA1006100//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//2.8e-18:180:78//AC005880
- 5 F-HEMBA1006108//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte-Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.26:84:71//AL031177
- F-HEMBA1006121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 691N24, WORKING DRAFT SEQUENCE.//5.2e-18:147:87//AL031672
- 10 F-HEMBA1006124//CIT-HSP-2355B17.TF CIT-HSP Homo sapiens genomic clone 2355B17, genomic survey sequence.//0.044:225:61//AQ058966
- F-HEMBA1006130//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//8.8e-07:173:69//B55085
- 15 F-HEMBA1006138//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//7.5e-22:164:75//AL022162
- F-HEMBA1006142//, complete sequence.//7.9e-125:586:99//AC005500
- F-HEMBA1006155//H.sapiens CpG island DNA genomic MseI fragment, clone 119b6, forward read cpg119b6.ft1a.//1.0:85:72//Z64428
- 20 F-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.1e-185:852:99//AF048693
- F-HEMBA1006173//striatum enriched phosphatase=protein-tyrosine-phosphatase [rat, striata, mRNA, 2815 nt].//8.4e-50:642:73//S49400
- F-HEMBA1006182//Homo sapiens Chromosome 15q26.1 PAC clone pDJ105i19, complete sequence.//1.4e-22:194:74//AC005318
- 25 F-HEMBA1006198
- F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.6e-175:836:98//AF070557
- F-HEMBA1006248//Pinctada fucata mRNA for insoluble protein, complete cds.//8.2e-05:359:61//D86074
- F-HEMBA1006252//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//0.98:397:58//AL031664
- 30 F-HEMBA1006253
- F-HEMBA1006259//HS_2231_A1_D10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=19 Row=G, genomic survey sequence.//1.2e-11:233:68//AQ152722
- F-HEMBA1006268//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//5.2e-27:156:85//AC004673
- 35 F-HEMBA1006272//Human endogenous retrovirus gag mRNA.//8.1e-115:847:80//X72791
- F-HEMBA1006278//Mus musculus poly(A) polymerase VI mRNA, complete cds.//2.1e-57:665:70//U58134
- F-HEMBA1006283
- F-HEMBA1006284//Streptomyces fradiae tylactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//9.6e-06:623:60//U78289
- 40 F-HEMBA1006291//HS_2208_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=5 Row=E, genomic survey sequence.//1.2e-13:105:92//AQ091804
- F-HEMBA1006293//Sequence 8 from patent US 5721351.//5.6e-77:580:75//I89415
- F-HEMBA1006309//Caenorhabditis elegans cosmid F01F1.//1.1e-21:420:63//U13070
- 45 F-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.8e-120:748:85//AF076183
- F-HEMBA1006328//Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds.//1.5e-46:485:73//L29074
- F-HEMBA1006334//HS-1051-B2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=2 Row=L, genomic survey sequence.//0.0032:61:91//B40563
- 50 F-HEMBA1006344//HS-1009-A2-B02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 331 Col=4 Row=C, genomic survey sequence.//3.3e-09:218:66//B31420
- F-HEMBA1006347//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//1.6e-31:484:68//U71219
- 55 F-HEMBA1006349//HS-1054-A1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=11 Row=M, genomic survey sequence.//5.4e-15:95:100//B41671
- F-HEMBA1006359//Human ZNF43 mRNA.//1.4e-115:823:81//X59244
- F-HEMBA1006364//Mouse mRNA for transforming growth factor-beta2.//2.7e-10:247:71//X57413

- F-HEMBA1006377//Mus musculus chromosome 7, clone 19K5, complete sequence //3.0e-57:401:81//AC002327
 F-HEMBA1006380//CIT-HSP-2172K18.TF CIT-HSP Homo sapiens genomic clone 2172K18, genomic survey sequence //1.3e-110:525:99//B92570
 F-HEMBA1006381//HS-1045-B2-F10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 828 Col=20 Row=L, genomic survey sequence //4.4e-05:163:70//B37813
 F-HEMBA1006398//Homo sapiens 12q24.2 BAC RPC111-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence //3.8e-62:370:86//AC004806
 F-HEMBA1006416//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence //3.7e-15:157:78//AC005179
 F-HEMBA1006419//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence //1.2e-39:752:63//AL022165
 F-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes //2.4e-41:438:76//AF107885
 F-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence //0.027:293:64//AL031781
 F-HEMBA1006426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE //1.7e-50:310:80//Z93930
 F-HEMBA1006438//Liverwort Marchantia polymorpha chloroplast genome DNA //0.051:440:59//X04465
 F-HEMBA1006445//Felis catus ras p21 (H-ras) mRNA, partial cds //1.0:238:59//U62088
 F-HEMBA1006446//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING DRAFT SEQUENCE //2.4e-05:702:58//AL031749
 F-HEMBA1006461//Homo sapiens chromosome 19, cosmid R30676, complete sequence //8.6e-55:409:83//AC004560
 F-HEMBA1006467//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence //1.0:293:59//AC006120
 F-HEMBA1006471//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces //1.4e-05:731:59//AC004709
 F-HEMBA1006474//CIT-HSP-2017H3.TF CIT-HSP Homo sapiens genomic clone 2017H3, genomic survey sequence //5.2e-60:435:83//B54247
 F-HEMBA1006483//Homo sapiens chromosome 5, BAC clone 8e5 (LBNL H167), complete sequence //2.9e-48:286:84//AC004752
 F-HEMBA1006485//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence //0.96:283:59//AC006031
 F-HEMBA1006486//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence //1.8e-14:259:67//AL022577
 F-HEMBA1006489//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING DRAFT SEQUENCE //6.6e-11:595:61//AL031283
 F-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence //6.0e-122:337:100//AC005828
 F-HEMBA1006494//Homo sapiens chromosome 7qtel0 BAC E3, complete sequence //3.8e-23:459:68//AF093117
 F-HEMBA1006497//HS_3023_B2_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=6 Row=P, genomic survey sequence //2.3e-81:433:95//AQ093846
 F-HEMBA1006502//H.sapiens 7SL repeat (clones 2-19b) //1.6e-13:86:87//X62364
 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds //2.3e-139:470:98//AB014566
 F-HEMBA1006521//Human BAC clone RG167B05 from 7q21, complete sequence //4.3e-27:406:71//AC003991
 F-HEMBA1006530//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE //2.9e-27:408:65//AL031650
 F-HEMBA1006535//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE //0.028:599:60//AL034557
 F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds //1.4e-171:654:98//AF093419

- F-HEMBA1006546//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//3.8e-104:811:80//Z73986
- F-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//4.8e-99:386:82//U06944
- F-HEMBA1006562//Human fructose-1,6-biphosphatase (FBP1) gene, exon 1.//0.012:322:60//U21925
- 5 F-HEMBA1006566//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0026:580:58//AC005504
- F-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//6.3e-08:231:70//U39357
- F-HEMBA1006579//CIT-HSP-2380A22.TR CIT-HSP Homo sapiens genomic clone 2380A22, genomic survey sequence.//0.036:250:62//AQ197107
- 10 F-HEMBA1006583//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.0:225:63//AL021841
- F-HEMBA1006595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//3.6e-50:689:69//AL022156
- F-HEMBA1006597//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-42:253:84//AC004166
- 15 F-HEMBA1006612//RPC11-88F20.TJ RPC11 Homo sapiens genomic clone R-88F20, genomic survey sequence.//1.1e-51:266:98//AQ286726
- F-HEMBA1006617//HS_2193_B2_H07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=14 Row=P, genomic survey sequence.//1.1e-59:413:85//AQ299685
- 20 F-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//1.4e-35:257:89//AL023284
- F-HEMBA1006631//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//9.6e-112:800:83//AC002036
- 25 F-HEMBA1006635//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.15:393:58//AL031745
- F-HEMBA1006639//Petromyzon marinus polyadenylate binding protein (PABP) mRNA, complete cds.//9.6e-15:318:68//AF032896
- 30 F-HEMBA1006643//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.58:254:65//AC006148
- F-HEMBA1006648//Mus musculus integrin binding protein kinase mRNA, complete cds.//1.5e-37:108:88//U94479
- F-HEMBA1006652//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//1.3e-154:671:96//AC005601
- 35 F-HEMBA1006653
- F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//5.2e-110:254:93//AC005189
- F-HEMBA1006665//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//1.4e-14:177:76//AC004554
- 40 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56.//5.5e-15:122:90//Y12065
- F-HEMBA1006676//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//0.098:218:63//AC004755
- F-HEMBA1006682//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING DRAFT SEQUENCE.//1.4e-05:719:57//AL034346
- 45 F-HEMBA1006695//Homo sapiens clone DJ0935K16, complete sequence.//3.1e-22:151:78//AC006011
- F-HEMBA1006696//CITBI-E1-2522D16.TF CITBI-E1 Homo sapiens genomic clone 2522D16, genomic survey sequence.//5.6e-17:324:66//AQ280738
- F-HEMBA1006708
- F-HEMBA1006709
- 50 F-HEMBA1006717//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.3e-08:136:79//AC005537
- F-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//5.8e-162:497:98//AC005828
- F-HEMBA1006744//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//7.4e-48:320:87//AC004796
- 55 F-HEMBA1006754//Human DNA sequence from PAC 82J11 and cosmid U134E6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBG) genes, ESTs and STSs.//4.1e-129:804:85//Z83850

EP 1 074 617 A2

- F-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence//2.2e-162:766:99//AC005752
- F-HEMBA1006767//Human Xq28 cosmid U247A3 from LLOXNC01 X chromosome library, complete sequence//1.2e-19:326:69//U73465
- 5 F-HEMBA1006779//Human DNA sequence from clone 80119 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence//1.4e-103:355:87//AL022727
- F-HEMBA1006780//CIT-HSP-2359P7.TR CIT-HSP Homo sapiens genomic clone 2359P7, genomic survey sequence//0.072:147:68//AQ077208
- 10 F-HEMBA1006789//nbxb0037113r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0037113r, genomic survey sequence//0.00011:288:63//AQ290474
- F-HEMBA1006795//CIT-HSP-2307E3.TF CIT-HSP Homo sapiens genomic clone 2307E3, genomic survey sequence//5.1e-80:420:96//AQ020511
- F-HEMBA1006796//Human clone 23803 mRNA, partial cds//4.5e-06:202:68//U79298
- F-HEMBA1006807//Homo sapiens mRNA for SPOP//1.2e-66:651:73//AJ000644
- 15 F-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62_O_9, complete sequence//6.0e-116:541:99//AC004797
- F-HEMBA1006824//Homo sapiens chromosome 19, cosmid R29368, complete sequence//0.40:159:66//AC004262
- F-HEMBA1006832//Homo sapiens (subclone 3_g8 from P1 H25) DNA sequence, complete sequence//1.8e-24:323:71//AC002196
- 20 F-HEMBA1006849//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 4/10//0.15:403:60//AB020872
- F-HEMBA1006865//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence//0.20:472:57//AE001369
- 25 F-HEMBA1006877//Mus musculus clone OST9241, genomic survey sequence//3.4e-79:641:76//AF046757
- F-HEMBA1006885//HS_2208_B2_G06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=12 Row=N, genomic survey sequence//4.9e-18:206:76//AQ089246
- F-HEMBA1006900//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence//5.4e-07:298:65//AL031321
- 30 F-HEMBA1006914//S.pombe chromosome II cosmid c16H5//0.00040:194:66//AL022104
- F-HEMBA1006921//Homo sapiens BAC clone GS114109 from 7p14-p15, complete sequence//1.1e-174:813:99//AC006027
- F-HEMBA1006926//Caenorhabditis elegans cosmid ZK185//0.0075:183:65//AF036704
- F-HEMBA1006929//P.falciparum complete gene map of plastid-like DNA (IR-A)//4.0e-06:739:57//X95275
- 35 F-HEMBA1006936
- F-HEMBA1006938//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P4, WORKING DRAFT SEQUENCE//1.1e-05:733:57//AL031747
- F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//1.3e-90:437:98//AJ010841
- F-HEMBA1006949//Human DNA sequence from PAC 363L9 on chromosome X. contains STS and polymorphic CA repeat//0.67:217:62//Z82205
- 40 F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//5.6e-143:740:94//AF004828
- F-HEMBA1006976//cDNA encoding alpha 2 to 3 sialyltransferase//2.8e-101:338:89//E06058
- F-HEMBA1006993//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence//7.1e-31:536:66//AC003071
- 45 F-HEMBA1006996//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE//9.5e-07:285:60//Z82209
- F-HEMBA1007002//Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence//0.99:388:58//AC002328
- 50 F-HEMBA1007017//Sequence 3 from Patent WO9416067//0.96:220:62//A39358
- F-HEMBA1007018//G.gallus mRNA for dynein light chain-A//1.3e-124:838:83//X79088
- F-HEMBA1007045
- F-HEMBA1007051//Caenorhabditis elegans cosmid Y57G11C, complete sequence//0.17:343:60//Z99281
- F-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region//4.3e-67:659:74//U85056
- 55 F-HEMBA1007062//Tubulin gene//1.0:113:67//A18572
- F-HEMBA1007066//HS_3116_A2_A03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=6 Row=A, genomic survey sequence//0.80:214:62//AQ140467
- F-HEMBA1007073//Homo sapiens 12q13 PAC RPC11-316M24 (Roswell Park Cancer Institute Human PAC library)

- complete sequence//9.3e-54:519:68//AC004242
 F-HEMBA1007078//CIT-HSP-2318N6.TF CIT-HSP Homo sapiens genomic clone 2318N6, genomic survey sequence//8.7e-80:387:98//AQ044076
 F-HEMBA1007080
- 5 F-HEMBA1007085//Streptomyces coelicolor cosmid 7A1.//3.5e-06:496:59//AL034447
 F-HEMBA1007087//Plasmodium falciparum MAL3P6, complete sequence//7.4e-07:553:56//Z98551
 F-HEMBA1007112//HS_2171_A1_B01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=1 Row=C, genomic survey sequence//1.0:172:61//AQ091865
 F-HEMBA1007113//Human DNA sequence from clone 1044O17 on chromosome Xp11.3-11.4 Contains GSS and
- 10 STS, complete sequence//0.54:502:56//AL023875
 F-HEMBA1007121//Caenorhabditis elegans cosmid ZK430.//1.4e-08:265:64//U42833
 F-HEMBA1007129//CITBI-E1-2504A5.TF CITBI-E1 Homo sapiens genomic clone 2504A5, genomic survey sequence//0.97:267:62//AQ264035
 F-HEMBA1007147//HS_3208_A2_C04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=8 Row=E, genomic survey sequence//9.1e-90:466:95//AQ176696
- 15 F-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence//6.0e-138:524:98//AC005239
 F-HEMBA1007151//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence//2.0e-20:157:87//AQ280780
- 20 F-HEMBA1007174//Homo sapiens epsin 2a mRNA, complete cds//2.0e-62:318:97//AF062085
 F-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPC111-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces//1.6e-21:205:80//AC005911
 F-HEMBA1007194//HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence//1.3e-11:87:96//AQ187492
- 25 F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-156:478:98//D86987
 F-HEMBA1007206//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence//0.024:342:63//AC004223
 F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//5.0e-176:839:98//AB018340
 F-HEMBA1007243//Chinese hamster hprt mRNA, complete cds//4.3e-58:687:68//J00060
- 30 F-HEMBA1007251//Rabbit troponin T messenger fragment (aa 49 to 129)//0.084:177:62//V00899
 F-HEMBA1007256//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE//1.3e-75:490:88//AL022240
 F-HEMBA1007267//HS_3218_A1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=13 Row=K, genomic survey sequence//2.9e-62:393:87//AQ181128
- 35 F-HEMBA1007273//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence//1.1e-63:314:99//B95401
 F-HEMBA1007279//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence//3.1e-31:401:72//AC004638
 F-HEMBA1007281//HS_3115_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=21 Row=A, genomic survey sequence//5.0e-70:372:96//AQ186691
- 40 F-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence//1.2e-152:727:98//AL031003
 F-HEMBA1007300//Canis familiaris PDE5 mRNA for 3',5'-Cyclic GMP Phosphodiesterase, complete cds//2.1e-21:542:63//AB008467
- 45 F-HEMBA1007301//COL1A1=type I collagen pro alpha 1(I) chain propeptide {3' region} [human, fetal cells 86-237, 86-146, 88-251, mRNA Partial Mutant, 855 nt]//1.7e-08:388:61//S64596
 F-HEMBA1007319//Genomic sequence from Mouse 9, complete sequence//6.0e-84:390:75//AC000399
 F-HEMBA1007320
 F-HEMBA1007322//Homo sapiens BAC clone RG118E13 from 7p15-p21, complete sequence//0.091:260:64//AC004485
- 50 F-HEMBA1007327//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces//0.12:472:59//AC005140
 F-HEMBA1007341//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence//1.5e-18:408:64//AC006120
- 55 F-HEMBA1007342//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces//8.7e-25:500:62//AC005377
 F-HEMBA1007347//Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H126), complete sequence//0.75:269:61//AC005738

EP 1 074 617 A2

F-HEM BB1000005//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//5.0e-05:441:60//AC004617

F-HEM BB1000008//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.0e-44:417:77//AC004491

5 F-HEM BB1000018//HS_2179_B2_E04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=8 Row=J, genomic survey sequence.//0.012:87:77//AQ023250

F-HEM BB1000024//Human DNA sequence from PAC 106120, on chromosome 22q12-qter contains NADH pseudogene, ESTs, STS.//8.1e-11:461:61//Z81369

10 F-HEM BB1000025//CIT-HSP-2348F3.TR CIT-HSP Homo sapiens genomic clone 2348F3, genomic survey sequence.//0.96:198:62//AQ062938

F-HEM BB1000030//Homo sapiens DNA sequence from PAC 32F7 on chromosome X. Contains NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3, ESTs.//0.00049:276:64//AL009173

F-HEM BB1000036//H.sapiens chromosome 22 CpG island DNA genomic MseI fragment, clone 302e2, reverse read 302e2.r.//0.0057:66:81//Z79857

15 F-HEM BB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.9e-100:450:98//AF084928

F-HEM BB1000039//HS_2167_B1_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2167 Col=23 Row=L, genomic survey sequence.//0.022:108:69//AQ092404

F-HEM BB1000044//Borrelia burgdorferi (section 50 of 70) of the complete genome.//1.0e-07:486:61//AE001164

20 F-HEM BB1000048//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.3e-05:585:58//AC005507

F-HEM BB1000050//Homo sapiens DNA sequence from clone 501N12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseudo?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene.

25 Contains ESTs, STSs and GSSs, complete sequence.//5.8e-38:549:67//AL022170

F-HEM BB1000054//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//7.0e-98:328:83//AC002349

F-HEM BB1000055//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, WORKING DRAFT SEQUENCE.//3.7e-05:600:58//AB000880

30 F-HEM BB1000059//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.3e-48:472:78//AC005096

F-HEM BB1000083

F-HEM BB1000089//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.0036:679:56//AL031744

35 F-HEM BB1000099//Homo sapiens chromosome 18 BAC RPC11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-15:312:68//AC005909

F-HEM BB1000103//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.0e-37:316:74//AC006210

F-HEM BB1000113//Homo sapiens chromosome 21q22.3 cosmid Q11M15, complete sequence.//3.1e-25:259:76//AF045450

40 F-HEM BB1000119//Homo sapiens ASMTL gene.//1.2e-137:654:98//Y15521

F-HEM BB1000136//Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.//0.59:217:66//Z74697

F-HEM BB1000141//Homo sapiens DNA from chromosome 19q13.1 cosmid f14121 containing ATP4A and GADPH-2 genes, genomic sequence.//8.4e-31:113:88//AD000090

45 F-HEM BB1000144//Human BAC clone RG114A06 from 7q31, complete sequence.//4.4e-58:339:87//AC002542

F-HEM BB1000173//Homo sapiens 12q24 BAC RPC11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//9.4e-160:562:93//AC002996

F-HEM BB1000175

50 F-HEM BB1000198//HS_3071_A2_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=20 Row=A, genomic survey sequence.//0.99:261:61//AQ137388

F-HEM BB1000215//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence.//6.7e-17:138:86//AC005839

F-HEM BB1000217//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00083:287:60//U80808

55 F-HEM BB1000218//Caenorhabditis elegans cosmid C52A11, complete sequence.//0.90:337:56//Z46792

F-HEM BB1000226//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.7e-90:175:92//Z69890

- F-HEMBB1000240//Human G-protein-coupled inwardly rectifying potassium channel (KCNJ3) gene, polymorphic repeat sequence //0.16:171:62//U07918
- F-HEMBB1000244//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.8e-08:355:63//AC005522
- 5 F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds.//6.6e-155:735:98//AF075587
- F-HEMBB1000258//Human adenosine monophosphate deaminase 1 (AMPD1) gene, exons 1-16 //0.58:396:59//M98818
- 10 F-HEMBB1000264//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds //4.4e-32:100:100//U75968
- F-HEMBB1000266//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence //3.8e-16:176:78//AC004470
- F-HEMBB1000272//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence //0.011:379:58//AE001369
- 15 F-HEMBB1000274//Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAll project) //0.92:272:61//AL022580
- F-HEMBB1000284//Human Xp22 BAC CT-285115 (from CalTech/Research Genetics) , PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence //0.00071:568:57//AC002366
- 20 F-HEMBB1000307//Human DNA sequence from PAC 29K1 on chromosome 6p21.3-22.2. Contains glutathione peroxidase-like; zinc finger, ESTs, mRNA, STS, tRNAs, olfactory receptor pseudogene //3.0e-13:439:65//Z98745
- F-HEMBB1000312//Homo sapiens clone GS051M12, complete sequence //0.031:252:65//AC005007
- F-HEMBB1000317//Fugu rubripes GSS sequence, clone 060J22aE10, genomic survey sequence //0.00033:173:65//AL026242
- 25 F-HEMBB1000318//HS_3244_B2_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=20 Row=P, genomic survey sequence //3.9e-85:438:95//AQ252951
- F-HEMBB1000335//Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence //0.63:285:61//AC005968
- F-HEMBB1000336
- 30 F-HEMBB1000337//Homo sapiens chromosome 4 clone B208G5 map 4q25, complete sequence //0.0014:309:64//AC004051
- F-HEMBB1000338//HS_3108_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=14 Row=K, genomic survey sequence //3.8e-09:331:63//AQ140356
- F-HEMBB1000339//Homo sapiens 12q24 PAC RPC11-46F2 (Roswell Park Cancer Institute Human PAC library) complete sequence //1.2e-52:295:77//AC002351
- 35 F-HEMBB1000341
- F-HEMBB1000343//Plasmodium falciparum MAL3P3, complete sequence //0.00081:397:61//Z98547
- F-HEMBB1000354//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence //9.1e-34:596:66//AL020989
- 40 F-HEMBB1000369//Genomic sequence from Human 17, complete sequence //0.012:298:60//AC002090
- F-HEMBB1000374//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence //9.3e-69:294:89//U96409
- F-HEMBB1000376//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence //3.5e-54:352:88//AL034377
- 45 F-HEMBB1000391//Trichotheceum roseum internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence //0.011:168:67//U51982
- F-HEMBB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//2.6e-163:762:98//AF076838
- 50 F-HEMBB1000402//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence //7.7e-15:466:63//AC002368
- F-HEMBB1000404//Homo sapiens mRNA for myosin-IXA.//3.5e-65:324:98//AJ001714
- F-HEMBB1000420//244Kb Contig from Human Chromosome 11p15.5 spanning D11S1 through D11S25, complete sequence //0.013:399:62//AC001228
- F-HEMBB1000434//Homo sapiens PAC clone 278C19 from 12q, complete sequence //6.1e-83:571:84//AC004263
- 55 F-HEMBB1000438//RPC11-21E14.TP RPC1-11 Homo sapiens genomic clone RPC1-11-21E14, genomic survey sequence //0.0030:295:63//B83110
- F-HEMBB1000441//Homo sapiens Chromosome 22q12 Cosmid Clone II47g11, complete sequence //2.5e-33:372:72//AC000035

- F-HEM BB1000449//Human DNA sequence from PAC 296K21 on chromosome X contains cytochrome c, delta-aminolevulinic acid synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37), 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS//1.3e-51:534:72//Z83821
- F-HEM BB1000455//Saccharomyces cerevisiae mitochondrion origin of replication (ori6) and oli1 gene, complete cds//0.016:522:58//L36899
- 5 F-HEM BB1000472
- F-HEM BB1000480
- F-HEM BB1000487//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 128O3, WORKING DRAFT SEQUENCE//0.00013:314:64//Z98742
- 10 F-HEM BB1000490//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE//4.1e-110:529:98//AL034423
- F-HEM BB1000491//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence//0.10:187:65//AE001388
- F-HEM BB1000493//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence//3.7e-06:637:58//AL022577
- 15 F-HEM BB1000510//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence//3.1e-96:737:81//AC005553
- 20 F-HEM BB1000518//Homo Sapiens Chromosome X clone bWXP171, WORKING DRAFT SEQUENCE, 1 ordered pieces//0.00014:163:68//AC004676
- F-HEM BB1000523//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, complete sequence//0.41:349:56//AL010212
- F-HEM BB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus//6.6e-37:138:96//Y11710
- 25 F-HEM BB1000550//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11//3.9e-56:683:71//AB020860
- F-HEM BB1000554//Homo sapiens *** SEQUENCING IN PROGRESS *** , WORKING DRAFT SEQUENCE//2.2e-51:282:84//AJ011929
- 30 F-HEM BB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds//6.1e-32:537:65//AB018293
- F-HEM BB1000564
- F-HEM BB1000573//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces//8.2e-33:268:73//AC005077
- F-HEM BB1000575//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence//5.8e-47:734:66//AL022476
- 35 F-HEM BB1000586//H.sapiens highly polymorphic microsatellite DNA//0.030:147:67//X79883
- F-HEM BB1000589//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence//6.3e-41:278:83//AC002300
- 40 F-HEM BB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence//1.1e-182:871:98//AC005184
- F-HEM BB1000592//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #19//0.012:185:64//AF009074
- 45 F-HEM BB1000593//Homo sapiens chromosome 7q22 sequence, complete sequence//1.2e-131:353:93//AF053356
- F-HEM BB1000598//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence//9.1e-58:600:72//AC006207
- F-HEM BB1000623//cDNA encoding Coliolum manganese peroxidase//0.89:284:62//E12284
- 50 F-HEM BB1000630//Mus musculus clone NSAT47 nonsatellite RNA sequence//1.9e-15:129:87//U26231
- F-HEM BB1000631//Sequence 26 from patent US 5708157//3.2e-27:180:88//I80057
- F-HEM BB1000632//Human mRNA for KIAA0351 gene, complete cds//1.6e-48:811:65//AB002349
- F-HEM BB1000637//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces//4.1e-58:649:73//AC005478
- 55 F-HEM BB1000638//HS_3051_A1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=M, genomic survey sequence//0.0032:497:56//AQ155234
- F-HEM BB1000643//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces//2.4e-50:791:68//AC005077

- F-HEM BB1000649//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence//5.2e-64:775:69//AC003009
- F-HEM BB1000652//Homo sapiens chromosome 10 clone CRI-JC2048 map 10q22.1, WORKING DRAFT SEQUENCE, 4 unordered pieces//2.7e-52:334:89//AC006186
- 5 F-HEM BB1000665//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence//0.0062:426:60//AL024493
- F-HEM BB1000671//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island//9.6e-95:399:78//Z84488
- 10 F-HEM BB1000673//HS_3039_A2_C08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence//3.8e-50:293:92//AQ155121
- F-HEM BB1000684//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE//8.0e-65:282:83//Z93241
- F-HEM BB1000693//Homo sapiens neuroan1 mRNA, complete cds//1.6e-118:575:97//AF040723
- 15 F-HEM BB1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces//8.6e-07:251:61//AC005507
- F-HEM BB1000706//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE//2.9e-20:434:64//AL031118
- F-HEM BB1000709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 994L9, WORKING DRAFT SEQUENCE//0.26:184:65//AL034554
- 20 F-HEM BB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds//1.8e-129:692:93//U53475
- F-HEM BB1000726//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence//2.7e-40:304:80//U91321
- F-HEM BB1000738//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence//8.9e-35:582:63//AF011889
- 25 F-HEM BB1000749//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces//6.2e-46:262:89//AC005849
- F-HEM BB1000763//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE//1.6e-99:316:98//AL034405
- 30 F-HEM BB1000770//Human DNA sequence from clone 80119 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence//0.044:325:60//AL022727
- F-HEM BB1000774
- F-HEM BB1000781//Sequence 3 from patent US 5753446//1.2e-92:599:86//AR008277
- 35 F-HEM BB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds//9.3e-64:672:71//AB014577
- F-HEM BB1000790//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence//2.4e-41:460:74//AC004801
- F-HEM BB1000794//HS_3034_B2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=24 Row=H, genomic survey sequence//1.8e-74:378:97//AQ117099
- 40 F-HEM BB1000807//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39d7, reverse read cpq39d7.rt1a//8.5e-14:95:97//Z58412
- F-HEM BB1000810//H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 303a8, complete read//3.2e-05:138:71//Z79983
- F-HEM BB1000821//HS_2168_B1_A12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=B, genomic survey sequence//0.85:208:60//AQ086361
- 45 F-HEM BB1000822//Human BAC clone GS113H23 from 5p15.2, complete sequence//3.0e-06:361:60//AC003015
- F-HEM BB1000826//Human BAC clone RG180F08 from 7q31, complete sequence//1.1e-27:360:69//AC002431
- F-HEM BB1000827
- F-HEM BB1000831
- 50 F-HEM BB1000835//Human DNA sequence from clone 4514 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence//0.00098:234:63//AL023581
- F-HEM BB1000840//Human Chromosome 11 Cosmid cSRL97a6, complete sequence//4.5e-61:328:79//U73649
- F-HEM BB1000848//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence//9.7e-144:809:87//AL021068
- 55 F-HEM BB1000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING

EP 1 074 617 A2

DRAFT SEQUENCE, 9 unordered pieces//0.12:492:58//AC004157
F-HEM BB1000870//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING
DRAFT SEQUENCE, 9 unordered pieces//0.0024:212:67//AC004157
F-HEM BB1000876//Homo sapiens ELISC-1 mRNA, partial cds.//1.5e-32:200:94//AF085351
5 F-HEM BB1000883//HS_3065_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3065 Col=8 Row=F, genomic survey sequence.//0.0017:152:66//AQ137687
F-HEM BB1000887
F-HEM BB1000888//CIT-HSP-2329A10.TR CIT-HSP Homo sapiens genomic clone 2329A10, genomic survey se-
quence.//1.5e-31:172:98//AQ044369
10 F-HEM BB1000890
F-HEM BB1000893//Plasmodium falciparum MAL3P2, complete sequence.//9.5e-06:768:56//AL034558
F-HEM BB1000908//Homo sapiens clone DJ1119N05, complete sequence.//4.5e-21:199:82//AC004968
F-HEM BB1000910//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING
DRAFT SEQUENCE.//0.72:366:59//AL034557
15 F-HEM BB1000913//HS_3078_B1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//9.9e-12:221:63//AQ144507
F-HEM BB1000915//Homo sapiens DNA for (CGG)_n trinucleotide repeat region, isolate P4.//1.2e-49:252:99//
AJ001215
F-HEM BB1000917//Homo sapiens chromosome 5, P1 clone 254f11 (LBNL H62), complete sequence.//2.3e-42:
20 316:76//AC006077
F-HEM BB1000927//Human BDR-2 mRNA for hippocalcin, complete cds.//3.6e-30:528:65/D16593
F-HEM BB1000947//CpG0856B CplOWAgDNA1 Cryptosporidium parvum genomic, genomic survey sequence.//
0.81:262:62//AQ254493
F-HEM BB1000959//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 346O6, WORKING
DRAFT SEQUENCE.//1.2e-43:454:75//Z84487
25 F-HEM BB1000973//Mus musculus schlafen2 (Slfn2) mRNA, complete cds.//8.3e-42:458:72//AF099973
F-HEM BB1000975//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence.//
0.98:196:63//AB005234
F-HEM BB1000981
30 F-HEM BB1000985//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//2.9e-06:566:57//
AC004476
F-HEM BB1000991//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//
0.099:391:57//Z98753
F-HEM BB1000996//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-
35 sequences (GSSs).//6.2e-33:227:80//Z94802
F-HEM BB1001004
F-HEM BB1001008//Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence.//4.0e-13:164:
79//AC002551
F-HEM BB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//7.5e-13:229:
40 69//AC002310
F-HEM BB1001014//Homo sapiens chromosome 16, BAC clone 375G12 (LANL), complete sequence.//0.32:474:
58//AC005751
F-HEM BB1001020//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//
2.6e-39:218:80//AF069291
45 F-HEM BB1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//5.3e-05:656:59//AF070717
F-HEM BB1001037//CIT-HSP-2358K16.TF CIT-HSP Homo sapiens genomic clone 2358K16, genomic survey se-
quence.//6.6e-05:228:64//AQ080539
F-HEM BB1001047//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from
Xq28, complete sequence.//4.0e-27:385:71//U82671
50 F-HEM BB1001051//H.sapiens mRNA for FAN protein.//1.2e-27:160:98//X96586
F-HEM BB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//
2.3e-89:180:91//AC006014
F-HEM BB1001058//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Li-
brary) complete sequence.//1.2e-41:468:74//AC006060
55 F-HEM BB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.3e-122:785:86//
U49973
F-HEM BB1001063//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 523G1, WORKING
DRAFT SEQUENCE.//7.1e-162:770:99//AL034375

- F-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//3.1e-146:736:95//AF034803
- F-HEM BB1001096//Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene, partial cds.//0.00088:690:57//AF008210
- 5 F-HEM BB1001102//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//2.1e-76:368:99//AF049612
- F-HEM BB1001105//CIT-HSP-2185N1.TR CIT-HSP Homo sapiens genomic clone 2185N1, genomic survey sequence.//1.0e-09:136:76//AQ002987
- F-HEM BB1001112//Rattus rattus sec61 homologue mRNA, complete cds.//1.0e-108:909:76//M96630
- 10 F-HEM BB1001114//Homo sapiens chromosome 17, clone hRPK.795_F_17, complete sequence.//7.2e-07:459:59//AC005284
- F-HEM BB1001117//HS_2178_B1_E12_MR CIT Approved-Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=23 Row=J, genomic survey sequence.//7.8e-50:331:86//AQ068244
- F-HEM BB1001119//Human collagen type XII alpha-1 precursor (COL12A1) mRNA, complete cds.//1.6e-25:150:98//U73778
- 15 F-HEM BB1001126
- F-HEM BB1001133//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//2.8e-24:228:80//AC004673
- F-HEM BB1001137
- 20 F-HEM BB1001142//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.0e-40:231:76//AC004617
- F-HEM BB1001151//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.9e-47:640:67//AF015264
- F-HEM BB1001153//CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.//0.76:136:67//AQ075724
- 25 F-HEM BB1001169//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//9.9e-63:259:79//AL008712
- F-HEM BB1001175//Human mRNA for ankyrin motif, complete cds.//2.2e-34:509:66//D78334
- F-HEM BB1001177//CIT-HSP-2321I17.TR CIT-HSP Homo sapiens genomic clone 2321I17, genomic survey sequence.//5.9e-27:320:75//AQ036473
- 30 F-HEM BB1001182//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//5.7e-06:62:96//B85188
- F-HEM BB1001199
- F-HEM BB1001208//HS_2026_B1_C07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=13 Row=F, genomic survey sequence.//0.00018:134:70//AQ229237
- 35 F-HEM BB1001209//CITBI-E1-2521F23.TF CITBI-E1 Homo sapiens genomic clone 2521F23, genomic survey sequence.//1.4e-95:464:98//AQ278357
- F-HEM BB1001210//HS_3102_A2_F09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3102 Col=18 Row=K, genomic survey sequence.//2.6e-90:446:98//AQ119196
- 40 F-HEM BB1001218//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.//1.0e-31:315:72//AL031291
- F-HEM BB1001221//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.7e-17:770:59//AC005504
- F-HEM BB1001234//H.sapiens CpG island DNA genomic MseI fragment, clone 39f9, forward read cpg39f9.ft1e//4.0e-30:171:97//Z65435
- 45 F-HEM BB1001242//Homo sapiens mRNA for LAK-1, complete cds.//3.8e-30:458:67//AB005754
- F-HEM BB1001249//CIT-HSP-2375N19.TF CIT-HSP Homo sapiens genomic clone 2375N19, genomic survey sequence.//0.0076:250:63//AQ109087
- F-HEM BB1001253//Homo sapiens genomic DNA, chromosome 21q11.1, segment 3/28, WORKING DRAFT SEQUENCE.//0.0097:89:80//AP000032
- 50 F-HEM BB1001254//CIT-HSP-2320E5.TF CIT-HSP Homo sapiens genomic clone 2320E5, genomic survey sequence.//3.7e-54:284:97//AQ037173
- F-HEM BB1001267//Homo sapiens chromosome 17, clone hRPK.488_L_1, complete sequence.//3.5e-30:236:78//AC005303
- 55 F-HEM BB1001271//HS_3011_A1_G02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3011 Col=3 Row=M, genomic survey sequence.//5.2e-07:364:62//AQ214217
- F-HEM BB1001282//CIT-HSP-2356J20.TF CIT-HSP Homo sapiens genomic clone 2356J20; genomic survey sequence.//1.8e-16:109:97//AQ060969

- F-HEM BB1001288//R.norvegicus mRNA for gephyrin.//3.4e-18:194:77//X66366
 F-HEM BB1001289//Genomic sequence from Human 9q34, complete sequence.//4.8e-66:434:74//AC000387
 F-HEM BB1001294//HS_3039_B1_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//2.0e-90:437:99//AQ155035
- 5 F-HEM BB1001302
 F-HEM BB1001304//CIT-HSP-2053E15.TF CIT-HSP Homo sapiens genomic clone 2053E15, genomic survey sequence.//2.2e-07:370:61//B69144
 F-HEM BB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//5.7e-116:663:85//U92703
- 10 F-HEM BB1001315//Homo sapiens chromosome 10 clone LA10NC01_40_G_3 map 10q26.1-10q26.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.5e-33:328:77//AC006096
 F-HEM BB1001317//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.4e-122:680:91//AC006210
 F-HEM BB1001326//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.8e-09:518:60//AC004129
- 15 F-HEM BB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//3.7e-56:458:79//D63850
 F-HEM BB1001335//HS_3055_A1_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=19 Row=O, genomic survey sequence.//1.0:222:63//AQ147384
- 20 F-HEM BB1001337//Human PAC clone DJ0093103 from Xq23, complete sequence.//1.0e-74:319:85//AC003983
 F-HEM BB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.0e-135:856:87//U85056
 F-HEM BB1001346//Human familial Alzheimer's disease (STM2) gene, complete cds.//3.3e-44:481:74//U50871
 F-HEM BB1001348//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//1.8e-17:210:73//AC006041
- 25 F-HEM BB1001356//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:386:59//AC005079
 F-HEM BB1001364//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//0.97:349:61//AC004662
 F-HEM BB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete sequence.//5.5e-161:766:98//AC005876
- 30 F-HEM BB1001367//Homo sapiens chromosome 17, clone hRPC.906_A_24, complete sequence.//3.0e-55:510:76//AC004408
 F-HEM BB1001369//Homo sapiens BAC clone RG163K11 from 7q31, complete sequence.//0.048:244:64//AC005192
- 35 F-HEM BB1001380//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//2.5e-26:257:78//AC006204
 F-HEM BB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//5.1e-99:571:89//AF071314
 F-HEM BB1001387//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//7.1e-05:546:58//X02354
- 40 F-HEM BB1001394//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence.//4.0e-129:788:88//AC005023
 F-HEM BB1001410//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.8e-11:632:59//AF045555
 F-HEM BB1001424//Mus musculus Chromosome 4 BAC clone BacB6, complete sequence.//0.0012:435:59//AC003019
- 45 F-HEM BB1001426//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.8e-17:360:64//AC005482
 F-HEM BB1001429//leucine aminopeptidase [cattle, kidney, mRNA, 2056 nt].//4.1e-114:668:88//S65367
 F-HEM BB1001436//Homo sapiens FUT2 gene, intron 1, complete sequence.//2.3e-37:438:74//AB000931
- 50 F-HEM BB1001443//Bos taurus pyruvate dehydrogenase phosphatase mRNA, complete cds.//9.1e-92:550:88//L18966
 F-HEM BB1001449//Homo sapiens chromosome 5, PAC clone 228g9 (LBNL H142), complete sequence.//0.00024:385:62//AC004768
 F-HEM BB1001454//Homo sapiens chromosome 19, cosmid R34169, complete sequence.//0.84:577:57//AC005790
- 55 F-HEM BB1001458//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//8.0e-40:377:78//AC000382
 F-HEM BB1001463//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.011:482:

- 59//AF001549
F-HEM BB1001464//Human chromosome 16p13 BAC clone CIT987SK-3H8 complete sequence.//0.019:263:61//U91320
- 5 F-HEM BB1001482//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//1.0e-30:521:66//U92564
F-HEM BB1001500//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-31:479:71//AC004873
F-HEM BB1001521//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.7e-51:680:70//AC005080
- 10 F-HEM BB1001527
F-HEM BB1001531//Homo sapiens Chromosome 22q11.2 Cosmid Clone 89h In DGCR Region, complete sequence.//1.3e-79:696:79//AC000089
F-HEM BB1001535//O. aries DNA for polymorphic marker 'OVINRA01' (339 bp).//0.00034:217:62//X89268
F-HEM BB1001536//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//0.54:266:60//AC004548
- 15 F-HEM BB1001537//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//4.6e-25:784:61//AC004262
F-HEM BB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//6.9e-50:213:80//AC004605
- 20 F-HEM BB1001562//Homo sapiens clone NH0523H20, complete sequence.//0.46:269:60//AC005041
F-HEM BB1001564//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//1.7e-107:620:83//AL020989
F-HEM BB1001565//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-50:734:67//AC004003
- 25 F-HEM BB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.4e-166:816:97//AL031677
F-HEM BB1001586
F-HEM BB1001588//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.6e-21:419:65//AC005261
- 30 F-HEM BB1001603
F-HEM BB1001618//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//4.5e-29:422:72//Z99289
- 35 F-HEM BB1001619//HS_3079_B1_A04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=B, genomic survey sequence.//0.0010:77:79//AQ123388
F-HEM BB1001630//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:667:59//AC005089
F-HEM BB1001635//Plasmodium falciparum MAL3P7, complete sequence.//3.8e-05:475:57//AL034559
- 40 F-HEM BB1001637//Homo sapiens DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the alternatively spliced CLCN6 gene for chloride channel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPPA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronatriodilatin), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence.//9.2e-13:168:76//AL021155
- 45 F-HEM BB1001641//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//0.00097:721:58//AB006702
F-HEM BB1001653//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//0.15:276:63//AC002038
- 50 F-HEM BB1001665//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.43:393:61//L14320
F-HEM BB1001668//F16C15-T7 IGF Arabidopsis thaliana genomic clone F16C15, genomic survey sequence.//0.040:275:60//B12308
- 55 F-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//7.2e-171:803:98//AB014546
F-HEM BB1001684//Sequence 1 from patent US 5700927.//7.5e-124:883:81//I86429
F-HEM BB1001685//CIT-HSP-2287O9.TF CIT-HSP Homo sapiens genomic clone 2287O9, genomic survey sequence.//2.3e-34:191:97//B99261
F-HEM BB1001695//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding

- exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (*Drosophila*) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.0091:334:63//AL009178
- 5 F-HEM BB1001704//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STss, GSSs and genomic marker DXS8098, complete sequence.//1.2e-17:144:87//AL023575
- F-HEM BB1001706
- F-HEM BB1001707//Guinea pig CD19 mRNA, complete cds.//0.57:232:62//M62543
- F-HEM BB1001717//*Saccharomyces cerevisiae* mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//1.1e-13:723:58//AJ223323
- 10 F-HEM BB1001735//Human PAC clone DJ0596O09 from 7p15, complete sequence.//1.3e-36:427:73//AC003074
- F-HEM BB1001736//*S.pombe* chromosome II cosmid c4B4.//0.0085:479:57//AL023706
- F-HEM BB1001747//Homo sapiens PAC clone DJ1002N02 from 7p21-p22, complete sequence.//4.0e-112:532:84//AC005376
- 15 F-HEM BB1001749//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//1.3e-98:395:82//AC005829
- F-HEM BB1001753//*S.maximus* repeat region, 342bp.//4.2e-11:69:85//Z78099
- F-HEM BB1001756//Homo sapiens full-length insert cDNA clone ZD86A11.//0.0015:302:62//AF088064
- F-HEM BB1001760//*P.falciparum* complete gene map of plastid-like DNA (IR-A).//0.011:615:56//X95275
- 20 F-HEM BB1001762//CIT-HSP-2290J16.TF CIT-HSP Homo sapiens genomic clone 2290J16, genomic survey sequence.//0.84:208:64//AQ005184
- F-HEM BB1001785//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE.//0.0019:469:60//AL031746
- F-HEM BB1001797//Human heterogenous nuclear RNA W16W.//0.00012:83:86//X17272
- 25 F-HEM BB1001802//*Plasmodium falciparum* MAL3P7, complete sequence.//1.8e-11:538:60//AL034559
- F-HEM BB1001812//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING DRAFT SEQUENCE.//1.0e-56:304:84//Z98882
- F-HEM BB1001816//Homo sapiens chromosome 19, cosmid F24083, complete sequence.//3.6e-75:300:87//AC005204
- 30 F-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//2.3e-162:763:98//AF056209
- F-HEM BB1001834//CIT-HSP-2291012.TF CIT-HSP Homo sapiens genomic clone 2291012, genomic survey sequence.//7.6e-08:73:94//AQ004168
- F-HEM BB1001836//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-30:297:79//AC004801
- 35 F-HEM BB1001839//Human Chromosome X, complete sequence.//0.016:293:63//AC004073
- F-HEM BB1001850//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0027:812:58//AC005504
- F-HEM BB1001863//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.3e-43:520:72//AC004581
- 40 F-HEM BB1001867//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//1.7e-56:399:86//U07563
- F-HEM BB1001868//*Rattus norvegicus* clone 923 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//6.1e-08:234:67//U01145
- 45 F-HEM BB1001869//Homo sapiens full-length insert cDNA clone YT86F01.//7.4e-87:432:97//AF085974
- F-HEM BB1001872
- F-HEM BB1001874//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.4e-14:631:61//AC005000
- F-HEM BB1001875//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//0.93:415:57//Z82209
- 50 F-HEM BB1001880//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//1.0e-18:729:60//Z93403
- F-HEM BB1001899//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 4-10, complete sequence.//0.0038:425:58//AL010216
- 55 F-HEM BB1001905//*S.pombe* chromosome III cosmid c330.//1.1e-23:520:62//AL031603
- F-HEM BB1001906
- F-HEM BB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//3.7e-82:672:81//U47742

- F-HEM BB1001910//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0033:566:55//AC005505
- F-HEM BB1001911//*Arabidopsis thaliana* chromosome II BAC F26C24 genomic sequence, complete sequence.//1.0:581:58//AC004705
- 5 F-HEM BB1001915//*Caenorhabditis elegans* cosmid T05H10, complete sequence.//1.2e-16:283:67//Z47812
- F-HEM BB1001921//*Homo sapiens* chromosome 17, clone hCIT.123_J_14, complete sequence.//3.4e-07:803:58//AC003950
- F-HEM BB1001922//*Plasmodium falciparum* chromosome 2, section 28 of 73 of the complete sequence.//5.0e-06:756:56//AE001391
- 10 F-HEM BB1001925//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.1e-45:609:73//AL009181
- F-HEM BB1001930//*Homo sapiens* genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11.//3.2e-158:745:99//AB020867
- F-HEM BB1001944//, complete sequence.//4.1e-60:638:73//AC005815
- 15 F-HEM BB1001945//HS_3185_B1_G05_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3185 Col=9 Row=N, genomic survey sequence.//1.0:280:58//AQ188882
- F-HEM BB1001947//Human mRNA for KIAA0392 gene, partial cds.//5.6e-20:333:66//AB002390
- F-HEM BB1001950//Human lipocortin (LIP) 2 gene, upstream region.//0.0094:180:63//M62899
- F-HEM BB1001952//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 101A4, WORKING DRAFT SEQUENCE.//5.4e-19:329:70//Z93341
- 20 F-HEM BB1001953//*Homo sapiens* chromosome 17, clone hRPK.795_F_17, complete sequence.//0.11:589:58//AC005284
- F-HEM BB1001957//Human DNA sequence from PAC 204E5 on chromosome 12. Contains exon similar to Wilms' Tumour-related protein QM-like P2X-like receptor, ATP ligand gated ion channel, ESTs, CpG island.//9.8e-25:446:67//Z98941
- 25 F-HEM BB1001962//*Homo sapiens* chromosome 16, BAC clone 462G18 (LANL), complete sequence.//2.8e-147:727:97//AC005736
- F-HEM BB1001967//*Homo sapiens* clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//3.2e-56:650:71//AC004963
- 30 F-HEM BB1001973//*Homo sapiens* chromosome 12p13.3-clone RPC11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//1.2e-42:327:84//AC005844
- F-HEM BB1001983//CIT-HSP-2315M4.TF CIT-HSP *Homo sapiens* genomic clone 2315M4, genomic survey sequence.//8.8e-35:198:96//AQ028071
- F-HEM BB1001988//D.polychroa microsatellite sequence (clone Dp 1C e12).//4.5e-07:337:62//X92189
- 35 F-HEM BB1001990//HS_3234_A1_G08_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3234 Col=15 Row=M, genomic survey sequence.//0.039:279:59//AQ204689
- F-HEM BB1001996//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.//0.18:392:58//AL024507
- F-HEM BB1001997//*Homo sapiens* clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.3e-43:446:71//AC005069
- 40 F-HEM BB1002002//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.077:444:58//AC004153
- F-HEM BB1002005//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 963K23, WORKING DRAFT SEQUENCE.//3.4e-16:173:78//AL031685
- 45 F-HEM BB1002009//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00033:790:56//AC005506
- F-HEM BB1002015//*Homo sapiens* genomic DNA, chromosome 21q11.1, segment 27/28, WORKING DRAFT SEQUENCE.//6.7e-05:126:76//AP000056
- F-HEM BB1002042//*Oncorhynchus mykiss* cytochrome P450 (CYP4V1) mRNA, partial cds.//6.4e-33:402:69//AF046012
- 50 F-HEM BB1002043
- F-HEM BB1002044//*Homo sapiens* chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//3.0e-167:809:97//AC005740
- F-HEM BB1002045
- 55 F-HEM BB1002049//*Homo sapiens* chromosome 17, clone hRPC.161_P_9, complete sequence.//0.87:177:65//AC006237
- F-HEM BB1002050//*Streptomyces coelicolor* cosmid D78.//8.5e-08:644:58//AL034355
- F-HEM BB1002068//*Homo sapiens* mRNA for KIAA0612 protein, partial cds.//2.5e-05:402:61//AB014512

EP 1 074 617 A2

F-HEMBB1002069
 F-HEMBB1002092//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.8e-104:550:83//AC004064
 F-HEMBB1002094//Homo sapiens genomic DNA, 21q region, clone: 125H6N2, genomic survey sequence.//2.9e-49:302:83//AG001476
 5 F-HEMBB1002115//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//0.00023:542:61//AC004035
 F-HEMBB1002134//Human h-neuro-d4 protein mRNA, complete cds.//7.3e-43:533:70//U43843
 F-HEMBB1002139//HS-1048-A2-B02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 831 Col=4 Row=C, genomic survey sequence.//0.055:228:66//B38714
 10 F-HEMBB1002142//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P5, WORKING DRAFT SEQUENCE.//0.0095:276:64//AL031748
 F-HEMBB1002152//Human Chromosome X, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.055:520:57//AC002421
 15 F-HEMBB1002189//Homo sapiens cosmid ICRFc104I0935Q8 from Xq28, complete sequence.//2.6e-05:311:63//AF002998
 F-HEMBB1002190//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.4e-05:647:59//AC005140
 F-HEMBB1002193//Sequence 5 from patent US 5709858.//1.8e-34:179:100//I80846
 20 F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10.//1.2e-23:405:67//X52332
 F-HEMBB1002218//HS_2056_B1_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=17 Row=F, genomic survey sequence.//3.3e-45:245:97//AQ244711
 F-HEMBB1002232//Human chromosome 11 72g7 cosmid, complete sequence.//1.9e-21:314:70//U73648
 F-HEMBB1002247
 25 F-HEMBB1002249//Homo sapiens DNA sequence from BAC 34I8 on chromosome 6p21.3-22.1. Contains ZNF184 gene coding for Kruppel related Zinc Finger protein 184, a hnRNP core protein A1 (mouse Fli-2, rat helix destabilizing protein, mouse Topoisomerase-inhibitor suppressed gene TIS) LIKE pseudogene, a HB15 (CD83 antigen precursor) LIKE pseudogene, Ser-tRNA, Glu-tRNA and Met-tRNA (Met-tRNA-i gene 1) genes. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-45:327:83//AL021918
 30 F-HEMBB1002254//Human chromosome 16 BAC clone LANL cosmid-440E5, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.8e-40:315:82//AC002506
 F-HEMBB1002255//Plasmodium falciparum MAL3P3, complete sequence.//0.0035:312:62//Z98547
 F-HEMBB1002266//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:469:59//AC005504
 35 F-HEMBB1002280//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//5.3e-18:527:61//AC004682
 F-HEMBB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//8.6e-139:818:88//U73642
 F-HEMBB1002306//HS_3109_A2_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=2 Row=O, genomic survey sequence.//1.3e-75:371:98//AQ148164
 40 F-HEMBB1002327//HS_3235_B2_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=20 Row=N, genomic survey sequence.//3.3e-83:418:97//AQ209752
 F-HEMBB1002329//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//3.3e-31:220:88//AQ263402
 45 F-HEMBB1002340
 F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//4.1e-154:724:98//AJ010841
 F-HEMBB1002358//Human thymidylate kinase (CDC8) mRNA, complete cds.//3.3e-36:192:98//L16991
 F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds.//1.8e-13:96:96//U55766
 50 F-HEMBB1002364//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 376D21, WORKING DRAFT SEQUENCE.//7.5e-24:202:71//Z98946
 F-HEMBB1002371//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9e-06:674:56//AC004153
 F-HEMBB1002381//Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete sequence.//0.34:238:61//AC005222
 55 F-HEMBB1002383
 F-HEMBB1002387//CIT-HSP-2173E20.TR CIT-HSP Homo sapiens genomic clone 2173E20, genomic survey sequence.//5.2e-17:434:66//B91052
 F-HEMBB1002409//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3

EP 1 074 617 A2

precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-56:324:88//AL008712
 F-HEMBB1002415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 36411, WORKING
 DRAFT SEQUENCE.//8.9e-35:334:75//AL031319
 F-HEMBB1002425//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//1.0e-36:317:76//
 5 U62317
 F-HEMBB1002442//Rattus norvegicus lin-10 protein homolog (lin-10) mRNA, complete cds.//4.3e-88:296:92//
 U92010
 F-HEMBB1002453//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 86D1, WORKING
 DRAFT SEQUENCE.//2.7e-43:419:78//AL034349
 10 F-HEMBB1002457//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//
 1.3e-27:542:68//AC005534
 F-HEMBB1002458//HS_3246_A2_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3246 Col=10 Row=M, genomic survey sequence.//3.2e-51:257:99//AQ217993
 F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//1.9e-87:493:92//U43885
 15 F-HEMBB1002489
 F-HEMBB1002492//Arabidopsis thaliana BAC T15B16.//0.028:516:57//AF104919
 F-HEMBB1002495//Homo sapiens chromosome 17, clone hRPK.421_E_14, complete sequence.//1.1e-16:297:
 68//AC006141
 F-HEMBB1002502//Homo sapiens clone DJ1163L11, complete sequence.//1.1e-91:675:82//AC005230
 20 F-HEMBB1002509//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//2.7e-
 11:648:60//AC004605
 F-HEMBB1002510//HS_3236_B1_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3236 Col=21 Row=P, genomic survey sequence.//1.2e-06:67:94//AQ205992
 F-HEMBB1002520//Homo sapiens BAC clone NH0004N07 from Y, complete sequence.//1.2e-70:580:72//
 25 AC006152
 F-HEMBB1002522//Homo sapiens Xp22 bin 150 clone GSHB-223P11 (Genome Systems Human BAC library)
 complete sequence.//5.6e-22:516:64//AC004553 F-HEMBB1002531
 F-HEMBB1002534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING
 DRAFT SEQUENCE.//6.9e-62:265:87//AL034346
 30 F-HEMBB1002545//Human BAC clone RG128M16 from 7q21-7q22, complete sequence.//2.7e-44:200:82//
 AC000059
 F-HEMBB1002550//Homo sapiens PAC clone DJ0910I17 from 7q11.21-q11.23, complete sequence.//0.22:161:
 68//AC004927
 F-HEMBB1002556//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//7.5e-43:306:77//
 35 AC004861
 F-HEMBB1002579
 F-HEMBB1002582//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING
 DRAFT SEQUENCE.//0.00018:431:61//AL033520
 F-HEMBB1002590//Yeast (S.cerevisiae) mitochondrial apocytochrome b gene, 3' flank.//0.78:147:64//J01471
 40 F-HEMBB1002596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 9E21, WORKING
 DRAFT SEQUENCE.//3.6e-50:692:69//AL008639
 F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//9.1e-151:710:98//AF089749
 F-HEMBB1002601//Human BAC clone RG020D02 from 7q22, complete sequence.//1.5e-07:416:60//AC002381
 F-HEMBB1002603//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//0.40:341:60//AC002454
 45 F-HEMBB1002607//Mus musculus homeobox containing nuclear transcriptional factor Hmx1 (Hmx1) gene, com-
 plete cds.//0.0042:460:60//AF009614
 F-HEMBB1002610//Homo sapiens Chromosome 12q24 PAC RPC13-462E2 (Roswell Park Cancer Institute Human
 PAC library) complete sequence.//6.3e-23:559:63//AC003029
 F-HEMBB1002613//Homo sapiens Chromosome 22q12 BAC Clone 566c1, complete sequence.//4.2e-17:441:63//
 50 AC000025
 F-HEMBB1002614//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//0.013:
 324:56//AE001417
 F-HEMBB1002617//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//2.1e-07:
 441:60//AF001550
 55 F-HEMBB1002623//C.hyalina microsatellite marker DNA (id ATCC4).//0.57:106:66//Z95304
 F-HEMBB1002635//Human JNK3 alpha2 protein kinase (JNK3A2) mRNA, complete cds.//4.8e-22:127:100//
 U34819
 F-HEMBB1002664//HS_2265_A1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

EP 1 074 617 A2

nomic clone Plate=2265 Col=11 Row=O, genomic survey sequence//0.54:115:67//AQ101557
 F-HEMBB1002677//Homo sapiens (subclone 3_d1 from P1 H25) DNA sequence, complete sequence//2.2e-49:
 784:68//L81774
 F-HEMBB1002683//Homo sapiens type IV collagen 5a chain (COL4A5) gene, exon 23//1.0:112:63//U04492
 5 F-HEMBB1002684//HS-1050-A2-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone
 Plate=CT 772 Col=12 Row=M, genomic survey sequence//4.4e-07:86:84//B39748
 F-HEMBB1002686//HS-1023-B2-F10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone
 Plate=CT 802 Col=20 Row=L, genomic survey sequence//0.98:183:61//B34077
 F-HEMBB1002692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108H3, WORKING
 10 DRAFT SEQUENCE//0.00039:408:60//AL033525
 F-HEMBB1002697//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces//
 7.3e-35:323:74//AC004955
 F-HEMBB1002699//Mus musculus D6MM5e protein (D6Mm5e) and DOK protein (Dok) genes, complete cds; and
 LOR2 protein (Lor2) gene, partial cds//0.031:325:62//AF084363
 15 F-HEMBB1002702//HS-1025-A2-D01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic
 clone Plate=CT 804 Col=2 Row=G, genomic survey sequence//1.8e-25:158:95//B34720
 F-HEMBB1002705//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding
 carbonyl reductase and carbonyl reductase 3 (complete cds)//1.7e-137:534:96//AB003151
 F-HEMBB1002712//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038
 20 on chromosome X contains ESTs and STS//0.0019:612:58//Z71187
 F-MAMMA1000009//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3
 unordered pieces//6.1e-43:354:81//AC003117
 F-MAMMA1000019
 F-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5)//2.0e-40:185:97//Z47553
 25 F-MAMMA1000025//Homo sapiens PAC clone DJ0806A17 from 7p13-p14, complete sequence//1.0:211:65//
 AC005483
 F-MAMMA1000043//Human angiotensin I-converting enzyme (ACE) gene, intron 12//0.075:204:65//M73275
 F-MAMMA1000045//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a
 gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence//4.1e-122:
 30 495:79//AL031073
 F-MAMMA1000055//M.musculus mRNA for testin//2.1e-35:559:66//X78989
 F-MAMMA1000057//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence//5.5e-121:703:
 89//AC005829
 F-MAMMA1000069//Homo sapiens minisatellite ceb1 repeat region//0.00013:329:60//AF048727
 35 F-MAMMA1000084//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains
 ESTs STS and CpG island//2.1e-53:445:79//Z93023
 F-MAMMA1000085//Caenorhabditis elegans cosmid Y23H5A//0.0017:164:64//AF077541
 F-MAMMA1000092//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence//1.2e-70:598:78//
 AC004744
 40 F-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence//1.1e-156:857:92//
 AC003976
 F-MAMMA1000117//HS_3223_B2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3223 Col=16 Row=H, genomic survey sequence//5.4e-100:527:94//AQ221160
 F-MAMMA1000129//ryanodine receptor//0.055:492:59//A20359
 45 F-MAMMA1000133
 F-MAMMA1000134//HS_3078_B1_C02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3078 Col=3 Row=F, genomic survey sequence//2.1e-93:462:97//AQ144362
 F-MAMMA1000139//Homo sapiens Xp22 PAC RPC11-5G11 (from Roswell Park Cancer Center) complete se-
 quence//3.3e-14:322:65//AC002369
 50 F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.9e-25:148:97//AB014585
 F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//1.0e-29:
 219:87//AF031924
 F-MAMMA1000163
 F-MAMMA1000171//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence//6.3e-14:92:88//
 55 AC005393
 F-MAMMA1000173//Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human
 Drebrin//2.2e-114:698:87//U58884
 F-MAMMA1000175//HS_3050_B1_B03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=3050 Col=5 Row=D, genomic survey sequence //6.2e-73:357:99//AQ102678
 F-MAMMA1000183//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING
 DRAFT SEQUENCE //4.6e-94:904:73//AL023808
 F-MAMMA1000198//Z.diploperennis repetitive DNA (clone ZEAR 266) //0.18:152:70//X53610
 5 F-MAMMA1000221//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence //0.017:99:75//
 AC004583
 F-MAMMA1000227//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING
 DRAFT SEQUENCE //0.36:312:62//AL031283
 F-MAMMA1000241//HS_3217_B1_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 10 nomic clone Plate=3217 Col=3 Row=D, genomic survey sequence //1.9e-94:456:98//AQ193401
 F-MAMMA1000251//Homo sapiens NF2 gene //0.00092:270:64//Y18000
 F-MAMMA1000254//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING
 DRAFT SEQUENCE, 14 unordered pieces //0.0034:777:57//AC005140
 F-MAMMA1000257//Homo sapiens DNA sequence from PAC 201D7 on chromosome 6p22.1-22.3. Contains EST
 15 and STS //0.00036:230:65//AL022717
 F-MAMMA1000264//Homo sapiens (subclone 9_f5 from P1 H17) DNA sequence, complete sequence //1.5e-30:
 499:68//LB1612
 F-MAMMA1000266//Bacillus lyncceorum strain pMEL12 Bag320 satellite DNA //0.28:218:64//AF034430
 F-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence //1.4e-157:
 20 788:96//AF001549
 F-MAMMA1000277//Mycobacterium tuberculosis H37Rv complete genome; segment 48/162 //0.70:320:61//
 AL021897
 F-MAMMA1000278//Sequence 23 from patent US 5708157 //9.3e-103:540:95//I80055
 F-MAMMA1000279//Human DNA sequence from clone 769D20 on chromosome Xp21.1-21.3 Contains EST, STS,
 25 GSS, complete sequence //2.4e-49:262:77//AL031643
 F-MAMMA1000284//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic
 clone cSRL-165E12, genomic survey sequence //1.1e-30:324:75//B03004
 F-MAMMA1000287//Homo sapiens, clone hRPK.15_A_1, complete sequence //2.7e-54:401:83//AC006213
 F-MAMMA1000302//Drosophila melanogaster complete mitochondrial genome //0.0051:307:61//U37541
 30 F-MAMMA1000307//Homo sapiens chromosome 12p13.3 clone RPCI5-1154L15, WORKING DRAFT SE-
 QUENCE, 67 unordered pieces //0.15:449:59//AC006205
 F-MAMMA1000309//cDNA coding human apolipoprotein E3 //0.00010:691:58//E00359
 F-MAMMA1000312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 798A17, WORKING
 DRAFT SEQUENCE //0.27:301:60//AL031274
 35 F-MAMMA1000313
 F-MAMMA1000331//Human Chromosome 16 BAC clone CIT987SK-A-735G6, complete sequence //9.8e-06:151:
 71//AC002400
 F-MAMMA1000339
 F-MAMMA1000340//HS_2181_B2_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 40 nomic clone Plate=2181 Col=14 Row=L, genomic survey sequence //4.3e-05:181:68//AQ024288
 F-MAMMA1000348//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence //5.3e-30:575:66//
 AC004139
 F-MAMMA1000356//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces //
 1.8e-52:264:76//AC005052
 45 F-MAMMA1000360//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence //6.5e-91:569:88//
 AC004879
 F-MAMMA1000361//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribos-
 omal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat //1.4e-42:315:83//Z98950
 F-MAMMA1000372//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING
 50 DRAFT SEQUENCE //2.9e-114:516:89//AL022345
 F-MAMMA1000385//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey
 sequence //6.9e-26:377:71//AQ279944
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds //3.7e-148:710:
 98//AB015132
 55 F-MAMMA1000395
 F-MAMMA1000402//Homo sapiens clone DJ0718N17, complete sequence //4.0e-115:845:85//AC005999
 F-MAMMA1000410//HS_3245_A1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3245 Col=3 Row=E, genomic survey sequence //9.6e-42:350:80//AQ205768

- F-MAMMA1000413//HS_3223_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=2 Row=L, genomic survey sequence.//1.6e-48:318:89//AQ188456
- F-MAMMA1000414//HS_2027_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=8 Row=F, genomic survey sequence.//1.4e-46:286:92//AQ231369
- 5 F-MAMMA1000416//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//9.4e-33:310:72//AC004640
- F-MAMMA1000421//Homo sapiens clone DJ1129D05, complete sequence.//3.3e-29:223:84//AC005630
- F-MAMMA1000422
- F-MAMMA1000423//Drosophila yakuba mitochondrial DNA molecule.//2.2e-10:639:57//X03240
- 10 F-MAMMA1000424//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.6e-47:556:68//AC003973
- F-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//8.0e-99:545:92//AF062484
- F-MAMMA1000431//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-41:289:79//AC005283
- 15 F-MAMMA1000444//Human DNA sequence from clone 714B7 on chromosome 22q12.2-13.2 Contains CYTOCHROME C OXIDASE VIIB precursor like pseudogene and ESTs, complete sequence.//2.3e-34:291:80//Z99755
- F-MAMMA1000446
- F-MAMMA1000458//Mus musculus clone OST9003, genomic survey sequence.//5.0e-53:231:84//AF046620
- F-MAMMA1000468//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 291J10, WORKING
- 20 DRAFT SEQUENCE.//0.75:303:60//Z93017
- F-MAMMA1000472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 414D7, WORKING DRAFT SEQUENCE.//4.0e-41:403:77//AL033543
- F-MAMMA1000478//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.5e-54:369:77//AC005081
- 25 F-MAMMA1000483//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//3.6e-34:332:77//AC004381
- F-MAMMA1000490//Homo sapiens 12q13.1 PAC RPC11-90J4 (Roswell Park Cancer Institute Human PAC library) complete sequence.//8.9e-128:822:87//AC003686
- F-MAMMA1000500//CIT-HSP-231905.TF CIT-HSP Homo sapiens genomic clone 2319O5, genomic survey sequence.//4.8e-29:175:94//AQ044812
- 30 F-MAMMA1000501//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//5.7e-45:334:82//AL022336
- F-MAMMA1000516//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATPSG1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.9e-43:529:69//Z92545
- 35 F-MAMMA1000522//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//2.0e-14:380:63//AL022576
- 40 F-MAMMA1000524//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//1.4e-22:420:66//AC006101
- F-MAMMA1000559//Human HepG2 3' region cDNA, clone hmd3f08.//5.4e-29:168:97//D16922
- F-MAMMA1000565//RPC111-61K6.TJ RPC111 Homo sapiens genomic clone R-61K6, genomic survey sequence.//1.7e-120:561:100//AQ194238
- 45 F-MAMMA1000567//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//3.1e-43:387:80//Z81370
- F-MAMMA1000576//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.2e-30:237:75//AC005104
- F-MAMMA1000583//RPC111-60M22.TJ RPC111 Homo sapiens genomic clone R-60M22, genomic survey sequence.//9.6e-102:487:99//AQ198091
- 50 F-MAMMA1000585//Homo sapiens clone UWGC:djs14 from 7p14-15, complete sequence.//5.2e-39:370:78//AC006195
- F-MAMMA1000594//Homo sapiens chromosome 19, cosmid R31646, complete sequence.//3.9e-43:328:83//AC005338
- 55 F-MAMMA1000597//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence.//1.5e-32:259:82//AC005839
- F-MAMMA1000605//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.4e-59:318:83//AL031297

F-MAMMA1000612//HS_2188_A2_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//4.8e-30:171:96//AQ116793
 F-MAMMA1000616//HS_3176_A1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3176 Col=11 Row=I, genomic survey sequence.//4.7e-28:287:79//AQ300310
 5 F-MAMMA1000621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 273F20, WORKING DRAFT SEQUENCE.//0.015:478:58//AL034371
 F-MAMMA1000623
 F-MAMMA1000625//DNA encoding Hepatitis C virus antigen.//0.93:196:61//E06898
 F-MAMMA1000643//Homo sapiens nephrocytin (NPHP1) mRNA, partial cds.//0.95:365:59//AF023674
 10 F-MAMMA1000664//HS_3096_B1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3096 Col=3 Row=F, genomic survey sequence.//2.7e-51:257:99//AQ145137
 F-MAMMA1000669//Homo sapiens chromosome 19, cosmid R26908, complete sequence.//2.0e-66:586:67//AC004785
 F-MAMMA1000670//HS_2243_B2_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2243 Col=16 Row=B, genomic survey sequence.//8.7e-05:94:80//AQ153650
 15 F-MAMMA1000672//Mus musculus clone OST8270, genomic survey sequence.//3.9e-64:471:81//AF046705
 F-MAMMA1000684//Suid herpesvirus 1 Rsp40 mRNA, partial cds.//1.2e-07:186:67//U27489
 F-MAMMA1000696//Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2; neurofibromatosis 1 (NF1) exons 28-49; ecotropic viral integration site 2B (EVI2B) exons 1-2; ecotropic viral integration site 2A (EVI2A) exons 1-2; adenylate kinase (AK3) exons 1-2.//3.0e-53:653:70//L05367
 20 F-MAMMA1000707//CIT-HSP-2302019.TR CIT-HSP Homo sapiens genomic clone 2302019, genomic survey sequence.//1.8e-08:131:77//AQ017947
 F-MAMMA1000713//Rattus norvegicus clonol polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.062:134:67//U00762
 25 F-MAMMA1000714//Chicken hsp90 gene for 90 kDa-heat shock protein 5'-end.//1.0:266:61//X15028
 F-MAMMA1000718//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence.//3.6e-05:289:60//B95401
 F-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//4.4e-184:842:98//AC005781
 30 F-MAMMA1000723//Homo sapiens clone DJ0892G19, complete sequence.//8.8e-05:430:60//AC004917
 F-MAMMA1000731//Drosophila melanogaster DNA sequence (P1-DS07049 (D133)), complete sequence.//3.8e-55:796:66//AC004274
 F-MAMMA1000732//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.6e-77:555:74//AF064859
 35 F-MAMMA1000733//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING DRAFT SEQUENCE.//0.98:479:58//AL031749
 F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//7.3e-168:802:98//AF100141
 F-MAMMA1000738//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-31:626:63//Z71408
 F-MAMMA1000744//Gorilla Alu-repetitive sequence in beta-globin gene cluster.//2.7e-54:410:82//X06123
 40 F-MAMMA1000746//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-10F4, complete sequence.//3.7e-109:779:83//AC004158
 F-MAMMA1000752//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.2e-20:444:63//AC005075
 F-MAMMA1000760//Homo sapiens clone RG015P03, complete sequence.//1.5e-44:403:79//AC005048
 45 F-MAMMA1000761//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.3e-22:159:81//AC004166
 F-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//1.3e-51:789:68//AC005703
 F-MAMMA1000776//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//5.7e-40:238:78//Z95116
 50 F-MAMMA1000778//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE.//7.6e-29:222:84//AL031118
 F-MAMMA1000782//Human 2,4-dienoyl-CoA reductase gene, exon 9.//0.90:137:62//U94987
 F-MAMMA1000798//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.00058:163:71//AC003656
 55 F-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//6.3e-151:714:99//

- AC005339
F-MAMMA1000824//Homo sapiens 12p13.3 BAC RPC111-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//4.2e-104:503:99//AC005912
- 5 F-MAMMA1000831//Homo sapiens clone UWGC:g1211a139, complete sequence.//0.76:302:58//AC005502
F-MAMMA1000839//Human BAC clone RG013L03 from 7q21, complete sequence.//1.9e-54:322:68//AC002456
F-MAMMA1000841//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//6.7e-140:647:92//AL023755
F-MAMMA1000842//, complete sequence.//0.0068:499:59//AC005817
F-MAMMA1000843//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.13:439:59//AC004710
- 10 F-MAMMA1000845//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//2.2e-05:208:64//AL034557
F-MAMMA1000851//Gallus domesticus filamin gene 5' region, partial cds.//0.86:193:63//U00146
F-MAMMA1000855//Human minisatellite region detected by myoglobin 33-repeat probe, clone lambda 33.10//0.081:229:62//M30549
F-MAMMA1000856//B.taurus microsatellite marker ETH8 (D6S3) DNA.//0.0024:253:60//Z22747
F-MAMMA1000859//Sequence 6 from Patent WO9722695.//2.3e-79:533:82//A63553
F-MAMMA1000862
F-MAMMA1000863//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//1.0e-28:439:64//AP000050
- 20 F-MAMMA1000865
F-MAMMA1000867//CIT-HSP-2385J8.TR.1 CIT-HSP Homo sapiens genomic clone 2385J8, genomic survey sequence.//0.00017:158:70//AQ240906
F-MAMMA1000875//Homo sapiens DNA sequence from PAC 232G24 on chromosome Xq27.1-q27.3. Contains two exons similar to MAGE gene family, EST, CA repeat, STS, complete sequence.//1.0:121:68//AL022152
- 25 F-MAMMA1000876//Homo sapiens clone HS19.6 Alu-Ya5 sequence.//8.4e-41:185:90//AF015152
F-MAMMA1000877//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//8.3e-57:522:75//AL022336
F-MAMMA1000880//Homo sapiens full-length insert cDNA clone ZD54A10.//5.2e-26:143:100//AF086327
F-MAMMA1000883//Human DNA sequence from clone 786D3 on chromosome 22q13.31-33 Contains GSS, complete sequence.//0.99:225:63//AL023801
F-MAMMA1000897//R.norvegicus mRNA for plasma protein.//4.8e-07:479:58//Y11283
F-MAMMA1000905//F26L5TRB IGF Arabidopsis thaliana genomic clone F26L5, genomic survey sequence.//0.94:115:66//B61433
- 35 F-MAMMA1000906//HS_3110_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=22 Row=B, genomic survey sequence.//2.5e-63:548:78//AQ182819
F-MAMMA1000908//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//5.2e-80:480:90//AL033397
- 40 F-MAMMA1000914//Plasmodium falciparum MAL3P8, complete sequence.//7.6e-09:596:58//AL034560
F-MAMMA1000921//CIT-HSP-2171D8.TR CIT-HSP Homo sapiens genomic clone 2171D8, genomic survey sequence.//6.6e-07:249:66//889575
F-MAMMA1000931//Homo sapiens clone DJ0892G19, complete sequence.//2.9e-43:415:66//AC004917
F-MAMMA1000940//HS-1056-A2-E02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=4 Row=I, genomic survey sequence.//6.1e-44:235:78//B47296
- 45 F-MAMMA1000941//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 complete genomic sequence, complete sequence.//9.4e-48:443:75//AC002299
F-MAMMA1000942//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.8e-14:175:76//AL031117
- 50 F-MAMMA1000943//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0082:684:56//AC005308
F-MAMMA1000956//Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.//3.3e-30:530:67//AC004643
F-MAMMA1000957//HS_3039_A2_C08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//1.3e-72:390:94//AQ155121
- 55 F-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-58:318:86//AC006001
F-MAMMA1000968//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the

- TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.4e-18:396:65//AL022394
- 5 F-MAMMA1000975//Human DNA sequence from clone 34417 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence.//1.4e-79:690:77//AL024458
- F-MAMMA1000979//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//0.089:214:66//AC004991
- 10 F-MAMMA1000987//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.1e-58:458:82//AC000114
- F-MAMMA1000998//Human DNA sequence from PAC 997K18 on chromosome 20p12. Contains ESTs and CA repeat.//1.1e-05:439:62//AL021406
- F-MAMMA1001003//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochooidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.24:166:68//AL022401
- 15 F-MAMMA1001008//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//1.6e-103:139:99//AJ011929
- F-MAMMA1001021//Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds.//6.5e-48:465:76//AF070567
- 20 F-MAMMA1001024//CITBI-E1-2501L21.TF.1 CITBI-E1 Homo sapiens genomic clone 2501L21, genomic survey sequence.//1.0:175:62//AQ241701
- F-MAMMA1001030//Homo sapiens G protein-coupled receptor LGR5 (LGR5) mRNA, complete cds.//1.1e-30:753:6//1AF061444
- 25 F-MAMMA1001035//Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complete sequence.//7.9e-24:256:76//AC002990
- F-MAMMA1001038//CIT-HSP-2284N21.TF CIT-HSP Homo sapiens genomic clone 2284N21, genomic survey sequence.//0.96:78:75//AQ000903
- F-MAMMA1001041//chicken mRNA for alpha-actinin, complete cds.//2.8e-09:355:63//D26597
- 30 F-MAMMA1001050//Homo sapiens BAC clone RG060P12 from 7q21, complete sequence.//2.6e-40:378:76//AC002457
- F-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//4.8e-97:661:83//L25125
- F-MAMMA1001067//Homo sapiens genomic intron breakpoint sequence of MLL rearrangement, 285 bp.//2.8e-18:110:100//AJ000169
- 35 F-MAMMA1001073//HS_3046_A2_G08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=16 Row=M, genomic survey sequence.//1.0:142:68//AQ098420
- F-MAMMA1001074//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//1.2e-23:386:70//AL031733
- 40 F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence.//1.1e-27:559:65//L09749
- F-MAMMA1001078//Homo sapiens chromosome 17, clone hRPK:346_K_10, complete sequence.//2.0e-22:334:69//AC006120
- F-MAMMA1001080//Human immunoglobulin heavy chain variable region (VH III family) from IgM rheumatoid factor.//6.4e-58:327:92//L29155
- 45 F-MAMMA1001082//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//3.8e-87:695:77//AC004087
- F-MAMMA1001091//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//7.0e-05:594:60//AC005256
- F-MAMMA1001092//Human DNA sequence from PAC 49C23 on chromosome X contains malate dehydrogenase pseudogene and STS.//1.6e-91:174:87//Z93019
- 50 F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds.//6.4e-23:507:66//AF016045
- F-MAMMA1001110//Homo sapiens chromosome 19, cosmid F16815, complete sequence.//0.77:316:60//AC004637
- 55 F-MAMMA1001126//Homo sapiens PAC 50H2 in the CUTL1 locus, complete sequence.//3.3e-21:237:73//AF047825
- F-MAMMA1001133//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//0.97:202:63//Z95116

EP 1 074 617 A2

F-MAMMA1001139//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt]//1.6e-84:406:82//S70011
F-MAMMA1001143//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence//1.3e-14:182:76//AL022339
5 F-MAMMA1001145//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS//5.2e-87:714:78//Z71187
F-MAMMA1001154//CIT-HSP-2341D13.TF CIT-HSP Homo sapiens genomic clone 2341D13 genomic survey sequence//0.00051:249:61//AQ055735
F-MAMMA1001161//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence//2.2e-30:410:70//AC004518
10 F-MAMMA1001162//Homo sapiens full-length insert cDNA clone ZA79C01//2.4e-13:87:100//AF086123
F-MAMMA1001181//Mus musculus C2C12 unknown mRNA, partial cds//9.3e-15:432:60//U31629
F-MAMMA1001186//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence//6.8e-57:670:72//AC005696
F-MAMMA1001191
15 F-MAMMA1001198//Mus musculus eps15R mRNA, complete cds//1.5e-117:759:84//U29156
F-MAMMA1001202
F-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces//1.5e-161:764:98//AC005412
F-MAMMA1001206//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence//5.1e-30:535:65//
20 AC004099
F-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence//8.4e-182:860:98//AC005393
F-MAMMA1001220//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence//7.7e-58:690:70//AC004875
25 F-MAMMA1001222//Mouse loricrin mRNA, complete cds//2.7e-07:624:58//M34398
F-MAMMA1001243//Homo sapiens chromosome 17, clone hRPK.192_H_23, complete sequence//0.91:177:66//AC005726
F-MAMMA1001244
F-MAMMA1001249//Human 28S ribosomal RNA psuedogenes and alu repeat region sequence//6.7e-09:502:58//
30 U67616
F-MAMMA1001256//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence//5.0e-37:342:80//Z99495
F-MAMMA1001259
F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//8.7e-40:659:64//AB014561
35 F-MAMMA1001268//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence//4.9e-43:265:81//AC004453
F-MAMMA1001271//Salmo salar DNA for a cryptic repeat//2.6e-06:311:63//AJ012206
F-MAMMA1001274//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces//6.6e-70:327:83//AC004840
40 F-MAMMA1001280//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence//1.0e-05:276:66//AC003035
F-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and
45 GSSs, complete sequence//3.6e-98:199:98//AL022314
F-MAMMA1001296//RPCI11-38B4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38B4, genomic survey sequence//4.7e-33:292:71//AQ030084
F-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence//1.6e-182:860:98//AC005703
50 F-MAMMA1001305//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence//1.9e-70:163:97//Z93244
F-MAMMA1001322//Human DNA sequence from clone 774I24 on chromosome 1q24.1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and
55 GSS, complete sequence//2.6e-19:379:68//AL031290
F-MAMMA1001324//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 197L1, WORKING DRAFT SEQUENCE//4.5e-131:751:90//AL031390
F-MAMMA1001330

F-MAMMA1001341//*Sus scrofa* //1.6e-36:420:73//Z46906
 F-MAMMA1001343//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORK-
 ING DRAFT SEQUENCE //1.1e-05:818:58//AL031744
 F-MAMMA1001346
 5 F-MAMMA1001383//*Homo sapiens*, WORKING DRAFT SEQUENCE, 52 unordered pieces //2.0e-44:505:74//
 AC004086
 F-MAMMA1001388//Human IGF binding protein complex acid-labile subunit a mRNA, complete cds //1.5e-07:415:
 58//M86826
 F-MAMMA1001397//Human DNA sequence from clone 462D8 on chromosome 22q11.21-12.1 Contains EST, STS
 10 and GSS, complete sequence //1.6e-23 :209:75//AL022332
 F-MAMMA1001408//HS_3242_A1_H11_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* ge-
 nomic clone Plate=3242 Col=21 Row=O, genomic survey sequence //2.7e-07:181:69//AQ207300
 F-MAMMA1001411//*Homo sapiens* autosomal dominant polycystic kidney disease type II protein (PKD2) gene,
 exon 14 //0.98:120:68//AF004872
 15 F-MAMMA1001419//HS_2053_B1_F12_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* ge-
 nomic clone Plate=2053 Col=23 Row=L, genomic survey sequence //1.9e-75 :424:93//AQ244585
 F-MAMMA1001420//*Homo sapiens* chromosome 4 clone B203C23 map 4q25, complete sequence //2.4e-09:199:
 70//AC004049
 F-MAMMA1001435//*Homo sapiens* chromosome 16p11.2 BAC clone CIT987SK-2011O4, WORKING DRAFT SE-
 20 QUENCE, 4 unordered pieces //5.1e-42:558:69//AC004529 F-MAMMA1001442//*Plasmodium falciparum* chromo-
 some 2, section 37 of 73 of the complete sequence //0.0019:516:56//AE001400
 F-MAMMA1001446//*Homo sapiens* Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete
 sequence //3.6e-42:486:70//AC003684
 F-MAMMA1001452//RPC111-48022.TJ RPC111 *Homo sapiens* genomic clone R-48O22, genomic survey se-
 25 quence //5.3e-87:423:98//AQ199294
 F-MAMMA1001465//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 414D7, WORKING
 DRAFT SEQUENCE //0.00038:114:75//AL033543
 F-MAMMA1001476//*Mus musculus* uridine kinase mRNA, partial cds //4.1e-99:604:87//L31783
 F-MAMMA1001487//*Homo sapiens* clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces //
 30 1.0e-13:158:77//AC005486
 F-MAMMA1001501//Human mRNA for calcium activated neutral protease large subunit (muCANP, calpain, EC
 3.4.22.17) //9.6e-52:438:81//X04366
 F-MAMMA1001502//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B7, WORKING
 DRAFT SEQUENCE //3.7e-152:720:99//AL031714
 35 F-MAMMA1001510//Human PAC clone DJ438O4 from 22q12.1-qter, complete sequence //1.1e-05:371:61//
 AC002378
 F-MAMMA1001522
 F-MAMMA1001547
 F-MAMMA1001551//*Homo sapiens* mRNA for KIAA0462 protein, partial cds //2.3e-128:614:98//AB007931
 40 F-MAMMA1001575//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence //0.97:154:68//
 AF001548
 F-MAMMA1001576//Human gamma-tubulin mRNA, complete cds //1.8e-95:529:91//M61764
 F-MAMMA1001590//Human DNA sequence from clone 125H2 on chromosome 22q11-12 Contains part of myosin
 heavy chain gene, EST, CA repeat, STS, GSS, complete sequence //1.8e-07:104:84//Z98949
 45 F-MAMMA1001600//HS_3022_A2_H01_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* ge-
 nomic clone Plate=3022 Col=2 Row=O, genomic survey sequence //1.6e-66:405:90//AQ163791
 F-MAMMA1001604//Human DNA sequence from clone 1114G22 on chromosome 1q24-25 Contains EST, CA re-
 peat, Ninenin like sequence, complete sequence //0.00043:715:58//AL008626
 F-MAMMA1001606//jd114 Trypanosome Shotgun M13 genomic *Trypanosoma brucei brucei* genomic clone 2G6,
 50 genomic survey sequence //0.19:266:62//B13685
 F-MAMMA1001620//*Homo sapiens* monocyte/neutrophil elastase inhibitor gene, complete cds //9.7e-54:442:69//
 AF053630
 F-MAMMA1001627//*X.borealis* ribosomal spacer DNA, with a DNaseI-hypersensitive site //0.14:221:62//M29833
 F-MAMMA1001630//*Homo sapiens* chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2
 55 ordered pieces //2.0e-47:611:71//AC005412
 F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds //1.1e-42:611:67//U57796
 F-MAMMA1001635//Human BAC clone RG072E11 from 7q21-7q22, complete sequence //4.0e-35:407:70//
 AC000118

- F-MAMMA1001649//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence//0.44:245:63//AL022577
- 5 F-MAMMA1001654//Mouse transcriptional control element//0.0025:189:63//M17284
- F-MAMMA1001663//CIT-HSP-2165E16.TR CIT-HSP Homo sapiens genomic clone 2165E16, genomic survey sequence//9.7e-05:146:66//B95491
- F-MAMMA1001670//HS_3136_A1_G06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=11 Row=M, genomic survey sequence//3.1e-28:237:85//AQ148779
- 10 F-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence//3.3e-181:863:98//AC005614
- F-MAMMA1001679//HS_3054_A1_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=O, genomic survey sequence//1.0:89:70//AQ106118
- F-MAMMA1001683//Spermatogenesis similis mRNA for 90 kD basal apparatus-protein//8.3e-07:480:62//AJ224970
- 15 F-MAMMA1001686//HS_3219_B1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=5 Row=B, genomic survey sequence//0.00072:180:65//AQ180345
- F-MAMMA1001692//HS_3047_B1_B10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=D, genomic survey sequence//2.5e-94:459:98//AQ134228
- 20 F-MAMMA1001711//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces//1.2e-42:316:82//AC004845
- F-MAMMA1001715//CIT-HSP-2347A14.TF CIT-HSP Homo sapiens genomic clone 2347A14, genomic survey sequence//1.1e-60:413:87//AQ059125
- F-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds//1.8e-133:646:97//AF095687
- 25 F-MAMMA1001735//chicken brain tubulin beta chain mrna//3.5e-110:740:84//J00913
- F-MAMMA1001740//Human DNA sequence from PAC 136017 on chromosome X contains ESTs and STS//0.98:416:57//Z72001
- F-MAMMA1001743//Homo sapiens clone DJ0981O07, complete sequence//3.2e-16:194:75//AC006017
- 30 F-MAMMA1001744//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence//0.0036:181:66//AL030998
- F-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence//1.2e-60:822:68//AF070718
- 35 F-MAMMA1001751//Human potassium channel KCNO1 mRNA, complete cds//1.2e-35:583:65//U90065
- F-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds//8.4e-102:627:87//AF041338
- F-MAMMA1001757//HS_2058_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=8 Row=F, genomic survey sequence//1.7e-24:173:88//AQ243865
- 40 F-MAMMA1001760//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence//6.6e-76:349:87//AL022722
- 45 F-MAMMA1001764//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds//0.23:633:57//M97514
- F-MAMMA1001768//Bovine herpesvirus 1 complete genome//2.3e-11:547:60//AJ004801
- F-MAMMA1001769//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence//1.1e-76:509:78//AC004801
- 50 F-MAMMA1001771//M.musculus mRNA for semaphorin B//2.7e-106:744:82//X85991
- F-MAMMA1001783//Human PAC clone 127H14 from 12q, complete sequence//6.0e-20:228:75//AC002563
- F-MAMMA1001785
- 55 F-MAMMA1001788//Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene. Contains ESTs, STSs and GSSs, complete sequence//5.0e-05:152:74//Z99129
- F-MAMMA1001790//Homo sapiens chromosome 12p13.3 clone RPC13-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces//4.5e-53:318:80//AC005845

- F-MAMMA1001806//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//1.0:131:67//AC004262
- F-MAMMA1001812//Human Chromosome X clone bWXD187, complete sequence.//3.0e-34:257:83//AC004383
- 5 F-MAMMA1001815//Homo sapiens PAC clone DJ0850G01 from 7q21.2-q22, complete sequence.//5.2e-61:516:79//AC004128
- F-MAMMA1001817//Homo sapiens 12q24 PAC RPCI1-261P5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.1e-32:295:78//AC004031
- F-MAMMA1001818//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1.333303.//0.71:179:67//AJ011930
- 10 F-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//3.0e-91:726:79//Y13148
- F-MAMMA1001824//HS_3108_A1_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=23 Row=M, genomic survey sequence.//3.4e-05:119:74//AQ107508
- F-MAMMA1001836//Homo sapiens chromosome 18, clone hRPK.537_E_1, complete sequence.//3.4e-45:312:85//AC006211
- 15 F-MAMMA1001837//Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA, complete cds.//4.5e-51:480:75//AF052042
- F-MAMMA1001848//CITBI-E1-2516P17.TF CITBI-E1 Homo sapiens genomic clone 2516P17, genomic survey sequence.//1.0e-100:486:98//AQ279620
- F-MAMMA1001851//Human DNA from overlapping chromosome 19-specific cosmids R30072 and R28588, genomic sequence, complete sequence.//5.1e-07:197:67//AC002390
- 20 F-MAMMA1001854
- F-MAMMA1001858//RPCI11-11L22.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11L22, genomic survey sequence.//0.091:161:65//B75631
- F-MAMMA1001864//Human PAC clone DJ0205E24 from Xq23, complete sequence.//2.6e-09:397:61//AC003013
- 25 F-MAMMA1001868//HS_2196_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=24 Row=B, genomic survey sequence.//5.8e-13:86:100//AQ032455
- F-MAMMA1001874//H.sapiens CpG island DNA genomic MseI fragment, clone 63h5, reverse read cpg63h5.rta.//1.0:127:63//Z62129
- F-MAMMA1001878//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//1.7e-19:372:67//Z94802
- 30 F-MAMMA1001880//RPCI11-90K3.TJ RPCI11 Homo sapiens genomic clone R-90K3, genomic survey sequence.//6.6e-11:362:62//AQ283465
- F-MAMMA1001890//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//1.8e-45:317:86//AL021707
- 35 F-MAMMA1001907//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//2.7e-23:255:77//Z82207
- F-MAMMA1001908//HS_2225_A1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2225 Col=5 Row=A, genomic survey sequence.//5.4e-08:264:62//AQ301597
- F-MAMMA1001931//HS_3049_B2_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=18 Row=H, genomic survey sequence.//1.7e-47:295:90//AQ100157
- 40 F-MAMMA1001956//H.sapiens DNA sequence.//0.056:233:66//Z22493
- F-MAMMA1001963//Homo sapiens adenylosuccinate lyase gene, complete cds.//0.99:173:68//AF106656
- F-MAMMA1001969//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//5.3e-63:479:78//Z73986
- 45 F-MAMMA1001970//Homo Sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.4e-126:699:93//AC003071
- F-MAMMA1001992//HS_3078_A1_A09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=17 Row=A, genomic survey sequence.//3.3e-08:257:65//AQ143646
- F-MAMMA1002009//Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.//1.5e-07:244:62//AC005224
- 50 F-MAMMA1002011//HS_3252_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//1.3e-07:170:69//AQ304711
- F-MAMMA1002032//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//2.1e-34:315:79//AC004803
- 55 F-MAMMA1002033//HS_3023_A2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=8 Row=M, genomic survey sequence.//4.3e-69:366:94//AQ105493
- F-MAMMA1002041//Genomic sequence from Human 9q34, complete sequence.//5.3e-85:439:82//AC001227
- F-MAMMA1002042//Homo sapiens chromosome 3, clone hRPK.165_I_16, complete sequence.//1.4e-20:314:70//

- AC005669
F-MAMMA1002047//Homo sapiens 12p13.3 BAC RPCII1-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//6.8e-14:526:62//AC005906
- 5 F-MAMMA1002056//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.1e-47:648:71//AL030996
- 10 F-MAMMA1002058//Homo sapiens PAC clone DJ0732C22 from 7p11.2-p13, complete sequence.//2.4e-19:256:74//AC004869
- F-MAMMA1002068//Homo sapiens, clone hRPK.2_A_1, complete sequence.//5.4e-41:407:78//AC006197
- F-MAMMA1002078//Human DNA sequence from PAC 106120 on chromosome 22q12 Contains ESTs and STS, complete sequence.//0.021:333:64//Z81313
- F-MAMMA1002082
- 15 F-MAMMA1002084//Caenorhabditis elegans cosmid F28C12, complete sequence.//0.032:469:58//Z93380
- F-MAMMA1002093//HS_3050_B1_F06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=11 Row=L, genomic survey sequence.//1.0:77:71//AQ105997
- F-MAMMA1002108//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//8.3e-10:464:60//AF017308
- 20 F-MAMMA1002118
- F-MAMMA1002125//Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.//1.0e-35:619:68//AC003962
- F-MAMMA1002132//RPCI11-78F11.TJ RPCI11 Homo sapiens genomic clone R-78F11, genomic survey sequence.//1.0e-90:357:97//AQ286460
- 25 F-MAMMA1002140//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-45:583:64//AC004216
- F-MAMMA1002143//Human serum constituent protein (MSE55) mRNA, complete cds.//6.0e-11:192:70//M88338
- F-MAMMA1002145//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102D24, WORKING DRAFT SEQUENCE.//0.0028:570:59//AL021391
- 30 F-MAMMA1002153//HS_3005_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=7 Row=G, genomic survey sequence.//4.9e-41:213:99//AQ132213
- F-MAMMA1002155//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462O23, WORKING DRAFT SEQUENCE.//1.2e-45:303:78//AL031431
- F-MAMMA1002156
- 35 F-MAMMA1002158//CITBI-E1-2508P18.TR CITBI-E1 Homo sapiens genomic clone 2508P18, genomic survey sequence.//7.1e-42:255:92//AQ266165
- F-MAMMA1002170//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//2.0e-81:604:81//AC004448
- F-MAMMA1002174//Homo sapiens clone UWGC:y67c126 from 6p21, complete sequence.//3.2e-43:333:83//AC004212
- 40 F-MAMMA1002198//H.sapiens thiol-specific antioxidant protein mRNA.//1.0e-34:121:98//Z22548
- F-MAMMA1002209//HS_2197_B1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2197 Col=13 Row=J, genomic survey sequence.//9.6e-18:163:84//AQ210058
- F-MAMMA1002215//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//6.3e-08:435:60//AF017308
- 45 F-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.8e-124:752:87//AF032667
- F-MAMMA1002230//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.67:356:59//AC004710
- F-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//9.3e-140:836:87//U38253
- 50 F-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//1.4e-145:691:98//AC005666
- F-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//6.0e-138:660:98//AC005600
- 55 F-MAMMA1002267//Homo sapiens chromosome 2, P1 clone 777H5 (LBNL H27), complete sequence.//0.066:333:60//AC003676
- F-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//1.1e-39:404:74//AF068748
- F-MAMMA1002269//HS_3163_B1_D03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=3163 Col=5 Row=H, genomic survey sequence.//1.0:150:63//AQ171576
 F-MAMMA1002282//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.5e-22:315:67//AC003108
 F-MAMMA1002292//B.garinii (strain Tls1) p83/100 gene (partial).//0.73:200:64//X81533
 5 F-MAMMA1002293//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//1.6e-56:408:75//AC006023
 F-MAMMA1002294//Sequence 2 from Patent WO9516779.//1.8e-06:401:62//A45258
 F-MAMMA1002297
 F-MAMMA1002298//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.0056:525:61//AC004221
 10 F-MAMMA1002299//CIT-HSP-2345B2.TR CIT-HSP Homo sapiens genomic clone 2345B2, genomic survey sequence.//1.2e-90:446:98//AQ053994
 F-MAMMA1002308//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//1.3e-35:329:78//AL031680
 15 F-MAMMA1002310//Human gastric (H⁺ K⁺)-ATPase gene, complete cds.//0.0060:301:60//J05451
 F-MAMMA1002311//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.6e-50:327:69//AC004737
 F-MAMMA1002312//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and STS.//1.3e-09:741:58//Z86064
 20 F-MAMMA1002317
 F-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//1.9e-158:746:99//AC005756
 F-MAMMA1002322//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//5.3e-52:617:70//AC004796
 25 F-MAMMA1002329//Homo sapiens RaP2 interacting protein 8 (RPIP8) mRNA, complete cds.//0.22:143:67//U93871
 F-MAMMA1002332//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE.//1.6e-31:287:74//AL034402
 F-MAMMA1002333//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//2.5e-09:674:59//AL022022
 30 F-MAMMA1002339//Homo sapiens chromosome 21q22.3, cosmid clone Q4H9 complete sequence bases 1.41604.//2.1e-57:522:77//AJ011932
 F-MAMMA1002347//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.0e-14:258:69//AC004129
 35 F-MAMMA1002351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1059H15, WORKING DRAFT SEQUENCE.//7.8e-132:723:91//AL022100
 F-MAMMA1002352//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 128O3, WORKING DRAFT SEQUENCE.//5.8e-17:326:70//Z98742
 F-MAMMA1002353//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.1e-14:399:63//AC004825
 40 F-MAMMA1002355//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 109G6, WORKING DRAFT SEQUENCE.//3.7e-43:420:75//AL023879
 F-MAMMA1002356//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:534:59//AC004153
 45 F-MAMMA1002359//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.3e-18:156:75//AC005831
 F-MAMMA1002360//Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST.//4.9e-43:353:69//Z68885
 F-MAMMA1002361//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//1.8e-22:282:74//AL008719
 50 F-MAMMA1002362//Platemys spixii CR1-like LINE, partial sequence.//0.00058:83:79//D82938
 F-MAMMA1002380//CIT-HSP-2383K24.TF CIT-HSP Homo sapiens genomic clone 2383K24, genomic survey sequence.//4.4e-10:85:92//AQ196889
 F-MAMMA1002384//RPCI11-80J20.TV RPCI11 Homo sapiens genomic clone R-80J20, genomic survey sequence.//2.7e-56:286:98//AQ284134
 55 F-MAMMA1002385//CIT-HSP-2328G13.TF CIT-HSP Homo sapiens genomic clone 2328G13, genomic survey sequence.//5.5e-46:335:84//AQ043985
 F-MAMMA1002392//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-29:273:78//

AC004888
 F-MAMMA1002411//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//8.2e-09:287:63//AL023 875
 F-MAMMA1002413//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var1) gene, complete cds.//9.6e-08:730:57//L40608
 5 F-MAMMA1002417//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE.//4.1e-06:181:72//AL034402
 F-MAMMA1002427//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//1.3e-51:593:72//AC004604
 10 F-MAMMA1002428
 F-MAMMA1002434//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//7.3e-56:388:81//Z93023
 F-MAMMA1002446//CIT-HSP-2324O22.TR CIT-HSP Homo sapiens genomic clone 2324O22, genomic survey sequence.//2.3e-56:302:95//AQ027479
 15 F-MAMMA1002454//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.1e-54:190:94//AC005229
 F-MAMMA1002461//Rattus norvegicus calcium channel alpha-1 subunit gene, partial cds.//0.00045:457:60//U14005
 F-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//9.7e-33:709:60//U10556
 20 F-MAMMA1002475//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.092:506:58//AC004671
 F-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2-unordered pieces.//0.025:100:76//AC005077
 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.9e-118:560:98//AF055460
 25 F-MAMMA1002494//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//1.5e-22:297:73//AC005913
 F-MAMMA1002498//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//7.2e-10:330:64//AC002477
 F-MAMMA1002524//Homo sapiens huntingtin gene, partial exon.//0.0080:124:72//L49359
 30 F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.4e-160:775:97//AF065214
 F-MAMMA1002545//Homo sapiens chromosome 17, clone hRPK.74_E_22 complete sequence.//1.9e-41:345:80//AC005696
 F-MAMMA1002554
 35 F-MAMMA1002556
 F-MAMMA1002566
 F-MAMMA1002571//CIT-HSP-2296N17.TR CIT-HSP Homo sapiens genomic clone 2296N17, genomic survey sequence.//1.7e-07:76:90//AQ006579
 F-MAMMA1002573//Homo sapiens DNA, trinucleotide repeats region, clone GAA C27.//2.7e-08:195:70//AB018507
 40 F-MAMMA1002585
 F-MAMMA1002590//Homo sapiens BAC clone GS250A16 from 7p21-p22, complete sequence.//2.1e-26:361:69//AC005019
 F-MAMMA1002597//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1103G7, WORKING DRAFT SEQUENCE.//1.3e-34:550:69//AL034548
 45 F-MAMMA1002598//H.sapiens mRNA for ribosomal protein L7.//1.1e-21:123:100//X57958
 F-MAMMA1002603//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//0.0018:358:61//AC005220
 F-MAMMA1002612//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//2.1e-13:336:63//AC004861
 50 F-MAMMA1002617//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.14:229:64//AC005486
 F-MAMMA1002618
 F-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.5e-71:319:85//AJ010598
 55 F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds.//1.5e-20:157:90//AF041449
 F-MAMMA1002623//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//8.3e-06:137:72//AE000660
 F-MAMMA1002625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1056L3, WORKING

EP 1 074 617 A2

DRAFT SEQUENCE //1.9e-171:819:98//AL031727
F-MAMMA1002629//Human BAC clone RG385F02 from 7p15, complete sequence //4.8e-85:478:78//AC003093
F-MAMMA1002636//Human POU domain factor (Brn-3a) gene, exon 2, complete cds //5.6e-09:499:62//U10063
F-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds //3.6e-115:785:82//AF055666
5 F-MAMMA1002646//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence //1.5e-45:291:90//
AC002038
F-MAMMA1002650//Homo sapiens candidate tumor suppressor HIC-1 (HIC-1) gene, complete cds //6.6e-06:661:
59//L41919
F-MAMMA1002655//HS_2003_A2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
10 nomic clone Plate=2003 Col=22 Row=A, genomic survey sequence //9.0e-15:198:74//AQ224233
F-MAMMA1002662
F-MAMMA1002665//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence //1.4e-37:235:84//
AC005029
F-MAMMA1002671//Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds //0.00027:272:64//U22398
15 F-MAMMA1002673
F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds //3.7e-161:752:99//D86987
F-MAMMA1002685//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 39417, WORKING
DRAFT SEQUENCE //6.2e-45:510:70//AL023585
F-MAMMA1002698//HS_3024_B1_C06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
20 nomic clone Plate=3024 Col=11 Row=F, genomic survey sequence //1.7e-10:155:75//AQ072214
F-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds //5.9e-75:509:83//
AF018261
F-MAMMA1002701//Homo sapiens gene for AF-6, complete cds //1.2e-159:749:99//AB011399
F-MAMMA1002708//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of
25 the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence //3.0e-57:347:79//AL031053
F-MAMMA1002711//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence //3.4e-31:484:69//
AC005030
F-MAMMA1002721//CIT-HSP-2350M5.TR CIT-HSP Homo sapiens genomic clone 2350M5, genomic survey se-
quence //1.4e-06:265:63//AQ061245
30 F-MAMMA1002727//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVP2
(Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene.
Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence //0.18:386:58//AL023584
F-MAMMA1002728//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-
aminolevulinic synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/
35 fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS //3.2e-05:362:63//Z83821
F-MAMMA1002744//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence //0.00010:
535:58//AE001368
F-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence //1.2e-182:880:
97//AC005856
40 F-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human
PAC Library) complete sequence //2.7e-175:829:98//AC006055
F-MAMMA1002754//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered
pieces //3.1e-31:372:75//AC004676
F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds //3.3e-26:151:98//AB007902
45 F-MAMMA1002764//Human Chromosome 11 Cosmid cSRL166a1, complete sequence //5.2e-49:355:81//U73636
F-MAMMA1002765//RPCI11-20A22.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20A22, genomic survey
sequence //6.7e-13:155:76//B92153
F-MAMMA1002769//CIT-HSP-2323G1.TF CIT-HSP Homo sapiens genomic clone 2323G1, genomic survey se-
quence //9.7e-21:151:90//AQ028244
50 F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene,
complete cds //5.6e-105:179:99//U07561
F-MAMMA1002780//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-08, com-
plete sequence //0.071:277:58//Z98546
F-MAMMA1002782//HS_3213_B2_B08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
55 nomic clone Plate=3213 Col=16 Row=D, genomic survey sequence //0.00018:219:63//AQ175845
F-MAMMA1002796
F-MAMMA1002807//Human Chromosome X PAC RPCI1-290C9 from the Pieter de Jong Human PAC library; com-
plete sequence //6.9e-22:332:69//AC002404

EP 1 074 617 A2

F-MAMMA1002820//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence//5.9e-11:483:62//AC003035
F-MAMMA1002830//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence//1.0e-64:320:83//AC002553
5 F-MAMMA1002833//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence//2.8e-47:413:80//AC004875
F-MAMMA1002835
F-MAMMA1002838//A-916H10.TP CIT978SK Homo sapiens genomic clone A-916H10, genomic survey sequence//1.1e-39:164:83//B14462
10 F-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds//1.9e-62:373:81//U58883
F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.7e-135:635:99//AB018353
F-MAMMA1002844//F1707-T7 IGF Arabidopsis thaliana genomic clone F1707, genomic survey sequence//6.7e-17:383:66//B11616
F-MAMMA1002858
15 F-MAMMA1002868//RPCI11-54F9.TJ RPCI11 Homo sapiens genomic clone R-54F9, genomic survey sequence//8.3e-81:392:99//AQ081566
F-MAMMA1002869//Sequence 1 from patent US 5552529//2.2e-86:696:78//I25863
F-MAMMA1002871//Lupinus angustifolius nodulin-45 gene, complete cds//0.029:370:59//L12388
F-MAMMA1002880//RPCI11-23M23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-23M23, genomic survey sequence//1.8e-20:271:74//B86518
20 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds//1.2e-28:680:61//D45027
F-MAMMA1002886//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 380A1, WORKING DRAFT SEQUENCE//0.00040:505:57//Z97653
F-MAMMA1002887//HS_3238_B2_G08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=16 Row=N, genomic survey sequence//5.5e-79:401:97//AQ219814
25 F-MAMMA1002890//Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes//4.6e-35:136:73//AF109906
F-MAMMA1002892//Mouse Cosmid ma66a100 from 14D1-D2, complete sequence//5.7e-14:450:60//AC004096
30 F-MAMMA1002895//H.sapiens CpG island DNA genomic MseI fragment, clone 46b6, forward read cpg46b6.ft1a//3.7e-36:190:100//Z58616
F-MAMMA1002908//Panaeus monodon microsatellite locus Pmo27//1.1e-05:195:62//AF068828
F-MAMMA1002909//Human Chromosome 11 pac pDJ205d23, complete sequence//1.0e-13:457:61//AC002402
F-MAMMA1002930//Homo sapiens Xp22 BAC GSHB-512P14 (Genome Systems Human BAC library) complete sequence//0.25:260:62//AC004467
35 F-MAMMA1002937//H.sapiens ZNF74-1 mRNA//6.3e-13:577:59//X71623
F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//5.1e-193:910:98//AB014598
F-MAMMA1002941//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence//2.7e-23:174:77//AC004032
40 F-MAMMA1002947//Rhodobacter capsulatus strain SB1003, partial genome//1.3e-09:475:61//AF010496
F-MAMMA1002964//Human thiopurine methyltransferase (TPMT) gene, exon 5//0.0029:314:60//AF019366
F-MAMMA1002970//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence//4.0e-10:194:71//Z94056
45 F-MAMMA1002972//H.sapiens CpG island DNA genomic MseI fragment, clone 2g10, forward read cpg2g10.ft1aa//0.38:156:66//Z55272
F-MAMMA1002973//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence//2.9e-41:234:79//AC005919
F-MAMMA1002982//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3//1.7e-05:322:63//AL022098
50 F-MAMMA1002987//CITBI-E1-2514J12.TR CITBI-E1 Homo sapiens genomic clone 2514J12, genomic survey sequence//0.0064:135:66//AQ275871
F-MAMMA1003003//cSRL-145D12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-145D12, genomic survey sequence//2.8e-31:201:89//B01998
55 F-MAMMA1003004//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y237C10, WORKING DRAFT SEQUENCE//1.6e-10:180:73//AL031601
F-MAMMA1003007//Homo sapiens (clone cosmid c11q-8D1) tetranucleotide repeat polymorphism at the D11S488 locus//3.5e-12:435:61//L04732

EP 1 074 617 A2

F-MAMMA1003011//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//2.3e-50:734:67//U79139
 F-MAMMA1003013//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.2e-86:341:79//
 AC003694
 F-MAMMA1003015//Homo sapiens Chromosome 16 BAC clone CIT987SK-591M7, complete sequence.//2.6e-
 13:443:61//AC003661
 5 F-MAMMA1003019//HS_3221_A1_A01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3221 Col=1 Row=A, genomic survey sequence.//2.8e-51:299:92//AQ184271
 F-MAMMA1003026
 F-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//
 10 0.0037:134:73//AC005214
 F-MAMMA1003035//RPCI11-11P4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11P4, genomic survey se-
 quence.//1.1e-07:66:100//B74936
 F-MAMMA1003039//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Li-
 brary) complete sequence.//2.1e-19:220:76//AC004671
 15 F-MAMMA1003040//Human DNA sequence from PAC 340N1 on chromosome 1p35-36.2. Contains ESTs, poly-
 morphic CA repeat, trna and endogenous retrovirus.//9.5e-91:469:78//Z98257
 F-MAMMA1003044//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS,
 complete sequence.//0.21:289:61//AL031321
 F-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//1.7e-
 20 139:663:98//AF077952
 F-MAMMA1003049
 F-MAMMA1003055//HS_3014_B2_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3014 Col=20 Row=L, genomic survey sequence.//4.2e-05:215:64//AQ164940
 F-MAMMA1003056//HS_3221_B2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 25 nomic clone Plate=3221 Col=24 Row=H, genomic survey sequence.//1.4e-16:206:74//AQ302772
 F-MAMMA1003057//M.domesticus MD6 mRNA.//8.5e-128:654:94//X54352
 F-MAMMA1003066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 273F20, WORKING
 DRAFT SEQUENCE.//1.0:142:71//AL034371
 F-MAMMA1003089//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.7e-42:
 30 373:78//AC004796
 F-MAMMA1003099//Homo sapiens beta-filamin mRNA, complete cds.//2.6e-42:288:88//AF042166
 F-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//1.6e-12:
 477:64//U72634
 F-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//3.4e-121:789:
 35 85//AF071316
 F-MAMMA1003127//R.norvegicus MYR1 mRNA for myosin I heavy chain.//9.4e-58:423:83//X68199
 F-MAMMA1003135//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.62:
 676:58//U67916
 F-MAMMA1003140
 40 F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//2.2e-80:397:97//Y15062
 F-MAMMA1003150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 598F2, WORKING
 DRAFT SEQUENCE.//7.3e-123:266:88//AL021579
 F-MAMMA1003166//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING
 DRAFT SEQUENCE.//1.6e-33:143:82//Z99716
 45 F-NT2RM1000001//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs,
 complete sequence.//0.50:216:61//Z95400
 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//4.8e-65:385:92//D31886
 F-NT2RM1000032
 F-NT2RM1000035//Cricetulus griseus SREBP cleavage activating protein (SCAP) mRNA, complete cds.//6.3e-
 50 135:565:84//U67060
 F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.1 e-106:542:95//AB014590
 F-NT2RM1000039//Mouse genetic suppressor element mRNA.//0.080:239:60//L27155
 F-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//8.4e-96:535:91//D87671
 F-NT2RM1000059//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 390E6, WORKING
 55 DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000062//Nephila clavipes dragline silk protein spidroin 1 gene, partial cds.//0.54:306:63//U37520
 F-NT2RM1000080//Sequence 2 from patent US 5763589.//1.5e-115:566:97//AR012692
 F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//1.8e-114:550:97//AB014561

F-NT2RM1000092//Homo sapiens chromosome 19, cosmid R26894, complete sequence//0.63:180:65//AC005594
 F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.027:126:70//AF007155
 F-NT2RM1000119//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING
 5 DRAFT SEQUENCE//0.022:644:58//Z97630
 F-NT2RM1000127//RPC111-44E5.TJ RPC111 Homo sapiens genomic clone R-44E5, genomic survey sequence//1.6e-45:254:94//AQ195884
 F-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete cds//5.5e-153:778:95//AB018335
 F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUF56 subunit mRNA, nuclear gene en-
 10 coding mitochondrial protein, complete cds//1.1e-90:448:97//AF044959
 F-NT2RM1000153//Human Nott linking clone 924A081D, genomic survey sequence//5.9e-07:66:96//U49890
 F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.025:126:70//AF007155
 F-NT2RM1000187//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey se-
 quence//1.1e-05:56:98//AQ261184
 15 F-NT2RM1000199//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds//1.6e-38:711:65//D64009
 F-NT2RM1000242
 F-NT2RM1000244//HS_2229_A1_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2229 Col=7 Row=E, genomic survey sequence//2.0e-13:95:95//AQ298474
 20 F-NT2RM1000252//Homo sapiens chromosome 17, clone hRPK.206_C_20, complete sequence//0.023:225:61//AC006070
 F-NT2RM1000256//Caenorhabditis elegans cosmid F22B3, complete sequence//8.5e-24:473:64//Z68336
 F-NT2RM1000257//Homo sapiens MAGOH mRNA, complete cds//6.4e-69:455:85//AF035940
 F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//6.5e-57:460:80//D50920
 25 F-NT2RM1000271
 F-NT2RM1000272
 F-NT2RM1000280//Bos gaurus vacuolar H-ATPase subunit D (VATD) mRNA, complete cds//6.7e-97:430:92//U11927
 F-NT2RM1000300//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING
 30 DRAFT SEQUENCE//2.1e-96:170:100//Z93097
 F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//8.1e-127:708:92//D63880
 F-NT2RM1000318//Homo sapiens mRNA for ribosomal protein L39, complete cds//5.7e-34:182:99//D79205
 F-NT2RM1000341//Homo sapiens full-length insert cDNA clone YP11F06//1.3e-100:504:97//AF085879
 F-NT2RM1000354//HS_2001_B1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 35 nomic clone Plate=2001 Col=11 Row=J, genomic survey sequence//1.6e-11:201:73//AQ218494
 F-NT2RM1000355//Mus musculus E25B protein mRNA, complete cds//1.8e-77:578:82//U76253
 F-NT2RM1000365//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces//9.4e-113:367:97//AC004821
 F-NT2RM1000377//H.sapiens mRNA for MAP kinase phosphatase 4//6.1e-14:362:62//Y08302
 40 F-NT2RM1000388//Azospirillum brasilense lateral flagellin (laf1) gene, complete cds//1.0:482:58//U26679
 F-NT2RM1000394//M.musculus mRNA for histone H3.3A//1.7e-94:549:89//Z85979
 F-NT2RM1000399
 F-NT2RM1000421//HS_2213_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2213 Col=1 Row=J, genomic survey sequence//3.6e-08:195:72//AQ032737
 45 F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//3.7e-84:418:97//AF084928
 F-NT2RM1000499//Human mRNA for KIAA0167 gene, complete cds//1.3e-35:525:69//D79989
 F-NT2RM1000539//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence//4.6e-73:533:83//AC004993
 50 F-NT2RM1000553
 F-NT2RM1000555//Homo sapiens clone 24514 unknown mRNA//2.3e-110:555:97//AF070542
 F-NT2RM1000563//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces//1.3e-123:477:100//AC004873
 F-NT2RM1000623//HS_2213_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 55 nomic clone Plate=2213 Col=1 Row=J, genomic survey sequence//8.2e-06:75:89//AQ032737
 F-NT2RM1000648//Halobium cutirubrum L11, L1, L10 and L12 equivalent ribosomal protein gene cluster//1.3e-06:414:61//X15078
 F-NT2RM1000661//Homo sapiens cap-binding protein 4EHP mRNA, complete cds//9.3e-54:275:97//AF047695

F-NT2RM1000666//HS_2016_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2016 Col=16 Row=P, genomic survey sequence.//5.7e-13:199:73//AQ227865
 F-NT2RM1000669//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four
 novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene
 5 SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic
 marker D6S1553, complete sequence.//2.7e-94:499:94//AL031133
 F-NT2RM1000672
 F-NT2RM1000691//Homo sapiens HRIHFB2060 mRNA, partial cds.//2.2e-119:582:98//AB015348
 F-NT2RM1000699//Caenorhabditis elegans cosmid Y41C4A, complete sequence.//0.95:284:61//AL032627
 10 F-NT2RM1000702//HS_3005_A1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.073:290:58//AQ089514
 F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase.//4.8e-65:435:85//AJ004832
 F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds.//8.0e-126:690:92//AB011139
 F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//2.5e-66:524:83//AF027208
 15 F-NT2RM1000746//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete
 sequence bases 1.333303.//0.92:395:58//AJ011930
 F-NT2RM1000770//Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds.//2.1e-70:
 407:92//L39210
 F-NT2RM1000772//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//
 20 6.6e-36:98:93//AC000380
 F-NT2RM1000780//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//9.3e-22:
 126:99//X52233
 F-NT2RM1000781//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING
 DRAFT SEQUENCE, 8 unordered pieces.//7.1e-09:540:59//AC004153
 25 F-NT2RM1000800//Mus musculus mRNA for B-IND1 protein.//4.0e-81:497:88//Z97207
 F-NT2RM1000802
 F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//3.7e-63:490:84//AF027208
 F-NT2RM1000826//Homo sapiens clone 24514 unknown mRNA.//7.2e-153:749:96//AF070542
 F-NT2RM1000829//HS_3047_A1_A05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 30 nomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.74:215:67//AQ099134
 F-NT2RM1000833//Canis familiaris sec61 homologue mRNA, complete cds.//5.1e-114:683:88//M96629
 F-NT2RM1000850//F.rubripes GSS sequence, clone 163A22aF11, genomic survey sequence.//1.1e-26:279:74//
 AL018762
 F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//9.3e-148:726:97//AJ010840
 35 F-NT2RM1000857//Rattus norvegicus gene for cytochrome P450/6 beta B, exon 2.//0.97:124:65//AB008378
 F-NT2RM1000867//H.sapiens DNA sequence surrounding NotI site, clone NRLA143D.//1.2e-31:172:98//K95834
 F-NT2RM1000874//Homo sapiens KE05 protein mRNA, complete cds.//2.8e-131:632:97//AF064605
 F-NT2RM1000882//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for fer-
 ritin heavy chain (FTH), complete sequence.//1.2e-98:214:99//AC004228
 40 F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//2.7e-156:762:97//
 AF082516
 F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds.//2.0e-17:310:67//AB014561
 F-NT2RM1000894//Mus musculus second largest subunit of RNA polymerase I (RPA2) mRNA, complete cds.//
 3.2e-95:469:83//U58280
 45 F-NT2RM1000898
 F-NT2RM1000905//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING
 DRAFT SEQUENCE.//1.8e-74:188:98//Z97630
 F-NT2RM1000924//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-
 148:601:98//AC004873
 50 F-NT2RM1000927//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//
 0.071:392:60//AC004846
 F-NT2RM1000962//H.sapiens CpG island DNA genomic MseI fragment, clone 140d1, forward read
 cpg140d1.ft1a.//4.1e-35:187:99//Z56803
 F-NT2RM1000978//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 or-
 55 dered pieces.//1.1e-23:266:77//AC005959
 F-NT2RM1001003//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//4.0e-160:760:98//U97067
 F-NT2RM1001008//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//1.7e-
 11:602:61//U52064

F-NT2RM1001043//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//3.9e-93:645:86//Z95125
 F-NT2RM1001044//S.pombe chromosome III cosmid c320.//0.90:128:66//AL022245
 F-NT2RM1001059//Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.//3.8e-53:261:80//AC005915
 5 F-NT2RM1001066//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.64:285:59//B94391
 F-NT2RM1001072//HS_3115_B1_D07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=13 Row=H, genomic survey sequence.//7.3e-23:140:95//AQ147905
 10 F-NT2RM1001074//Homo sapiens chromosome 19, cosmid F20489, complete sequence.//5.0e-50:186:98//AC005263
 F-NT2RM1001082//Sequence 1 from Patent WO9718303.//2.1e-144:736:95//A62731
 F-NT2RM1001085//CIT-HSP-2310F21.TR CIT-HSP Homo sapiens genomic clone 2310F21, genomic survey sequence.//8.8e-45:235:97//AQ020757
 15 F-NT2RM1001092//HS_3055_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.1e-89:471:95//AQ155489
 F-NT2RM1001102//Human HEM45 mRNA, complete cds.//1.2e-28:482:63//U88964
 F-NT2RM1001105//Homo sapiens hRED1 gene, exon 1 (5'UTR).//0.0014:349:61//Z95973
 F-NT2RM1001112//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//0.060:429:58//AC004678
 20 F-NT2RM1001115//Plasmodium falciparum merozoite surface protein 3 (MSP-3) gene, partial cds.//0.93:156:62//AF024624
 F-NT2RM1001139//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//1.2e-10:466:59//AC004755
 25 F-NT2RM2000006//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.//5.3e-150:724:98//AL031291
 F-NT2RM2000013//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.5e-58:749:69//X58826
 F-NT2RM2000030//Homo sapiens clone DJ0708P22, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.1e-97:270:77//AC004863
 30 F-NT2RM2000032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-25:172:76//AL034379
 F-NT2RM2000042//Human DNA sequence from cosmid U55E4, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//5.0e-05:325:65//Z73418
 35 F-NT2RM2000092//Homo sapiens (D8S321 locus) DNA sequence, tetranucleotide repeat polymorphism.//0.63:117:68//L12269
 F-NT2RM2000093//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//0.38:312:62//AF109905
 40 F-NT2RM2000101
 F-NT2RM2000124//Mouse cAMP-dependent protein kinase catalytic subunit mRNA, complete cds.//3.8e-58:297:97//M12303
 F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A2 (PDE9A) mRNA, complete cds.//3.8e-138:653:98//AF067224
 45 F-NT2RM2000192//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//2.2e-33:191:95//B93289
 F-NT2RM2000239//F.rubripes GSS sequence, clone 156P04aG12, genomic survey sequence.//8.9e-44:445:69//AL018549
 F-nnnnnnnnnnnnn//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds.//0.00020:380:61//AF075292
 50 F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds.//3.1e-128:615:98//AB011162
 F-NT2RM2000259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310O13, WORKING DRAFT SEQUENCE.//0.0013:305:63//AL031658
 F-NT2RM2000260//Mus musculus WW domain binding protein 15 mRNA, partial sequence.//3.0e-14:645:61//AF073934
 55 F-NT2RM2000287//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B172P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SE-

- QUENCE, 50 unordered pieces.//1.3e-11:96:86//AC003656
 F-NT2RM2000322//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//8.5e-115:233:97//AL031864
- 5 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//8.8e-175:805:99//AB011132
 F-NT2RM2000363//RPC111-90B10.TJ RPC111 Homo sapiens genomic clone R-90B10, genomic survey sequence.//6.7e-15:96:98//AQ285300
 F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//1.2e-94:599:86//U48251
- 10 F-NT2RM2000371//RPC111-57I4.TJ RPC111 Homo sapiens genomic clone R-57I4, genomic survey sequence.//1.1e-52:312:91//AQ083343
 F-NT2RM2000374//M. musculus nodal gene, a TGF-beta-like gene.//6.7e-31:196:91//X70514
 F-NT2RM2000395//Leishmania major chromosome 1, complete sequence.//0.99:345:58//AE001274
 F-NT2RM2000402//Arabidopsis thaliana BAC T19D16 genomic sequence.//2.1e-23:414:63//U95973
- 15 F-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//1.4e-131:439:88//AF030430
 F-NT2RM2000420//HS_3063_B2_F11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//3.2e-25:154:95//AQ103204
 F-NT2RM2000422//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//1.7e-128:782:86//L22022
 F-NT2RM2000452//HS_3009_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=10 Row=H, genomic survey sequence.//1.2e-16:122:90//AQ130794
- 20 F-NT2RM2000469//HS_2019_A1_G02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2019 Col=3 Row=M, genomic survey sequence.//9.6e-22:176:85//AQ229041
 F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds.//7.5e-15:386:63//AB018290
 F-NT2RM2000502
 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//5.1e-171:824:97//AF061243
 F-NT2RM2000522
 F-NT2RM2000540
 F-NT2RM2000556//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.9e-42:344:82//AC004466
- 30 F-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//2.8e-154:751:97//AF072132
 F-NT2RM2000567//Pseudomonas aeruginosa enoyl-CoA hydratase gene, partial cds; pilin biosynthetic protein (fimL) gene, complete cds; and unknown gene.//3.0e-06:664:58//AF083252
 F-NT2RM2000569//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//1.3e-15:348:67//AL031681
- 35 F-NT2RM2000577//RPC111-43G22.TJ RPC111 Homo sapiens genomic clone R-43G22, genomic survey sequence.//1.6e-14:155:80//AQ199391
 F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.4e-174:820:98//D86987
 F-NT2RM2000588//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-60:344:82//AC004466
- 40 F-NT2RM2000594//Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.//4.9e-118:761:85//AF068626
 F-NT2RM2000599//O.sativa osr40g3 gene.//0.30:585:56//Y08988
 F-NT2RM2000609
 F-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.8e-102:709:83//U35776
- 45 F-NT2RM2000623//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//3.4e-17:450:65//AC005952
 F-NT2RM2000624
 2.9e-06:231:64//Z82061
- 50 F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//6.3e-142:664:98//AB018272
 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//7.4e-138:664:98//AB014558
 F-NT2RM2000639//RPC111-69E5.TJ RPC111 Homo sapiens genomic clone R-69E5, genomic survey sequence.//3.7e-14:97:97//AQ267491
 F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-167:518:99//AB014576
- 55 F-NT2RM2000669
 F-NT2RM2000691//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.1e-106:748:82//AC002038
 F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds.//6.8e-49:748:64//D86984

F-NT2RM2000718//Homo sapiens HRIHB2436 mRNA, partial cds.//2.4e-124:594:98//AB015342
 F-NT2RM2000735//Human ZNF43 mRNA.//8.4e-111:756:82//X59244
 F-NT2RM2000740//Mus musculus lymphocyte specific helicase mRNA, complete cds.//1.3e-141:815:89//U25691
 F-NT2RM2000795//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 439F8, WORKING
 5 DRAFT SEQUENCE.//1.0e-78:723:76//AL021392
 F-NT2RM2000821//Rat mRNA for beta COP.//2.0e-150:879:88//X57228
 F-NT2RM2000837//Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.//1.1e-05:361:62//
 AC005017
 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinaše, complete cds.//8.7e-184:847:99//AB015046
 10 F-NT2RM2000952
 F-NT2RM2000984//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-
 RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//
 7.6e-41:239:76//AF109905
 F-NT2RM2001004//CIT-HSP Homo sapiens genomic clone 2333N18, genomic survey se-
 15 quence.//1.1e-11:298:66//AQ035862
 F-NT2RM2001035//Mus musculus mCAF1 protein mRNA, complete cds.//1.4e-120:627:91//U21855
 F-NT2RM2001065//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//6.8e-118:690:88//
 AF071314
 F-NT2RM2001100//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.3e-
 20 145:614:99//AC004873
 F-NT2RM2001105//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING
 DRAFT SEQUENCE.//2.7e-95:461:99//AL034380
 F-NT2RM2001131//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//7.2e-
 24:726:62//U52064
 25 F-NT2RM2001141
 F-NT2RM2001152//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the
 CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase com-
 ponent A 1, Choroideraemia protein, Tapetochooidal Dystrophy (TCD) protein). Contains ESTs and an STS, com-
 plete sequence.//0.98:300:62//AL022401
 30 F-NT2RM2001177//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//
 1.2e-147:741:96//AC005488
 F-NT2RM2001194//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial
 cds.//0.026:408:59//U66829
 F-NT2RM2001196//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-
 35 135:627:98//AC004987
 F-NT2RM2001201//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700
 F-NT2RM2001221//Chimpanzee (P.paniscus) involucrin, complete cds.//0.53:670:55//M26514
 F-NT2RM2001238//Rat glutaminase mRNA, complete cds.//3.4e-128:719:90//M65150
 F-NT2RM2001243
 40 F-NT2RM2001247//CITBI-E1-2521M18.TR CITBI-E1 Homo sapiens genomic clone 2521M18, genomic survey
 sequence.//0.0011:274:59//AQ276184
 F-NT2RM2001256//M.musculus mRNA for 200 kD protein.//2.3e-129:742:90//X80169
 F-NT2RM2001291//CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey se-
 quence.//4.6e-09:156:72//B57734
 45 F-NT2RM2001306//RPCI11-28I5.TP RPCI-11 Homo sapiens genomic clone RPCI-11-28I5, genomic survey se-
 quence.//0.069:234:64//B84850
 F-NT2RM2001312//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//1.1e-22:111:
 81//AC005919
 F-NT2RM2001319//Borrelia burgdorferi (section 4 of 70) of the complete genome.//0.99:340:58//AE001118
 50 F-NT2RM2001324//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 209H1, WORKING
 DRAFT SEQUENCE.//3.7e-44:340:85//Z84465
 F-NT2RM2001345//HS_3005_A1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.042:290:58//AQ089514
 F-NT2RM2001360//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-60:365:87//
 55 U56429
 F-NT2RM2001370//Homo sapiens PAC clone DJ0815D20 from 7p11-p13, complete sequence.//0.98:415:58//
 AC004899
 F-NT2RM2001393//Homo sapiens Chromosome 22q11.2 PAC Clone p_m11 In BCRL2-GGT Region, complete

EP 1 074 617 A2

sequence.//4.0e-54:394:75//AC004033
 F-NT2RM2001420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//2.8e-169:789:99//AL033520
 F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.1e-96:453:99//AJ007509
 5 F-NT2RM2001499//Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.//7.1e-91:601:83//AB000113
 F-NT2RM2001504//Homo sapiens chromosome 19, cosmid R30017, complete sequence.//0.81:200:69//AC005624
 F-NT2RM2001524//Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2.//3.8e-16:316:65//Z99708
 10 F-NT2RM2001544
 F-NT2RM2001547//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//3.3e-24:318:67//AL032657
 F-NT2RM2001575//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//2.1e-26:582:64//M34551
 F-NT2RM2001582//M.musculus red-1 gene.//1.4e-102:581:90//X92750
 15 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds.//7.0e-10:282:65//AB007902
 F-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//9.6e-131:736:90//AF032667
 F-NT2RM2001605//RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre-B cell leukemia, mRNA, 6455 nt].//2.3e-85:749:75//S66431
 F-NT2RM2001613//Rattus rattus sec61 homologue mRNA, complete cds.//8.6e-118:779:85//M96630
 20 F-NT2RM2001632//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//1.5e-50:561:71//AC004691
 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//9.2e-153:740:98//AB014518
 F-NT2RM2001637//F.rubripes GSS sequence, clone 155D22bD8, genomic survey sequence.//2.5e-13:224:64//Z91020
 25 F-NT2RM2001641//CIT-HSP-2347F23.TF CIT-HSP Homo sapiens genomic clone 2347F23, genomic survey sequence.//1.3e-67:340:98//AQ060913
 F-NT2RM2001648//Canis familiaris sec61 homologue mRNA, complete cds.//1.4e-110:459:89//M96629
 F-NT2RM2001652//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.2e-153:807:93//AF023451
 30 F-NT2RM2001659//nbxb0002cE07f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002J13f, genomic survey sequence.//1.0:485:56//AQ051653
 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//3.7e-172:802:99//AF044195
 F-NT2RM2001668
 35 F-NT2RM2001670//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.2e-18:279:70//AJ003147
 F-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein-3 mRNA; complete cds.//1.6e-137:683:94//U21157
 F-NT2RM2001675//RPC111-51J16.TJ RPC111 Homo sapiens genomic clone R-51J16, genomic survey sequence.//1.0:394:58//AQ053677
 40 F-NT2RM2001681//Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project).//0.87:220:61//AL021890
 F-NT2RM2001688//B.parapertussis bvg locus (transcription regulators of virulence factors) with bvgA and bvgS genes.//1.0:286:62//X52948
 45 F-NT2RM2001695//CIT-HSP-345H13.TVB CIT-HSP Homo sapiens genomic clone 345H13, genomic survey sequence.//3.2e-53:241:82//B59854
 F-NT2RM2001696//Mouse DNA with homology to EBV IR3 repeat, segment 2, clone Mu2.//1.2e-05:306:58//M10668
 F-NT2RM2001698//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//6.0e-06:548:59//AL021920
 50 F-NT2RM2001699//HS_3195_8B2_DO1_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3195 Col=2 Row=H, genomic survey sequence.//2.7e-07:322:61//AQ189056
 F-NT2RM2001700//Mycobacterium tuberculosis H37Rv complete genome; segment 109/162.//7.8e-05:354:58//Z95556
 55 F-NT2RM2001706//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//7.5e-42:335:81//AC004469
 F-NT2RM2001716

- F-NT2RM2001718//*Drosophila melanogaster* DNA sequence (P1 DS04106 (D172)), complete sequence.//4.2e-08:536:58//AC004290
- F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence.//1.4e-26:163:95//AF052123
- F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//6.2e-111:530:98//AB007931
- 5 F-NT2RM2001730//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//3.1e-102:248:95//AJ010598
- F-NT2RM2001743
- F-NT2RM2001753//*Caenorhabditis elegans* cosmid F45E6, complete sequence.//0.11:138:66//Z68117
- F-NT2RM2001760//*Canis familiaris* sec61 homologue mRNA, complete cds.//9.4e100:418:88//M96629
- F-NT2RM2001768//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
- 10 nomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993
- F-NT2RM2001771//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC301323), complete sequence.//1.3e-66:680:72//AC006116
- F-NT2RM2001782
- F-NT2RM2001784//Bovine herpesvirus type 1 (Cooper) DNA (30 kb).//0.027:384:60//Z48053
- 15 F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770
- F-NT2RM2001797//HS_3045_AT_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
- nomic clone Plate=3045 Col=1 Row=G, genomic survey sequence.//1.4e-74:381:97//AQ129456
- F-NT2RM2001800
- 20 F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.3e-178:827:99//AF044195
- F-NT2RM2001805//*Malus domestica* leucine-rich receptor-like protein kinase (LRPKm1) gene, 5' flanking region and 5' UTR.//1.0:290:58//AF053126
- F-NT2RM2001813//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey se-
- 25 quence.//3.3e-16:109:95//B89870
- F-NT2RM2001823//*Drosophila melanogaster* DNA sequence (P1 DS07049 (D133)), complete sequence.//5.8e-62:819:68//AC004274
- F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//3.6e-131:738:90//AF013759
- F-NT2RM2001840//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.1e-57:422:79//
- 30 AC002347
- F-NT2RM2001855//HS_3224_A1_H07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
- nomic clone Plate=3224 Col=13 Row=O, genomic survey sequence.//0.00012:68:91//AQ205285
- F-NT2RM2001867//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the
- 35 gene for a novel protein similar to *X. laevis* Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.068:102:70//AL031177
- F-NT2RM2001879//Human DNA sequence from cosmid cU72E5, between markers DXS366 and DXS87 on chro-
- 40 mosome X.//0.0029:500:59//Z68328
- F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//1.9e-187:866:97//AB014610
- F-NT2RM2001896//*S.cerevisiae* chromosome III complete DNA sequence.//8.6e-30:613:63//X59720
- F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.9e-176:859:97//AB007931
- F-NT2RM2001930//*M.musculus* mRNA for semaphorin G.//4.7e-117:730:85//X97818
- F-NT2RM2001935//Sequence 11 from Patent WO9610637.//1.0:356:60//A50028
- 45 F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence.//6.9e-138:653:98//AF091080
- F-NT2RM2001950//RPCI11-24L12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24L12, genomic survey sequence.//2.7e-19:188:81//B86700
- F-NT2RM2001982//*Arabidopsis thaliana* chromosome II BAC T24121 genomic sequence, complete sequence.//0.42:179:65//AC005825
- 50 F-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//3.8e-20:123:98//AF089816
- F-NT2RM2001989//Sequence 3 from patent US 5747317.//1.9e-167:786:98//AR004981
- F-NT2RM2001997//Human HepG2 partial cDNA, clone hmd1b08m5.//9.6e-25:160:95//D16955
- F-NT2RM2001998//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding
- 55 carbonyl reductase and carbonyl reductase 3 (complete cds).//0.88:380:60//AB003151
- F-NT2RM2002004//Human Chromosome X, complete sequence.//5.0e-88:831:77//AC002407
- F-NT2RM2002014
- F-NT2RM2002030//*Mus musculus* glutamine:fructose-6-phosphate amidotransferase mRNA, complete cds.//

1.5e-89:822:74//U00932
F-NT2RM2002049//Bovine elastin mRNA, partial cds.//8.8e-11:125:81//M26132
F-NT2RM2002055
5 F-NT2RM2002088//Mus musculus WW domain binding protein 17 mRNA, partial sequence.//1.4e-15:421:63//AF073936
F-NT2RM2002091//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//4.6e-160:771:98//AL034380
F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//7.7e-164:776:98//AJ010840
10 F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//2.4e-143:684:98//AF030435
F-NT2RM2002128//Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete cds.//7.0e-27:330:73//U13152
F-NT2RM2002142//Danio rerio gastrulation specific (G12) mRNA, complete cds.//6.3e-10:135:80//U27121
15 F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//4.2e-143:800:92//AF084928
F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds.//5.2e-164:787:97//AB007936
F-NT2RM2002580//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//7.4e-13:337:62//AC004423
20 F-NT2RM4000024//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.2e-62:801:70//X58826
F-NT2RM4000027//Caenorhabditis elegans cosmid F09E5.//0.36:336:60//U37429
F-NT2RM4000030//H.sapiens CpG island DNA genomic MseI fragment, clone 56h10, forward read cpg56h10.ft1a.//9.3e-22:127:100//Z55685
25 F-NT2RM4000046//Curcubita maxima 25S - 18S rDNA intergenic spacer.//4.1e-05:386:60//X13059
F-NT2RM4000061
F-NT2RM4000085//B.taurus mRNA for nuclear DNA helicase II.//1.9e-10:485:59//X82829
F-NT2RM4000086
F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds.//4.2e-23:345:69//AF060865
30 F-NT2RM4000139//R.norvegicus trg mRNA.//1.4e-56:708:69//X68101
F-NT2RM4000155//CIT-HSP-2282N15.TR CIT-HSP Homo sapiens genomic clone 2282N15, genomic survey sequence.//3.0e-09:88:90//AQ000070
F-NT2RM4000156//H.sapiens HPBR11-7 gene.//2.0e-21:586:60//X67336
35 F-NT2RM4000167//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.7e-143:810:90//D12646
F-NT2RM4000169//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0054:746:57//AC004157
F-NT2RM4000191//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//0.00018:468:60//AF051726
40 F-NT2RM4000197
F-NT2RM4000199//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//0.67:461:60//AL031667
F-NT2RM4000200
F-NT2RM4000202//H.sapiens CpG island DNA genomic MseI fragment, clone 34c2, forward read cpg34c2.ft1a.//1.7e-27:190:90//Z65361
45 F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//1.4e-182:856:98//AB018255
F-NT2RM4000215//S.cerevisiae MAK16 protein gene, complete cds, and LTE1 protein gene, 3' end.//3.1e-31:731:62//J03852
F-NT2RM4000229//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//4.6e-102:233:94//AC005383
50 F-NT2RM4000233//Mus musculus semaphorin VIa mRNA, complete cds.//1.6e-135:835:86//AF030430
F-NT2RM4000244//RPC111-24P15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P15, genomic survey sequence.//5.5e-08:422:62//B86757
F-NT2RM4000251//Mus musculus clone UWGC:mbac92 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//0.98:207:60//AC005855
55 F-NT2RM4000265//Homo sapiens Chromosome 11q12.2 PAC clone pDJ1081b4 containing human mRNA for T-cell glycoprotein CD6, complete sequence.//5.2e-41:707:65//AC003689
F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//7.9e-153:609:93//

- M99438
 F-NT2RM4000324
 F-NT2RM4000327//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//3.9e-44:727:68//AF022085
- 5 F-NT2RM4000344//Mus musculus ATP-dependent metalloprotease FtsH1 mRNA, complete cds.//1.0e-143:801:90//AF090430
 F-NT2RM4000349//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700
 F-NT2RM4000354//HS_2221_A2_C07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221 Col=14 Row=E, genomic survey sequence.//1.0e-20:180:83//AQ253449
- 10 F-NT2RM4000356
 F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//1.6e-133:628:99//AB014542
 F-NT2RM4000368//RPC111-91B5.TJ RPC111 Homo sapiens genomic clone R-91B5, genomic survey sequence.//5.0e-12:431:61//AQ283217
 F-NT2RM4000386//Mus musculus DOC4 (Doc4) mRNA, complete cds.//7.4e-86:845:72//AF059485
- 15 F-NT2RM4000395//Saccharomyces cerevisiae chromosome VI cosmid 9965.//2.5e-34:767:61//D44597
 F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.5e-15:114:94//AB015046
 F-NT2RM4000421
 F-NT2RM4000425//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//1.5e-37:295:82//AC005921
- 20 F-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//3.9e-94:740:78//AF062476
 F-NT2RM4000457//CIT-HSP-2346B17.TR CIT-HSP Homo sapiens genomic clone 2346B17, genomic survey sequence.//1.5e-22:149:92//AQ062111
 F-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//1.3e-76:386:97//AJ010952
- 25 F-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22A, //1.1e-22:356:67//AB000459
 F-NT2RM4000496//Homo sapiens 12p13.3 BAC RPC111-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.53:198:70//AC005908
 F-NT2RM4000511
 F-NT2RM4000514
- 30 F-NT2RM4000515//CIT-HSP-2285L3.TR CIT-HSP Homo sapiens genomic clone 2285L3, genomic survey sequence.//0.0012:200:66//AQ000113
 F-NT2RM4000520
 F-NT2RM4000531//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//2.9e-31:732:64//M58297
 F-NT2RM4000532//HS_3231_B1_C05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3231 Col=9 Row=F, genomic survey sequence.//1.3e-59:362:90//AQ192093
- 35 F-NT2RM4000534
 F-NT2RM4000585//CITBI-E1-2508I18.TR CITBI-E1 Homo sapiens genomic clone 2508I18, genomic survey sequence.//1.1e-34:208:93//AQ260706
 F-NT2RM4000590//CIT-HSP-2291M14.TF CIT-HSP Homo sapiens genomic clone 2291M14, genomic survey sequence.//8.3e-34:180:99//AQ004125
- 40 F-NT2RM4000595//Homo sapiens chromosome 17, clone hCIT.131_K_11, complete sequence.//1.2e-09:203:66//AC005288
 F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds.//5.3e-14:305:68//AB002390
 F-NT2RM4000611//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870
- 45 F-NT2RM4000616//D.melanogaster mRNA for acetyl-CoA synthetase.//2.3e-59:721:68//Z46786
 F-NT2RM4000674
 F-NT2RM4000689//CIT-HSP-2381O13.TF CIT-HSP Homo sapiens genomic clone 2381O13, genomic survey sequence.//2.6e-31:174:97//AQ110303
- 50 F-NT2RM4000698
 F-NT2RM4000700
 F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.1e-89:744:77//AF022789
 F-NT2RM4000717
- 55 F-NT2RM4000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//2.1e-140:299:99//AL034379
 F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//3.8e-158:743:98//AB018303
 F-NT2RM4000741

EP 1 074 617 A2

F-NT2RM4000751//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//7.1e-95:754:77//M99593
F-NT2RM4000764
F-NT2RM4000778//Caenorhabditis elegans cosmid F36H12.//0.30:523:60//AF078790
5 F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//5.5e-172:810:98//AB007920
F-NT2RM4000787//Human DNA sequence from PAC 370M22 on chromosome 22q12-qter. contains GRB2 ADAPTOR LIKE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (UQCRFS1) exon, ESTs, STS, CA repeat and CpG island.//0.0057:163:69//Z82206
F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//6.9e-39:237:94//
10 AC005306
F-NT2RM4000795//Rattus norvegicus neuroligin 3 mRNA, complete cds.//5.9e-97:857:74//J41663
F-NT2RM4000796//HS_3214_B1_F11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=21 Row=L, genomic survey sequence.//1.1e-14:254:68//AQ175988
F-NT2RM4000798//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//6.2e-78:816:72//AF023451
15 F-NT2RM4000813//Leishmania major glycoprotein 96-92 (GP 96-92) gene, partial cds.//0.33:276:63//M63109
F-NT2RM4000820//, complete sequence.//2.6e-142:450:97//AC005406
F-NT2RM4000833//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//1.9e-52:501:71//AC004373
20 F-NT2RM4000848//Homo sapiens chromosome 17, clone hRPK.167_N_20, complete sequence.//1.0:477:56//AC005940
F-NT2RM4000852
F-NT2RM4000855//Homo sapiens chromosome 17, clone hCIT.457_L_16, complete sequence.//3.4e-29:229:83//AC003957
25 F-NT2RM4000887
F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds.//2.1e-20:407:64//AB011004
F-NT2RM4000950//Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.//0.41:311:64//AC004929
30 F-NT2RM4000971//RPC111-53H3.TJ RPC111 Homo sapiens genomic clone R-53H3, genomic survey sequence.//1.0:208:64//AQ053735
F-NT2RM4000979//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence.//1.3e-19:207:78//AC005245
F-NT2RM4000996//CITBI-E1-2506B10.TF CITBI-E1 Homo sapiens genomic clone 2506B10, genomic survey sequence.//1.4e-73:361:98//AQ263651
35 F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//5.1e-170:803:98//AB018272
F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//3.3e-125:584:99//AB014539
F-NT2RM4001032//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.00034:777:58//U47276
F-NT2RM4001047//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.5e-92:776:74//S51858
40 F-NT2RM4001054//Canis familiaris sec61 homologue mRNA, complete cds.//3.1e-102:859:76//M96629
F-NT2RM4001084//CIT-HSP-2330F9.TR CIT-HSP Homo sapiens genomic clone 2330F9, genomic survey sequence.//4.6e-78:379:99//AQ044479
F-NT2RM4001092//cSRL-71b1-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone cSRL-71b1, genomic survey sequence.//1.1e-12:152:75//B05776
45 F-NT2RM4001116
F-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.9e-136:717:93//AC004593
F-NT2RM4001151//Streptomyces antibioticus ATP-binding protein and membrane protein (oleC-ORF1, oleC-ORF2, oleC-ORF3, oleC-ORF4, and oleC-PRF5) genes, complete cds; 3427 base-pairs.//0.0083:368:60//L06249
50 F-NT2RM4001155//Bos taurus 50 kDa protein (adp50) mRNA, complete cds.//3.9e-120:764:85//U04706
F-NT2RM4001160
F-NT2RM4001187
F-NT2RM4001191//CIT-HSP-2010E7.TF CIT-HSP Homo sapiens genomic clone 2010E7, genomic survey sequence.//6.2e-12:181:72//B53378
55 F-NT2RM4001200//H.sapiens HZF10 mRNA for zinc finger protein.//1.3e-66:799:69//X78933
F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//4.2e-152:707:99//AF004828
F-NT2RM4001204

- F-NT2RM4001217//Homo sapiens ectoderm-neural cortex-1 protein (ENC-1) mRNA, complete cds.//1.6e-62:715:70//AF005381
- F-NT2RM4001256//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884
- F-NT2RM4001258//HS_3171_B2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=18 Row=N, genomic survey sequence.//2.5e-18:215:77//AQ149676
- 5 F-NT2RM4001309//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//4.9e-28:526:66//AL022163
- F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase.//2.5e-77:474:89//Z46973
- 10 F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11.//1.2e-16:230:73//U97002
- F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.1e-41:642:66//D89016
- F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.//0.0040:141:68//AQ025127
- 15 F-NT2RM4001344//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3, WORKING DRAFT SEQUENCE.//5.5e-06:469:60//AL021388
- F-NT2RM4001347
- F-NT2RM4001371//Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence.//0.10:400:61//AC004786
- F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.2e-167:790:98//AF098799
- 20 F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//0.99:255:59//AL021393
- F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//0.027:336:58//AP000023
- F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//5.9e-124:783:85//AF020526
- 25 F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete cds.//2.2e-34:418:71//AF050183
- F-NT2RM4001414//Homo sapiens full-length insert cDNA clone ZE16C11.//9.1e-76:363:100//AF086563
- F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBNL H146), complete sequence.//2.0e-47:623:69//AC004226
- 30 F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH), cell division protein DivIVA (divIVA), and isoleucine-tRNA synthetase (ileS) genes, complete cds; and unknown gene.//3.6e-09:566:58//AF068901
- 35 F-NT2RM4001454
- F-NT2RM4001455
- F-NT2RM4001483//Human zinc finger protein ZNF136.//3.2e-36:329:78//U09367
- F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//1.2e-155:724:99//AB014585
- F-NT2RM4001519//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00019:418:59//AC004688
- 40 F-NT2RM4001522//Human HepG2 3' region MboI cDNA, clone hmd6a08m3.//1.4e-16:130:88//D17274
- F-NT2RM4001557
- F-NT2RM4001565
- F-NT2RM4001566
- 45 F-NT2RM4001569//HS_2050_B1_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2050 Col=15 Row=F, genomic survey sequence.//2.7e-09:109:84//AQ234720
- F-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.2e-127:740:89//AF071317
- F-NT2RM4001592//M.musculus mRNA of enhancer-trap-locus 1.//7.3e-117:710:88//X69942
- 50 F-NT2RM4001594//Homo sapiens chromosome 9q34, clone 107G20, WORKING DRAFT SEQUENCE, 2 ordered pieces.//0.34:388:59//AC002355
- F-NT2RM4001597//M.musculus red-1 gene.//6.2e-139:788:90//X92750
- F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//3.3e-162:750:99//AB018334
- F-NT2RM4001611//Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592.//2.5e-05:490:58//D90910
- 55 F-NT2RM4001629//Mus musculus palmytoylated protein p55 mRNA, complete cds.//0.65:186:64//U38196
- F-NT2RM4001650//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0435P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.99:422:59//AC004689

EP 1 074 617 A2

F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds.//2.6e-81:449:93//AB002320
 F-NT2RM4001666
 F-NT2RM4001682//Mus musculus clone OST9187, genomic survey sequence.//3.2e-35:240:87//AF046699
 F-NT2RM4001710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING
 5 DRAFT SEQUENCE.//1.9e-151:564:97//AL031447
 F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds.//7.0e-85:748:74//D86957
 F-NT2RM4001715//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,
 complete sequence.//1.2e-91:488:94//AL034430
 F-NT2RM4001731//Orang-utan in volucrin gene, complete cds.//0.40:530:59//M25312
 10 F-NT2RM4001741//Mouse mRNA for talin.//1.1e-129:737:90//X56123
 F-NT2RM4001746//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316G12, WORKING
 DRAFT SEQUENCE.//2.3e-49:320:89//AL031709
 F-NT2RM4001754//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Li-
 brary) complete sequence.//6.3e-64:379:76//AC005831
 15 F-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//3.7e-146:871:87//Z83868
 F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.3e-173:803:99//AB018270
 F-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence.//2.0e-165:593:99//AC006017
 F-NT2RM4001810
 F-NT2RM4001813//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//7.1e-31:176:84//
 20 AC005036
 F-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//
 4.4e-34:195:95//M37712
 F-NT2RM4001823//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.3e-51:490:75//U49046
 F-NT2RM4001828//Human zinc finger containing protein ZNF157 (ZNF157) mRNA, complete cds.//5.6e-74:688:
 25 72//U28687
 F-NT2RM4001836//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete se-
 quence.//1.0:406:60//AC000076
 F-NT2RM4001841//Mus musculus A kinase anchor protein (AKAP-KL) mRNA, alternatively spliced isoform 2,
 complete cds.//1.6e-131:831:86//AF033275
 30 F-NT2RM4001842//HS_3163_A2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3163 Col=20 Row=M, genomic survey sequence.//1.5e-05:355:60//AQ168513
 F-NT2RM4001856//Caenorhabditis elegans cosmid K08F11.//4.0e-23:823:60//U70855
 F-NT2RM4001858//Notophthalmus viridescens NvTbox1 mRNA, partial cds.//6.4e-11:266:66//U64433
 F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//6.9e-149:704:98//Y17711
 35 F-NT2RM4001876//F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence.//5.7e-48:600:68//
 Z88651
 F-NT2RM4001880//CIT-HSP-2348J1.TF CIT-HSP Homo sapiens genomic clone 2348J1, genomic survey se-
 quence.//0.0025:61:88//AQ060809
 F-NT2RM4001905//R.norvegicus CYP3A1 gene, 5' flanking region.//2.5e-29:535:67//X98335
 40 F-NT2RM4001922//HS_2237_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//2.2e-73:364:98//AQ033732
 F-NT2RM4001930//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence.//
 4.9e-10:269:63//AB005248
 F-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC:1081_P_3, complete sequence.//7.6e-152:311:
 45 100//AC005207
 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//1.1e-170:808:98//AF098162
 F-NT2RM4001953//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B13E4;
 HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.7e-45:310:86//AC004046
 50 F-NT2RM4001965//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and
 non-small cell lung cancer, segment 11/11.//1.6e-107:622:90//AB020868
 F-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//3.9e-24:221:76//X99330
 F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.0e-61:527:76//AB018341
 F-NT2RM4001984//Human DNA sequence from cosmid U151E3, between markers on chromosome X.//5.8e-07:
 55 502:60//Z82253
 F-NT2RM4001987//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey se-
 quence.//2.6e-33:177:99//AQ051701
 F-NT2RM4002013//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//0.019:65:90//
 AC005921

F-NT2RM4002018//Human high molecular weight B cell growth factor mRNA sequence.//1.0:527:57//L15344
 F-NT2RM4002034//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//0.11:322:60//AL008712
 F-NT2RM4002044//Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds.//0.015:513:61//
 5 U01882
 F-NT2RM4002054//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.0e-44:473:76//AC005283
 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds.//1.0e-171:803:98//AB014540
 F-NT2RM4002062//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORK-
 10 ING DRAFT SEQUENCE, 8 unordered pieces.//0.0031:298:59//AC005122
 F-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//1.1e-147:705:98//
 U82267
 F-NT2RM4002066//Human mRNA for KIAA0192 gene, partial cds.//3.4e-73:889:69//D83783
 F-NT2RM4002067//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//1.1e-
 15 53:295:76//AC005216
 F-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//7.8e-25:277:75//AF072758
 F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.0e-23:588:61//
 AF059569
 F-NT2RM4002093//Rat PYBP1 mRNA for pyrimidine binding protein 1.//3.1e-68:544:69//X60789
 F-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.0e-121:762:
 20 86//D12646
 F-NT2RM4002128//HS_3084_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312
 F-NT2RM4002140
 25 F-NT2RM4002145//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//1.8e-49:736:65//
 AC004152
 F-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.5e-70:454:85//AF035940
 F-NT2RM4002161//Homo sapiens mRNA for LAFPTase, isoform 1, partial.//4.2e-151:763:96//AJ130763
 F-NT2RM4002174//Helicobacter pylori 26695 section 18 of 134 of the complete genome.//2.1e-16:580:60//
 30 AE000540
 F-NT2RM4002189//Homo sapiens DNA sequence from BAC 722E9 on chromosome 22q13.2-13.33. Contains
 ESTs.//1.0e-07:792:61//AL008636
 F-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//3.2e-132:782:87//AF030430
 F-NT2RM4002205//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//
 35 1.5e-40:292: 84//L14684
 F-NT2RM4002213
 F-NT2RM4002226//Mus musculus p190-B gene, complete cds.//0.099:350:59//U67160
 F-NT2RM4002251//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//1.0:428:58//
 AC004448
 40 F-NT2RM4002256//Mouse genomic DNA, chromosome 17, clone cosmid 49.1, genomic survey sequence.//9.4e-
 60:294:81//AB005959
 F-NT2RM4002266//Fugu rubripes GSS sequence, clone 006118aG12, genomic survey sequence.//3.3e-12:217:
 67//AL024779
 F-NT2RM4002278//HS_3089_A1_E05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 45 nomic clone Plate=3089 Col=9 Row=I, genomic survey sequence.//1.9e-64:381:92//AQ121653
 F-NT2RM4002281
 F-NT2RM4002287//CIT-HSP-2327E14.TF CIT-HSP Homo sapiens genomic clone 2327E14, genomic survey se-
 quence.//9.0e-49:336:86//AQ042515
 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds.//2.1e-48:511:72//D87457
 50 F-NT2RM4002301//Human NotI linking clone 924A053D, genomic survey sequence.//8.9e-05:62:91//U49881
 F-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudo-
 gene similar to GPISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and
 D6S299 and a ca repeat polymorphism, complete sequence.//4.9e-115:729:87//AL032822
 F-NT2RM4002339//Homo sapiens PAC clone DJ0728D04, complete sequence.//1.1e-97:457:93//AC004865
 55 F-NT2RM4002344//Caenorhabditis elegans cosmid K04A8.//2.2e-06:190:69//U64849
 F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//2.8e-149:708:98//AB014549
 F-NT2RM4002374//Homo sapiens 12q24 PAC P336P3 (Research Park Cancer Institute Human Genome PAC
 library) complete sequence.//0.00040:312:63//AC002978

- F-NT2RM4002383//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//6.8e-29:378:66//AL031284
- F-NT2RM4002390
- 5 F-NT2RM4002398//CIT-HSP-2288N22.TR CIT-HSP Homo sapiens genomic clone 2288N22, genomic survey sequence.//3.4e-35:184:100//AQ001110
- F-NT2RM4002409//Archaeoglobus fulgidus section 15 of 172 of the complete genome.//2.0e-16:468:59//AE001092
- 10 F-NT2RM4002438//Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.//1.6e-16:123:91//U89336
- F-NT2RM4002446//Human DNA sequence from cosmid 443D9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands, //9.6e-64:467:84//Z92845
- F-NT2RM4002452
- 15 F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 22, complete sequence.//2.2e-24:201:86//Z85988
- F-NT2RM4002460//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//1.3e-45:487:70//AC004690
- F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.7e-163:777:98//AF083255
- 20 F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//2.3e-93:464:97//AB014591
- F-NT2RM4002493
- F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-41:442:75//AC005484
- 25 F-NT2RM4002504//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudo-genes similar to ribosomal protein, ESTs, GSSs, complete sequence.//3.8e-31:233:87//AL031577
- F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic survey sequence.//7.7e-08:274:62//AL027162
- F-NT2RM4002532
- F-NT2RM4002534
- 30 F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partial cds.//3.8e-53:394:81//AF072759
- F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//6.4e-160:902:89//AF022962
- F-NT2RM4002567//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//8.5e-31:220:88//AQ263402
- 35 F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 mRNA, complete cds.//5.2e-05:199:65//AF049344
- F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31; complete sequence.//0.89:275:61//AC004875
- F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//3.7e-44:768:64//AC005454
- 40 F-NT2RM4002623//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-34:574:65//AC005122
- F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//3.9e-111:582:95//AB013385
- F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//1.1e-153:747:96//AJ012449
- 45 F-NT2RP1000040//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//1.6e-125:243:88//AP000047
- F-NT2RP1000063//Caenorhabditis elegans cosmid F31C3, complete sequence.//9.6e-09:414:59//Z92784
- F-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//2.8e-183:548:91//X98834
- F-NT2RP1000101//H.sapiens CpG island DNA genomic Mse1 fragment, clone 28b4, forward read cpg28b4.ft1a.//6.0e-27:163:95//Z60555
- 50 F-NT2RP1000111//CIT-HSP-2307O14.TR CIT-HSP Homo sapiens genomic clone 2307O14, genomic survey sequence.//1.2e-11:128:81//AQ016069
- F-NT2RP1000112//Human kinase (TTK) mRNA, complete cds.//1.0e-38:324:81//M86699
- F-NT2RP1000124//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.59:476:59//AL034557
- 55 F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor.//2.7e-35:535:681//E08546
- F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//6.7e-05:77:90//AF011792
- F-NT2RP1000170//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//

1.9e-20:431:64//AC006030
 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//2.5e-138:679:97//AF070535
 F-NT2RP1000191
 F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase, partial cds//5.3e-05:220:61//
 5 D89496
 F-NT2RP1000243//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence//4.7e-51:
 508:69//AC004373
 F-NT2RP1000259
 F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeats mRNA, complete cds//7.8e-142:866:
 10 88//AF042383
 F-NT2RP1000324//RPC111-81O21.TJ RPC111 Homo sapiens genomic clone R-81O21, genomic survey se-
 quence//2.8e-29:182:92//AQ285136
 F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, com-
 plete cds//4.2e-147:693:98//AF053551
 15 F-NT2RP1000333//Caenorhabditis elegans cosmid C03D6, complete sequence//1.4e-08:281:61//Z75525
 F-NT2RP1000348//H.sapiens CpG island DNA genomic MseI fragment, clone 12f1, reverse read cpg12f1.r1c//
 1.7e-09:71:100//Z56610
 F-NT2RP1000357
 F-NT2RP1000358 5.7e-16:403:61//AC005456
 20 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.8e-125:497:86//AB014538
 F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//1.8e-176:877:
 96//AF064594
 F-NT2RP1000409//Homo sapiens repetitive sequences, alphoid DNA, 2482bp//4.6e-106:700:84//AJ001558
 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//9.4e-178:710:98//AB011159
 25 F-NT2RP1000416
 F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds//1.0:198:60//L40178
 F-NT2RP1000439//HS_2182_A1_D06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2182 Col=11 Row=G, genomic survey sequence//2.1e-68:441:87//AQ024305
 F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SE-
 30 QUENCE//3.8e-57:185:88//AP000047
 F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence//2.7e-132:204:99//
 AC004453
 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete se-
 quence//4.9e-80:196:95//AC002985
 35 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//1.9e-55:440:80//U47634
 F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a
 Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloro-
 plast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691
 and STSs//2.6e-92:562:88//Z99297
 40 F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds//2.0e-130:622:98//D87686
 F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN genes, complete cds's//0.11:360:
 58//M81648
 F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces//4.9e-
 34:209:93//AC004895
 45 F-NT2RP1000547//Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds//1.2e-
 08:331:63//U26264
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//4.4e-81:295:92//
 AF017418
 F-NT2RP1000577//HS_2228_B2_C05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 50 nomic clone Plate=2228 Col=10 Row=F, genomic survey sequence//1.9e-31:179:75//AQ185128
 F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partial cds//4.7e-34:223:90//U31620
 F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene,
 complete sequence//1.6e-18:229:65//AC004770
 F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds//9.3e-89:584:84//M62419
 55 F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 22 Contains EST, complete se-
 quence//1.0:203:63//Z85989
 F-NT2RP1000677//Homo sapiens chromosome 19, cosmid R30538, complete sequence//0.0034:350:61//
 AC005943

F-NT2RP1000688//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form)//5.2e-10:120:80//X69907
 F-NT2RP1000695
 F-NT2RP1000701//Sequence 1 from patent US 5580968//2.4e-99:624:86//I30536
 F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces//1.1e-
 5 19:188:81//AC004932
 F-NT2RP1000730
 F-NT2RP1000733//Human chromosome 16p13-1 BAC clone CIT987SK-551G9 complete sequence//1.3e-30:
 315:75//U95742
 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete
 10 cds//8.0e-122:604:96//AF101434
 F-NT2RP1000746//HS_3084_A1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3084 Col=5 Row=O, genomic survey sequence//1.5e-83:466:92//AQ186344
 F-NT2RP1000767//Homo sapiens full-length insert cDNA clone ZD81B04//2.8e-21:144:91//AF086442
 F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds//2.1e-121:591:97//
 15 AF054840
 F-NT2RP1000796//T.thermophilus phosphofructokinase 1 (PFK1) gene, complete cds//0.76:263:64//M71213
 F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown
 gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic
 marker D22S1168 and a CA repeat polymorphism, complete sequence//1.5e-77:163:96//Z93244
 20 F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds//1.3e-147:
 424:96//AF048837
 F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds//1.9e-89:702:79//
 AF047020
 F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.41. Contains the
 25 HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE
 pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs,
 complete sequence//8.7e-169:842:96//AL022398
 F-NT2RP1000846//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//3.3e-15:196:76//
 U96629
 30 F-NT2RP1000851//Homo sapiens PAC clone 267D11 from 12, complete sequence//1.6e-144:724:96//AC004812
 F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds//2.1e-121:591:97//
 AF054840
 F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//6.7e-106:551:95//AF064094
 F-NT2RP1000902//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING
 35 DRAFT SEQUENCE//0.0097:55:100//Z82199
 F-NT2RP1000915//H.sapiens genomic DNA fragment (clone J32A032R)//1.3e-30:174:97//Z94761
 F-NT2RP1000916
 F-NT2RP1000943//Hylobates lar huntingtin gene, partial exon//0.19:103:72//L49362
 F-NT2RP1000944//HS_2179_B2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 40 nomic clone Plate=2179 Col=24 Row=F, genomic survey sequence//0.032:140:63//AQ065269
 F-NT2RP1000947//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds//3.7e-53:461:78//
 U62483
 F-NT2RP1000954//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic
 clone cSRL-143G4, genomic survey sequence//0.030:89:78//B01950
 45 F-NT2RP1000958//Caenorhabditis elegans cosmid K01C8, complete sequence//3.9e-11:445:61//Z49068
 F-NT2RP1000959//Homo sapiens PAC clone 278C19 from 12q, complete sequence//3.3e-57:326:92//AC004263
 F-NT2RP1000966//Human nucleolin gene, complete cds//3.4e-64:197:981//M60858
 F-NT2RP1000980//CIT-HSP-2314B10.TF CIT-HSP Homo sapiens genomic clone 2314B10, genomic survey se-
 quence//0.32:137:68//AQ017126
 50 F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//8.0e-72:665:80//L13435
 F-NT2RP1001011//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene,
 partial cds//1.3e-31:497:65//U34925
 F-NT2RP1001013//HS_3068_B1_809_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3068 Col=17 Row=D, genomic survey sequence//1.0e-24:414:66//AQ127667
 55 F-NT2RP1001014//HS_3252_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3252 Col=9 Row=D, genomic survey sequence//0.00052:83:81//AQ304711
 F-NT2RP1001033//Homo sapiens chromosome 17, clone hRPC-1073_F_15, complete sequence//1.3e-134:241:
 99//AC004686

EP 1 074 617 A2

- F-NT2RP1001073//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//2.5e-59:451:83//AC004993
- F-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//4.5e-93:476:96//U82267
- 5 F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//6.6e-54:217:89//AC004938
- F-NT2RP1001113
- F-NT2RP1001173
- F-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//8.1e-26:373:681//U79139
- 10 F-NT2RP1001185//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-32:388:73//AC006039
- F-NT2RP1001199
- F-NT2RP1001247//Homo sapiens signaling molecule LEFTY-A gene, exon 1.//2.0e-29:166:96//AF081508
- F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//7.3e-50:128 : 99//AC002036
- 15 F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//4.3e-91:344:93//AF029914
- F-NT2RP1001286//Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's.//0.54:292:63//L44140
- F-NT2RP1001294
- 20 F-NT2RP1001302
- F-NT2RP1001310//Rabbit skeletal muscle mRNA for ryanodine receptor.//1.5e-07:335:64//X15750
- F-NT2RP1001311//RPC111-67O14.TK RPC111 Homo sapiens genomic clone R-67O14, genomic survey sequence.//0.26:80:75//AQ239291
- F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//8.8e-75:304:98//AC004228
- 25 F-NT2RP1001361//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//2.7e-57:412:84//X68647
- F-NT2RP1001385
- F-NT2RP1001395//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.4e-72:535:83//AF071316
- 30 F-NT2RP1001410//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//5.8e-105:570:94//AL021878
- F-NT2RP1001424
- 35 F-NT2RP1001432
- F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence.//1.7e-84:422:97//AF052149
- F-NT2RP1001457//Xenopus laevis notchless (nle) mRNA, complete cds.//1.3e-47:471:73//AF069737
- F-NT2RP1001466//HS_3006_A2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=16 Row=G, genomic survey sequence.//0.56:289:60//AQ154336
- 40 F-NT2RP1001475//H.sapiens genomic DNA fragment (clone NLMA194R).//0.00011:91:79//Z95375
- F-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.//1.4-0e-87:563:85//L11316
- F-NT2RP1001494
- F-NT2RP10015431//Drosophila melanogaster DNA sequence (P1 DS01142 (D148)), complete sequence.//1.9e-27:387:67//AC004280
- 45 F-NT2RP1001546//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//8.0e-63:314:98//AF054840
- F-NT2RP1001569//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//1.2e-68:514:81//U17343
- F-NT2RP1001616//Human clone 23665 mRNA sequence.//7.6e-40:496:74//U90913
- 50 F-NT2RP1001665//CIT-HSP-2059N5.TF CIT-HSP Homo sapiens genomic clone 2059N5, genomic survey sequence.//2.4e-45:305:88//B69912
- F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence.//1.5e-135:685:96//AF091081
- F-NT2RP2000006//HS_3061_B2_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=6 Row=F, genomic survey sequence.//1.9e-17:394:67//AQ178856
- 55 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds.//3.5e-14:241:68//AB002390
- F-NT2RP2000008//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE.//1.7e-34:147:99//AL034424
- F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//1.4e-32:345:75//

AC005066
 F-NT2RP2000032//F.rubripes GSS sequence, clone 060E22aG10, genomic survey sequence//5.0e-41:445:72//Z88655
 F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//1.9e-76:383:97//AB018290
 5 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//2.4e-95:467:97//AF061749
 F-NT2RP2000054//CIT-HSP-2328J24.TF CIT-HSP Homo sapiens genomic clone 2328J24, genomic survey sequence//3.3e-39:236:91//AQ043092
 F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds//3.2e-50:311:90//D78610
 10 F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds//3.0e-55:766:66//AF059485
 F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence//2.0e-118:597:95//AC005754
 F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence//0.0017:423:60//AC006037
 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//2.1e-77:278:97//AF050079
 15 F-NT2RP2000079//H.sapiens CpG island DNA genomic Mse1 fragment, clone 40c2, forward read cpg40c2.ft1k//3.2e-33:197:95//Z55440
 F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//2.2e-158:752:98//AB018338
 F-NT2RP2000091//HS_2228_A2_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=4 Row=C, genomic survey sequence//0.26:55:90//AQ146363
 20 F-NT2RP2000097
 F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces//2.5e-05:482:60//AC004961
 F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence//1.0e-22:274:69//AC003973
 25 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//4.9e-114:551:97//AB018356
 F-NT2RP2000120//HS_3000_B1_E03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=5 Row=J, genomic survey sequence//1.8e-21:129:97//AQ090365
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//4.2e-119:607:96//AF054177
 30 F-NT2RP2000133//Homo sapiens PAC clone DJ044L15' from :Xq23, complete sequence//1.3e-07:339:63//AC004827
 F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds//9.0e-101:638:85//M62419
 F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains ESTs, STSs and GSSs, complete sequence//0.45:377:58//AL034370
 35 F-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence//4.0e-73:317:87//AC005924
 F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP Homo sapiens genomic clone 2353L5, genomic survey sequence//3.0e-14:123:90//AQ263431
 40 F-NT2RP2000173
 F-NT2RP2000175
 F-NT2RP2000183//F.rubripes GSS sequence, clone 168M02aC2, genomic survey sequence//3.7e-06:152:66//AL007295
 45 F-NT2RP2000195//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence//7.6e-62:170:99//AL023581
 F-NT2RP2000205
 F-NT2RP2000208//Homo sapiens chromosome 19, overlapping cosmids R29828 and F25496, complete sequence//7.2e-80:170:90//AC003030
 50 F-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence//5.5e-64:400:85//AC004382
 F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island, ESTs and STSs//2.2e-07:280:66//Z97632
 55 F-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds//8.8e-30:508:67//U88401
 F-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence//4.0e-79:504:

- 87//AC004066
F-NT2RP2000248
F-NT2RP2000257//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3, WORK-
ING DRAFT SEQUENCE //0.0078:286:60//AL021388
- 5 F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 2349P21, genomic survey se-
quence //5.7e-82:416:97//AQ059184
F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence //4.5e-
29:310:73//AC006116
F-NT2RP2000274
- 10 F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor //6.3e-20:260:73//X74904
F-NT2RP2000288
F-NT2RP2000289
F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9 //4.6e-69:744:70//
M27877
- 15 F-NT2RP2000298//Streptomyces coelicolor cosmid 2E9 //4.4e-05:502:59//AL021530
F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces //2.1e-13:173:76//AC006082
F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the
HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE
pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs,
complete sequence //8.3e-144:731:95//AL022398
- 20 F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,
complete sequence //1.9e-102:555:90//AL034430
F-NT2RP2000329//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds //6.4e-105:639:87//
M25757
- 25 F-NT2RP2000337//HS_2060_B1_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=2060 Col=1 Row=J, genomic survey sequence //0.78:218:60//AQ243333
F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds //3.6e-129:627:
97//U83981
F-NT2RP2000369//HS_2182_B1_B11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=2182 Col=21 Row=D, genomic survey sequence //2.5e-87:421:99//AQ024835
- 30 F-NT2RP2000412//Human DNA sequence from PAC 124O9 on chromosome 6q21. Contains DNAJ2 (HDJ1) like
pseudogene, ESTs, STSs and GSSs //0.72:170:65//AL021327
F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds //5.0e-66:375:93//L28010
F-NT2RP2000420//Homo sapiens full-length insert cDNA YQ86E07 //9.2e-77:423:93//AF075093
- 35 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds //2.1e-126:609:
96//AF102265
F-NT2RP2000438//CITBI-E1-2519O19.TR CITBI-E1 Homo sapiens genomic clone 2519O19, genomic survey se-
quence //0.96:61:78//AQ276878
F-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence //7.1e-17:341:67//
AC004691
- 40 F-NT2RP2000459//H.sapiens mRNA for imogen 38 //5.7e-21:158:87//Z68747
F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs //3.2e-11:160:
73//Z92844
F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence //0.0031:187:66//
AC005229
- 45 F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066G04aC1, genomic survey sequence //8.8e-07:179:
64//AL026277
F-NT2RP2000516//Mus musculus t complex testis-specific protein (Tctex2) gene, wild type, promoter sequence //
0.19:72:81//U21671
- 50 F-NT2RP2000523//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING
DRAFT SEQUENCE //5.0e-115:570:96//AL022318
F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds //8.4e-37:196:98//AB005543
F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence //0.81:354:60//
AC005321
- 55 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds //1.3e-149:732:97//AB014514
F-NT2RP2000644//HS_3211_A1_F06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3211 Col=11 Row=K, genomic survey sequence //3.6e-42:282:86//AQ175486
F-NT2RP2000656

F-NT2RP2000658//CITBI-E1-2518N15.TF CITBI-E1 Homo sapiens genomic clone 2518N15, genomic survey sequence.//0.57:141:66//AQ278386
 F-NT2RP2000668
 F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12 unordered pieces.//4.3e-22:433:62//AC004916
 5 F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.7e-22:270:75//AC005913
 F-NT2RP2000710//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-32:574:64//AC005122
 10 F-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//4.8e-113:546:98//AC004540
 F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.97:115:70//AC004965
 F-NT2RP2000758//Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds.//9.7e-16:162:77//U62293
 15 F-NT2RP2000764//HS_2254_B2_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=14 Row=H, genomic survey sequence.//0.071:45:95//AQ068887
 F-NT2RP2000809
 F-NT2RP2000812//Egernia stokesii clone EST3 microsatellite.//0.040:158:64//AF069698
 20 F-NT2RP2000814
 F-NT2RP2000816
 F-NT2RP2000819
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds.//1.1e-26:390:70//AB002292
 F-NT2RP2000842//H.sapiens mRNA for G protein-coupled receptor Edg-2.//1.2e-44:255:93//Y09479
 25 F-NT2RP2000845
 F-NT2RP2000863//Human partial cDNA sequence, clone x874.//5.9e-29:173:94//Z47045
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds.//2.4e-140:732:94//AB018284
 F-NT2RP2000892
 F-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//3.4e-129:610:98//AB018266
 30 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-37:212:84//AC005014
 F-NT2RP2000938//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.6e-126:682:93//Z69890
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//5.8e-112:533:98//AB018298
 35 F-NT2RP2000965
 F-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//9.2e-101:505:96//AL021393
 F-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//1.6e-72:498:82//AC005277
 40 F-NT2RP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//7.4e-12:171:77//AC002394
 F-NT2RP2001036//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//1.2e-37:390:76//AC004167
 F-NT2RP2001044//HS_2253_B1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence.//0.21:276:61//AQ069224
 45 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//3.2e-144:696:97//AB007957
 F-NT2RP2001065
 F-NT2RP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//4.3e-104:775:81//U91561
 50 F-NT2RP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds.//3.7e-69:488:82//AF000423
 F-NT2RP2001094//Human DNA sequence from PAC 410B11 on chromosome X contains STS.//7.4e-11:490:61//Z86063
 F-NT2RP2001119//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745C22, WORKING DRAFT SEQUENCE.//5.1e-30:316:76//AL031596
 55 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds.//1.1e-31:519:63//D87072
 F-NT2RP2001137//HS_2193_B2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=H, genomic survey sequence.//1.8e-11:136:78//AQ032187

F-NT2RP2001149//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//6.2e-29:247:78//AC000076
 F-NT2RP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); trans-located to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STSs, GSSs, and a putative CpG island, complete sequence.//0.23:207:66//AL009178
 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//2.3e-112:567:96//AB007949
 F-NT2RP2001174//RPC111-58L2.TK RPC111 Homo sapiens genomic clone R-58L2, genomic survey sequence.//7.6e-07:196:64//AQ237306
 F-NT2RP2001196
 F-NT2RP2001218
 F-NT2RP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//1.1e-09:320:65//U92893
 F-NT2RP2001233//Human ZFP-36 mRNA for a zinc finger protein.//6.1e-71:681:72//X51760
 F-NT2RP2001245//HS_3062_B1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence.//1.5e-05:268:63//AQ143177
 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//2.5e-106:514:97//AB018353
 F-NT2RP2001277//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//0.32:183:64//AE001430
 F-NT2RP2001290//M.musculus mRNA for I47 clone.//8.6e-102:641:86//X61455
 F-NT2RP2001295//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE.//0.20:171:63//AL022594
 F-NT2RP2001312//Bovine synaptophysin mRNA, complete cds.//0.98:253:58//M22967
 F-NT2RP2001327//Human B12 protein mRNA, complete cds.//5.8e-29:359:71//M80783
 F-NT2RP2001328//CIT-HSP-2335A5.TF CIT-HSP Homo sapiens genomic clone 2335A5, genomic survey sequence.//1.3e-65:366:94//AQ038539
 F-NT2RP2001347//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.8e-31:325:77//AJ003147
 F-NT2RP2001366//H.sapiens CpG island DNA genomic MseI fragment, clone 4e11, forward read cpg4e11.f1a.//1.7e-12:98:92//Z61305
 F-NT2RP2001378//HS_3054_B2_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=6 Row=B, genomic survey sequence.//9.8e-17:131:89//AQ100721
 F-NT2RP2001381//Arabidopsis thaliana BAC T2L5.//0.080:434:59//AF096371
 F-NT2RP2001392//S.pristinaespiralis snbC gene & snbDE gene.//0.019:267:59//Y11548
 F-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//1.9e-16:133:78//Z93242
 F-NT2RP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds.//1.3e-63:419:84//AF080219
 F-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//3.1e-98:747:79//U76759
 F-NT2RP2001423//Xenopus laevis ER1 mRNA, complete cds.//3.7e-34:269:85//AF015454
 F-NT2RP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//3.2e-13:164:78//AC003065
 F-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//3.0e-06:136:71//AF046702
 F-NT2RP2001440//cDNA sequence coding for gamma protein.//7.9e-83:553:86//E02350
 F-NT2RP2001445//P.falciparum complete gene map of plastid-like DNA (IR-A).//1.5e-09:829:57//X95275
 F-NT2RP2001449//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.3e-136:766:90//X75931
 F-NT2RP2001450
 F-NT2RP2001467
 F-NT2RP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 2374H21, genomic survey sequence.//7.9e-14:151:80//AQ109561
 F-NT2RP2001511//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-22:462:64//AF005355
 F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//2.0e-136:657:97//Y14494
 F-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//1.2e-37:357:64//AC004596
 F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//1.6e-103:384:94//AF035586
 F-NT2RP2001560
 F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//4.4e-123:590:98//

AB007957
 F-NT2RP2001576//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds//0.038:580:58//U32943
 F-NT2RP2001581//Mus musculus semaphorin VIa mRNA, complete cds//6.5e-09:222:66//AF030430
 5 F-NT2RP2001597//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds//0.0057:361:60//U72648
 F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.2e-137:647:98//AB018340
 F-NT2RP2001613
 F-NT2RP2001628//H.sapiens (xs128) mRNA, 380bp//1.7e-15:279:68//Z36784
 F-NT2RP2001634//Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds//5.4e-123:606:96//AF030233
 10 F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds//4.2e-144:687:97//AF058718
 F-NT2RP2001663//H.sapiens mRNA for 2-phosphopyruvate-hydratase-alpha-enolase//1.0e-36:372:74//X84907
 F-NT2RP2001675//S.pombe chromosome I cosmid c2G11//0.070:507:59//Z54354
 15 F-NT2RP2001677//Mouse BAC C11bCJ7 219m7, genomic sequence, complete sequence//2.0e-60:232:96//AC005259
 F-NT2RP2001678//HS_2007_A2_A04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=8 Row=A, genomic survey sequence//7.3e-62:370:91//AQ269699
 F-NT2RP2001699//RPC111-57B17.TK RPC111 Homo sapiens genomic clone R-57B17, genomic survey sequence//0.99:141:63//AQ115592
 20 F-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence//9.4e-117:604:95//AC004079
 F-NT2RP2001721//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence//1.0:273:61//AL030998
 25 F-NT2RP2001740//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence//1.0:356:62//AC000090
 F-NT2RP2001748//Human mRNA for KIAA0003 gene, complete cds//3.7e-18:151:86//D14697
 30 F-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence//6.0e-145:715:97//AC004783
 F-NT2RP2001813//Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence//0.38:340:60//AE001378
 F-NT2RP2001839//HS_3000_B1_C07_MR CIT Approved Human Genomic Sperm Library D_ Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence//0.026:253:60//AQ090347
 35 F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.89:146:71//Y16610
 F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds//0.040:174:62//AF027219
 F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete cds//2.8e-44:483:71//AB012309
 40 F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence//1.8e-87:496:92//AL031864
 F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end//9.2e-112:633:90//M74161
 45 F-NT2RP2001900//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone R08A5, WORKING DRAFT SEQUENCE//0.0026:360:62//Z82281
 F-NT2RP2001907//H.sapiens CpG island DNA genomic MseI fragment, clone 97f11, forward read cpg97f11.ft1a.//4.2e-26:206:84//Z64125
 F-NT2RP2001926//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces//5.5e-06:621:59//AC004688
 50 F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-47D9, genomic survey sequence//3.1e-50:282:93//B04856
 F-NT2RP2001943//Drosophila melanogaster cosmid 25E8//0.00036:248:60//AL009196
 F-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence//3.8e-78:232:99//AC005033
 55 F-NT2RP2001947//Homo sapiens full-length insert cDNA clone ZD81B04.//2.0e-28:172:94//AF086442
 F-NT2RP2001969//H.sapiens CpG island DNA genomic MseI fragment, clone 152a8, reverse read cpg152a8.r11a.//1.0e-20:123:99//Z59378
 F-NT2RP2001976

F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117
 F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//3.1e-35:180:80//L22022
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.8e-61:314:97//AB018299
 F-NT2RP2002032//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//0.76:189:65//AC005895
 5 F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.9e-12:160:79//AC004825
 F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//0.0014:123:73//AC004029
 F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete
 10 sequence.//2.2e-86:722:77//AC004552
 F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon
 of a putative new gene and STSs and GSSs, complete sequence.//0.13:350:61//AL033375
 F-NT2RP2002058//S.cerevisiae chromosome XII reading frame ORF YLR129w.//9.7e-11:480:60//Z73301
 F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//6.5e-97:610:86//
 15 U87306
 F-NT2RP2002070//beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta -ADD=adducin
 beta subunit 63 kda isoform/membrane skeleton protein [alternatively spliced, exon 10 to 13 region] [human,
 Genomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083
 F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.0e-127:643:96//AF052183
 20 F-NT2RP2002078//F12O16-T7.1 IGF Arabidopsis thaliana genomic clone F12016, genomic survey sequence.//
 0.14:191:64//AQ249805
 F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094:325:60//AC004917
 F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//9.8e-111:533:97//AJ007509
 F-NT2RP2002105//H.sapiens CpG island DNA genomic MseI fragment, clone 10h8, forward read cpG10h8.ft1a.//
 25 2.4e-29:178:94//Z58857
 F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 2023E9, genomic survey se-
 quence.//2.5e-32:202:92//B64468
 F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds.//0.095:319:59//
 M25874
 30 F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0:258:63//D85923
 F-NT2RP2002172//HS_3020_B1_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3020 Col=3 Row=P, genomic survey sequence.//1.2e-11:124:82//AQ093169
 F-NT2RP2002185//RPC111-67B15.TJ RPC111 Homo sapiens genomic clone R-67B15, genomic survey se-
 quence.//2.8e-18:109:100//AQ201833
 35 F-NT2RP2002192//Human PM-Sc1-75 autoantigen (PM-sc1) mRNA, complete cds.//2.7e-36:363:78//U09215
 F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//9.5e-
 82:477:89//AF032872
 F-NT2RP2002208
 F-NT2RP2002219//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING
 40 DRAFT SEQUENCE.//1.0:378:58//AL034557
 F-NT2RP2002231//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING
 DRAFT SEQUENCE, 5 unordered pieces.//0.60:560:56//AC005308
 F-NT2RP2002235//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.59:341:60//J03998
 F-NT2RP2002252//Mus musculus mSin3A (sin3A) mRNA, complete cds.//3.5e-81:398:87//U22394
 45 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//6.6e-50:315:89//AF005418
 F-NT2RP2002259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING
 DRAFT SEQUENCE.//9.7e-67:340:89//AL033527
 F-NT2RP2002270//RPC111-77C23.TV RPC111 Homo sapiens genomic clone R-77C23, genomic survey se-
 quence.//2.9e-18:79:93//AQ268098
 50 F-NT2RP2002292//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING
 DRAFT SEQUENCE.//1.0:290:60//AL031033
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.5e-93:467:96//
 AF069532
 F-NT2RP2002316//HS_2171_B2_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 55 nomic clone Plate=2171 Col=22 Row=H, genomic survey sequence.//7.3e-94:463:97//AQ119673
 F-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//3.9e-123:640:95//AB015594
 F-NT2RP2002333
 F-NT2RP2002373//F.rubripes GSS sequence, clone 026F10aB8, genomic survey sequence.//0.46:234:61//

- Z87330
 F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds //9.4e-138:673:97//AF038958
 F-NT2RP2002394//P.falciparum complete gene map of plastid-like DNA (IR-A) //0.79:421:56//X95275
 5 F-NT2RP2002408//F.rubripes GSS sequence, clone 080G11aA8, genomic survey sequence //5.7e-15:220:71//AL015615
 F-NT2RP2002426//Sus scrofa SCAMP1 gene, exon 9 //7.1e-71:582:80//AJ223742
 F-NT2RP2002439//Caenorhabditis elegans cosmid T07D3 //0.0018:210:67//AF016682
 F-NT2RP2002442//Caenorhabditis elegans cosmid T03F1 //2.8e-18:295:67//U88169
 10 F-NT2RP2002457//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence //1.9e-06:281:66//AC004381
 F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds //0.039:207:63//D42045
 F-NT2RP2002475
 F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds //2.4e-123:607:96//AB005289
 15 F-NT2RP2002498//Arabidopsis thaliana BAC F3D13 //0.73:395:57//AF069300
 F-NT2RP2002503//Homo sapiens, clone hRPK.15_A_1, complete sequence //7.2e-18:134:90//AC006213
 F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds //1.2e-157:761:97//AB018334
 F-NT2RP2002520
 20 F-NT2RP2002537
 F-NT2RP2002546//Homo sapiens Chromosome 11q12 pac pDJ741n15, WORKING DRAFT SEQUENCE, 7 un-ordered pieces //0.83:252:60//AC004127
 F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence //5.9e-93:186:99//AC005317
 25 F-NT2RP2002591//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE //4.0e-38:175:78//Z98304
 F-NT2RP2002595//Sequence 2 from patent US 5763220 //1.5e-84:430:95//AR012155
 F-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds //1.9e-43:282:87//U19181
 F-NT2RP2002609//Mus musculus defender against death 1 (DAD1) gene, partial cds //1.5e-11:99:90//AF051310
 30 F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1316 bp //5.6e-27:460:63//Y10806
 F-NT2RP2002621
 F-NT2RP2002643//Rat calmodulin III gene for calmodulin, promoter region and exon 1 //0.023:322:60//D90397
 F-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete se-
 35 quence //3.9e-149:794:94//AC005384
 F-NT2RP2002701//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING DRAFT SEQUENCE //9.2e-10:129:75//AL034380
 F-NT2RP2002706//S.griseus secA gene //1.3e-05:311:63//Y10980
 F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds //2.5e-40:631:65//AB014572
 40 F-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds //4.8e-65:600:73//AF041107
 F-NT2RP2002736//S.pombe chromosome II cosmid c887 //0.17:352:58//AL033388
 F-NT2RP2002740//Absidia glauca ORF, 3' end; (+) mating type surface protein (PSSP15) gene, complete cds; ORF, 5' end //0.0073:274:66//M94861
 F-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds //7.5e-29:628:62//D89016
 45 F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence //3.6e-31:568:67//AC005296
 F-NT2RP2002752//Human BAC clone RG317M02 from 7p15-p21, complete sequence //1.7e-08:206:63//AC002433
 F-NT2RP2002753//Human DNA sequence from cosmid B11B7 on chromosome 22 contains ESTs //2.8e-71:195:89//Z82171
 50 F-NT2RP2002769//Streptomyces fradiae ty lactone synthase, starter module and modules 1-7, (tylG) gene, complete cds //0.0016:412:60//U78289
 F-NT2RP2002778//CIT-HSP-2059C5.TF CIT-HSP Homo sapiens genomic clone 2059C5, genomic survey se-
 quence //6.8e-18:186:79//B69837
 55 F-NT2RP2002800
 F-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces //1.2e-41:134:94//AC006078
 F-NT2RP2002857//Rat T-cell receptor active beta-chain V-region (V-beta6-J-beta2.5) mRNA, partial cds, clone

- TRB-4 //0.85:93:68//M18845
 F-NT2RP2002862//HS_3084_A1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//5.0e-67:390:91//AQ186344
 F-NT2RP2002880
- 5 F-NT2RP2002891//CIT-HSP-2310O14.TF CIT-HSP Homo sapiens genomic clone 2310O14, genomic survey sequence.//0.11:53:90//AQ019792
 F-NT2RP2002925//Pig mRNA for carbonyl reductase, complete cds.//0.66:194:65//D16511
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//2.3e-135:628:99//AF038392
- 10 F-NT2RP2002929//F.rubripes GSS sequence, clone 123I23aA1, genomic survey sequence.//3.9e-06:66:83//AL017246
 F-NT2RP2002939
 F-NT2RP2002954
 F-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//1.3e-47:411:79//U62483
- 15 F-NT2RP2002979//CIT-HSP-2340D12.TF CIT-HSP Homo sapiens genomic clone 2340D12, genomic survey sequence.//4.6e-96:476:97//AQ057233
 F-NT2RP2002980//Sequence 20 from Patent EP0705842.//4.0e-13:100:94//A52230
 F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.4e-09:272:61//AF059569
- 20 F-NT2RP2002987//Homo sapiens (subclone 6_d9 from P1 H21) DNA sequence, complete sequence.//1.0e-22:293:67//AC000958
 F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//4.0e-74:502:84//AF025424
- 25 F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-46:474:76//AC004765
 F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//4.2e-23:202:82//AC005703
 F-NT2RP2003073//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//3.4e-59:330:82//Z83822
- 30 F-NT2RP2003099//HS_3008_B2_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3008 Col=18 Row=F, genomic survey sequence.//1.4e-71:362:96//AQ089786
 F-NT2RP2003108//Sequence 59 from patent US 5773577.//0.95:123:69//AR014362
 F-NT2RP2003117//HS_2034_B2_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=24 Row=H, genomic survey sequence.//1.5e-88:461:96//AQ230797
- 35 F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//4.3e-46:470:72//AF079765
 F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//5.7e-10:436:61//AC005329
- 40 F-NT2RP2003129//P.thunbergii cab gene.//0.00044:541:60//X61915
 F-NT2RP2003137//CIT-HSP-2300J6.TR CIT-HSP Homo sapiens genomic clone 2300J6, genomic survey sequence.//5.0e-78:393:97//AQ012976
 F-NT2RP2003157//Human DNA sequence from cDNA 16pHQG;16 from chromosome 16p13.3.//5.4e-07:137:71//Z84716
- 45 F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//1.8e-111:581:93//D67025
 F-NT2RP2003161//CITBI-E1-2506E20.TR CITBI-E1 Homo sapiens genomic clone 2506E20, genomic survey sequence.//0.0025:156:67//AQ262657
 F-NT2RP2003164
- 50 F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.4e-43:334:79//U91328
 F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds.//0.91:346:62//U50040
- 55 F-NT2RP2003194//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 996D20, WORKING DRAFT SEQUENCE.//1.7e-108:511:90//AL031597
 F-NT2RP2003206
 F-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//2.9e-136:726:93//X74794
 F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.6e-51:348:

86//AF023657
 F-NT2RP2003237//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE //2.6e-56:415:83//AL031447
 F-NT2RP2003243//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence //2.1e-16:112:93//AQ047107
 5 F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds //6.0e-114:696:87//L38481
 F-NT2RP2003272//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence //3.8e-16:110:94//AQ201833
 10 F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds //1.5e-145:714:96//AB014525
 F-NT2RP2003280//RPCI11-14I2.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-14I2, genomic survey sequence //6.4e-77:400:95//B85286
 F-NT2RP2003286//CIT-HSP-2336D3.TF CIT-HSP Homo sapiens genomic clone 2336D3, genomic survey sequence //5.3e-29:287:73//AQ041024
 15 F-NT2RP2003293//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence //1.5e-54:508:74//AC003973
 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds //6.1e-85:416:97//AB006572
 F-NT2RP2003297//S.pombe pho2 gene for specific p-nitrophenylphosphatase //0.60:309:64//X62722
 20 F-NT2RP2003307//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds //1.0e-45:442:75//AF055666
 F-NT2RP2003308//D.melanogaster crn mRNA //1.1e-63:697:70//X58374
 F-NT2RP2003329//Homo sapiens chromosome 17, clone hCIT.131_K_11, complete sequence //0.040:145:64//AC005288
 F-NT2RP2003339
 25 F-NT2RP2003347//Plasmodium falciparum MAL3P7, complete sequence //0.12:275:60//AL034559
 F-NT2RP2003367//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence //0.83:225:63//AC005510
 F-NT2RP2003391
 F-NT2RP2003393//HS_3218_A2_B09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=18 Row=C, genomic survey sequence //0.021:93:79//AQ204356
 30 F-NT2RP2003394
 F-NT2RP2003401
 F-NT2RP2003433//Rattus rattus sec61 homologue mRNA, complete cds //4.2e-61:533:75//M96630
 F-NT2RP2003445//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE //2.1e-49:301:72//AP000023
 35 F-NT2RP2003446
 F-NT2RP2003456//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4 //0.0018:366:60//AJ235272
 F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP:3f1e8 (BC269730) containing the hFEN1 gene, complete sequence //7.5e-16:189:68//AC004770
 40 F-NT2RP2003480//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end //1.9e-25:197:85//M21977
 F-NT2RP2003499 2.1e-08:408:61//AB000826
 F-NT2RP2003506//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces //1.9e-33:192:96//AC005236
 45 F-NT2RP2003511//Ceratopteris richardii mRNA for CRHB11, partial cds //1.0:328:60//AB013801
 F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds //7.3e-76:403:93//D87460
 F-NT2RP2003517//Human osteosarcoma cell line U-2 OS mRNA, fragment for PDGF-B chain (PDGF= platelet-derived growth factor) //1.5e-24:151:95//X03702
 F-NT2RP2003522//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end //1.3e-101:564:91//M21977
 50 F-NT2RP2003533//Human DNA sequence from cosmid F1121 on chromosome 6 //2.0e-40:315:75//Z80899
 F-NT2RP2003543
 F-NT2RP2003559//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cpg90a5.rt1a //1.1e-20:122:99//Z56144
 F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds //8.8e-27:664:63//M34551
 55 F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds //4.1e-113:541:98//AB007931
 F-NT2RP2003581
 F-NT2RP2003596//F.rubripes GSS sequence, clone 036L10aF12, genomic survey sequence //J1.9e-11:210:65//AL012756

F-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds//1.9e-123:587:98//AF030233
 F-NT2RP2003629
 F-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase//7.8e-88:582:84//AJ006215
 5 F-NT2RP2003668//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces//5.6e-47:335:83//AC005081
 F-NT2RP2003687//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence//1.2e-06:133:74//AC003684
 10 F-NT2RP2003691//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 525L6, WORKING DRAFT SEQUENCE//1.7e-47:337:81//AL023807
 F-NT2RP2003702//Rattus norvegicus ovarian-specific protein mRNA, complete cds//1.3e-65:458:82//U44803
 F-NT2RP2003704//H.sapiens CpG island DNA genomic MseI fragment, clone 2a9, reverse read cpq2a9.rt1e//3.8e-17:170:84//Z60615
 15 F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//2.6e-108:518:98//AB011097
 F-NT2RP2003713//HS_2016_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=9 Row=D, genomic survey sequence//1.3e-11:102:90//AQ226895
 F-NT2RP2003714//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence//1.4e-27:249:78//AC003973
 20 F-NT2RP2003727//RPC111-77119.TV RPC111 Homo sapiens genomic clone R-77119, genomic survey sequence//3.4e-26:294:74//AQ268303
 F-NT2RP2003737//Homo sapiens clone DJ1022114, WORKING DRAFT SEQUENCE, 14 unordered pieces//2.6e-74:194:91//AC004951
 F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-911E12, complete sequence//1.7e-92:165:96//AC003964
 25 F-NT2RP2003760//B.primigenius mRNA for coat protein gamma-cop//4.5e-76:696:73//X92987
 F-NT2RP2003764//Homo sapiens gene for MTG16, exon 1b, partial sequence//1.0:109:69//AB013275
 F-NT2RP2003769
 F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050_D_4, complete sequence//3.0e-96:467:98//AC004771
 30 F-NT2RP2003777
 F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt]//7.2e-107:731:82//S70011
 F-NT2RP2003793//CIT-HSP-2326L12.TF CIT-HSP Homo sapiens genomic clone 2326L12, genomic survey sequence//7.0e-20:124:95//AQ038761
 35 F-NT2RP2003825//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence//8.9e-06:151:74//AC004491
 F-NT2RP2003840//Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence//0.018:145:69//AC005167
 F-NT2RP2003857//HS_3227_A2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=8 Row=M, genomic survey sequence//0.96:257:61//AQ303467
 40 F-NT2RP2003859
 F-NT2RP2003871//Homo sapiens 12q24 PAC RPC11-74B13 (Roswell Park Cancer Institute Human PAC library) complete sequence//2.0e-12:369:65//AC002375
 F-NT2RP2003885//CITBI-E1-2514D6.TF CITBI-E1 Homo sapiens genomic clone 2514D6, genomic survey sequence//0.13:167:64//AQ265722
 45 F-NT2RP2003912//nek1=serine/threonine- and tyrosine-specific protein kinase [mice, erythroleukemia cells, mRNA, 4263 nt]//1.3e-136:838:86//S45828
 F-NT2RP2003952
 F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//2.1e-28:165:96//AB014458
 50 F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence//2.6e-24:298:74//AL031282
 55

- F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//9.9e-160:783:96//AB018347
 F-NT2RP2003984
 F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.7e-26:260:77//AC000382
- 5 F-NT2RP2003988//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701:70//AL031681
 F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//3.0e-123:693:91//AL023580
 F-NT2RP2004014
- 10 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid, F17127, complete sequence.//5.8e-83:427:87//AC004780
 F-NT2RP2004042
 F-NT2RP2004066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134O19, WORKING DRAFT SEQUENCE.//5.6e-110:528:98//AL034555
- 15 F-NT2RP2004081
 F-NT2RP2004098//HS_2216_A1_B12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, genomic survey sequence.//1.0e-07:86:84//AQ145694
 F-NT2RP2004124//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.0e-25:155:94//AQ136993
- 20 F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence.//1.0:220:62//AB007645
 F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.93:480:56//AC002493
 F-NT2RP2004165//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.051:265:61//AC005140
- 25 F-NT2RP2004170//Homo sapiens distal-less homeobox protein (DLX7) gene, complete cds.//1.0:162:66//AF028235
 F-NT2RP2004172//S.pombe chromosome II cosmid c24E9.//1.7e-06:466:59//AL021816
 F-NT2RP2004187//Homo sapiens full-length insert cDNA YQ86E07.//3.5e-17:354:64//AF075093
- 30 F-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//9.4e-53:397:82//AF003998
 F-NT2RP2004196
 F-NT2RP2004207//Human von Willebrand factor pseudogene corresponding to exons 23 through 34.//0.0023:386:61//M60676
 F-NT2RP2004226//HS_2186_A1_D03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2186 Col=5 Row=G, genomic survey sequence.//7.8e-58:370:87//AQ063813
- 35 F-NT2RP2004232//H.sapiens mRNA for protein kinase C mu.//1.2e-34:448:67//X75756
 F-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//5.2e-108:510:99//AB015718
 F-NT2RP2004240//Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).//1.1e-12:489:61//AP000006
- 40 F-NT2RP2004242
 F-NT2RP2004245
 F-NT2RP2004270//Streptomyces coelicolor cosmid 1A9.//7.5e-07:462:62//AL034446
 F-NT2RP2004300//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//3.5e-11:299:64//AC005781
- 45 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//4.5e-150:735:97//AF000416
 F-NT2RP2004321//Drosophila melanogaster DNA sequence (P1_DS02110 (D147)), complete sequence.//0.98:267:59//AC004423
 F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, complete sequence.//1.6e-40:419:75//AC002519
- 50 F-NT2RP2004347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//1.2e-72:439:82//AL031650
 F-NT2RP2004364
 F-NT2RP2004365
 F-NT2RP2004366//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//0.92:427:57//AL031864
- 55 F-NT2RP2004373//Homo sapiens cosmids Qc15C1 and 94B6 from Xq28, complete sequence.//2.6e-26:493:65//AF035397

EP 1 074 617 A2

F-NT2RP2004389//HS_2183_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//2.9e-11:83:96//AQ063969
F-NT2RP2004392
5 F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//1.1e-171:875:95//AC005164
F-NT2RP2004399//Homo sapiens SYBL1 gene.//1.4e-24:467:64//AJ004799
F-NT2RP2004400//Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence.//0.00074:455:59//AF069441
10 F-NT2RP2004412//H.sapiens CpG island DNA genomic Mse1 fragment, clone 34g4, reverse read cpg34g4.rt1a.//5.0e-27:154:98//Z65369
F-NT2RP2004425
F-NT2RP2004463//Streptomyces coelicolor cosmid 2E9.//0.0053:196:65//AL021530
F-NT2RP2004476//Drosophila melanogaster cosmid 67A9.//5.2e-15:377:63//AL034388
15 F-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//4.3e-100:497:97//AC005591
F-NT2RP2004512//Plasmodium falciparum MAL3P5, complete sequence.//2.3e-07:815:57//AL034556
F-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//8.5e-138:718:95//AC004890
F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds.//1.4e-137:687:96//AB011163
20 F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP Homo sapiens genomic clone 2387G7, genomic survey sequence.//2.1e-85:484:91//AQ239555
F-NT2RP2004568//H.vulgare GAA-satellite DNA.//2.0e-07:292:62//Z50100
F-NT2RP2004580//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//4.5e-44:512:72//AL023755
25 F-NT2RP2004587//Candida albicans cytoskeleton assembly control protein (SLA2) gene, partial cds.//1.0:344:56//AF092908
F-NT2RP2004594//nbxb0019H13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019H13r, genomic survey sequence.//0.053:324:60//AQ258020
F-NT2RP2004600
30 F-NT2RP2004602//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//0.12:109:73//AC005176
F-NT2RP2004614
F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//2.6e-102:496:98//AJ006291
F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.6e-153:728:98//AB007929
35 F-NT2RP2004675//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//0.092:239:61//AC005805
F-NT2RP2004681//Human DNA sequence from clone 51J23 on chromosome Xq26.3-27.3. Contains an EST and GSSs, complete sequence.//1.0:236:61//AL031312
F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.3e-59:327:94//AB014525
40 F-NT2RP2004709//HS_2033_B2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=8 Row=J, genomic survey sequence.//1.9e-15:187:74//AQ230714
F-NT2RP2004710//HS_3185_82_D07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=14 Row=H, genomic survey sequence.//9.9e-10:110:84//AQ172885
F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//6.4e-117:582:96//AB007947
45 F-NT2RP2004743//Human DNA sequence from PAC 37M17 chromosome X.//0.14:138:71//Z78022
F-NT2RP2004767//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65c11, reverse read cpg65c11.rt1a.//1.3e-24:217:81//Z62210
F-NT2RP2004768//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//1.6e-45:541:71//AF024636
F-NT2RP2004775//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//5.8e-13:697:59//AE001398
50 F-NT2RP2004791//Human HeLa mRNA isolated as a false positive in a two-hybrid screen.//5.0e-53:353:84//U56252
F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.5e-116:594:95//AF058953 F-NT2RP2004802
F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.1e-101:495:97//AF054179
55 F-NT2RP2004841//Human DNA sequence from cosmid J138O17, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//7.6e-82:531:84//Z72519
F-NT2RP2004861//Fugu rubripes GSS sequence, clone 040O17bA3, genomic survey sequence.//0.96:183:64//AL025645

F-NT2RP2004897//Human Chromosome X clone bWXD187, complete sequence//4.8e-142:710:96//AC004383
 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//2.0e-82:418:95//AB007144
 F-NT2RP2004936
 5 F-NT2RP2004959//HS_3197_A2_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//3.5e-25:218:83//AQ150183
 F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//2.5e-
 59:339:79//U56732
 F-NT2RP2004962//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemo-
 chromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//3.6e-
 10 19:187:72//U91328
 F-NT2RP2004967//Plasmodium falciparum MAL3P6, complete sequence.//0.0020:297:61//Z98551
 F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mRNA, complete cds.//0.22:162:69//L29029
 F-NT2RP2004982//F26D4-Sp6 IGF Arabidopsis thaliana genomic clone F26D4, genomic survey sequence.//0.13:
 273:61//B12642
 15 F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds.//1.5e-20:431:65//D63478
 F-NT2RP2004999
 F-NT2RP2005000//R.rattus gene for beta-1 subunit of Na,K-ATPase.//0.019:240:63//X63375
 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//6.0e-159:782:97//AB014515
 F-NT2RP2005003//H.sapiens Staf50 mRNA.//3.1e-42:430:75//X82200
 20 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//1.4e-98:501:96//AF100141
 F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//1.0:209:63//
 AC004849
 F-NT2RP2005020
 F-NT2RP2005022//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//
 25 3.0e-43:98:93//AC000380
 F-NT2RP2005031//HS_2052_B2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2052 Col=20 Row=N, genomic survey sequence.//0.019:363:61//AQ231464
 F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene.//0.70:174:65//U64454
 F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//0.20:519:57//
 30 AC005696
 F-NT2RP2005108
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//2.0e-103:495:98//AB014564
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//2.9e-27:157:98//
 X98743
 35 F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5.//
 0.00024:547:59//AJ223012
 F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete se-
 quence.//0.95:191:62//AC004527
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.6e-89:447:96//AF045583
 40 F-NT2RP2005147//HS_3184_A1_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3184 Col=1 Row=I, genomic survey sequence.//0.10:294:60//AQ252226
 F-NT2RP2005159//H.sapiens CpG island DNA genomic MseI fragment, clone 132g6, forward read
 cpg132g6.ft1a.//1.1e-13:93:97//Z59162
 F-NT2RP2005162//Caenorhabditis elegans cosmid F01F1.//2.6e-20:394:64//U13070
 45 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.4e-125:633:96//AJ007509
 F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00016:316:
 60//U80808
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.51:52:92//
 AC005189
 50 F-NT2RP2005239//S.pombe chromosome II cosmid c21D10.//1.3e-22:356:67//AL031536
 F-NT2RP2005254
 F-NT2RP2005270//H.sapiens genomic DNA (chromosome 3; clone NL197R).//0.58:132:65//X87513
 F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//9.0e-103:656:85//D30666
 F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//3.4e-37:302:84//L26335
 55 F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.1e-122:604:96//
 AF060219
 F-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//4.0e-140:670:98//AJ007590
 F-NT2RP2005293//HS_3245_B1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

- nomic clone Plate=3245 Col=19 Row=J, genomic survey sequence//8.2e-37:223:92//AQ217454
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//1.1e-95:483:96//AB014576
 F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//8.2e-22:166:90//U11701
 5 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//0.39:353:62//AF032387
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//8.8e-29:456:66//AB011138
 F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs//0.72:431:61//Z92844
 10 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//4.7e-99:489:96//AF072247
 F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon//0.93:105:67//L49358
 F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds//2.4e-08:97:83//M77184
 F-NT2RP2005407
 15 F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete sequence//0.014:235:62//AC005346
 F-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence//4.0e-107:532:97//AQ055548
 F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence//1.0:239:61//B97865
 20 F-NT2RP2005457//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone)//4.7e-25:245:79//X68647
 F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12 Contains EST, CA repeat, STS, GSS, retroviral sequence, complete sequence//4.6e-111:724:86//AL031679
 F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence//6.5e-18:152:75//AC006116
 25 F-NT2RP2005472//Human DNA sequence from clone 1118D24 on chromosome 1p36.11-36.33. Contains part of a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo) gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Binding Protein 2, TBPII, TNF-R2, CD120B, TNFR). Contains ESTs, STSs, GSSs, genomic marker D1S434 and a ca repeat polymorphism, complete sequence//4.4e-12:89:97//AL031276
 30 F-NT2RP2005476//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence//4.3e-40:463:73//AC004130
 F-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces//3.2e-115:228:99//AC006030
 35 F-NT2RP2005491//HS_2253_A2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=20 Row=M, genomic survey sequence//4.6e-23:234:80//AQ116847
 F-NT2RP2005495
 F-NT2RP2005496//HS_3064_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=15 Row=K, genomic survey sequence//5.3e-90:436:98//AQ143097
 40 F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds//1.4e-63:503:78//M64931
 F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence//0.86:183:63//AC005880
 F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28//1.0:160:65//U82695
 F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.9e-81:444:92//AF092563
 45 F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds//6.9e-18:112:99//AB018307
 F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds//1.1e-06:282:60//M14993
 F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//2.9e-153:747:97//AJ012449
 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//5.9e-130:618:98//AB007963
 50 F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence//3.1e-43:277:89//AF046734
 F-NT2RP2005555//HS_2188_A2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=8 Row=G, genomic survey sequence//8.0e-05:195:65//AQ086723
 F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds//2.5e-44:473:71//AF062529
 55 F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence//0.99:213:65//AC005016
 F-NT2RP2005600//H.sapiens CpG island DNA genomic MseI fragment, clone 172d12, reverse read cpg172d12.rt1a//0.32:134:63//Z57359
 F-NT2RP2005605

- F-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//9.8e-91:447:97//AF062085
F-NT2RP2005622
F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//8.6e-17:411:61//U10556
F-NT2RP2005637//NATI (NATI*10)=acetyltransferase 1 {3' region, polyadenylation polymorphism} [human, unre-
- 5 related Caucasians, mRNA Partial Mutant, 300 nt]//0.22:156:65//S78829
F-NT2RP2005640//Mouse U6 RNA gene.//5.5e-19:249:76//X06980
F-NT2RP2005645//HS_2201_B2_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=2201 Col=14 Row=H, genomic survey sequence.//0.30:159:65//AQ066763
F-NT2RP2005651//H.sapiens DNA sequence.//0.00037:150:66//Z22493
- 10 F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds.//4.7e-07:351:62//AB006626
F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds.//8.2e-98:472:98//AF064605
F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//2.4e-94:462:98//
AF089814
F-NT2RP2005683//HS-1024-B1-H05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone
- 15 Plate=CT 803 Col=9 Row=P, genomic survey sequence.//0.99:156:64//B34405
F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//7.7e-10:328:61//M77836
F-NT2RP2005694
F-NT2RP2005701//Homo sapiens 12p13.3 BAC RPC11-288K12 (Roswell Park Cancer Institute Human BAC Li-
brary) complete sequence.//0.72:160:65//AC005183
- 20 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//1.6e-124:599:97//AB018342
F-NT2RP2005719//R.norvegicus mRNA for metallothionein-III.//0.86:117:64//X89603
F-NT2RP2005722//Human zinc finger protein ZNF136.//2.6e-44:415:77//U09367
F-NT2RP2005723//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//6.9e-15:153:81//
AC002528
- 25 F-NT2RP2005726//Homo sapiens clone DJ0577P23, WORKING DRAFT SEQUENCE, 28 unordered pieces.//
5.1e-41:138:95//AC005627
F-NT2RP2005732//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 291J10, WORKING
DRAFT SEQUENCE.//0.61:303:60//Z93017
F-NT2RP2005741//Homo sapiens PALM gene, exon 1 and joined CDS.//0.52:116:67//Y16270
- 30 F-NT2RP2005748//Human Kox11 mRNA for zinc finger protein, partial.//0.11:136:66//X52342
F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//7.8e-22:134:96//
AF068868
F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.2e-100:486:98//
AF082516
- 35 F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds.//0.00073:425:56//D21853
F-NT2RP2005767//G.gallus PB1 gene.//2.1e-73:544:80//X90849
F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//6.2e-15:153:82//M77836
F-NT2RP2005775//Sus scrofa mRNA for soluble angiotensin-binding protein, complete cds.//1.2e-121:649:88//
D11336
- 40 F-NT2RP2005781//Pseudomonas aeruginosa gene for MexX and MexY, complete cds.//0.96:184:60//AB015853
F-NT2RP2005784//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING
DRAFT SEQUENCE.//1.9e-63:222:96//AL034423
F-NT2RP2005804//Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds.//2.6e-07:232:64//
AF010579
- 45 F-NT2RP2005812
F-NT2RP2005815//Streptomyces sp. gene for alkaline serine protease I.//0.031:358:59//X74103
F-NT2RP2005835//Rattus norvegicus mRNA for p47, complete cds.//2.5e-107:449:91//AB002086
F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//5.1e-05:144:73//Z68873
F-NT2RP2005853//RPC11-24D4.TKBF RPC1-11 Homo sapiens genomic clone RPC1-11-24D4, genomic survey
- 50 sequence.//6.4e-13:130:85//AQ013490
F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//1.7e-174:
829:98//AF092564
F-NT2RP2005859//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 914P20, WORKING
DRAFT SEQUENCE.//0.25:174:62//AL034553
- 55 F-NT2RP2005868//Fugu rubripes GSS sequence, clone 103I24aF4, genomic survey sequence.//7.8e-06:92:79//
AL027276
F-NT2RP2005886//HS_3187_A2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3187 Col=16 Row=G, genomic survey sequence.//7.1e-95:494:95//AQ155885

EP 1 074 617 A2

F-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-32:660:66//L11316
 F-NT2RP2005901//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15b5, reverse read cpG15b5.r11a.//
 0.0026:66:84//Z54729
 F-NT2RP2005908//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC li-
 5 brary) complete sequence.//6.4e-49:481:75//AC004241
 F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//6.6e-61:657:73//U63840
 F-NT2RP2005942//H.sapiens PAP mRNA.//1.6e-46:618:67//X76770
 F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence.//1.0e-48:533:
 71//AC005207
 10 F-NT2RP2006023//HS_3048_A1_A11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3048 Col=21 Row=A, genomic survey sequence.//2.1e-25:167:91//AQ126553
 F-NT2RP2006038//CIT-HSP-384K4.TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey se-
 quence.//3.9e-06:102:74//B51912
 F-NT2RP2006043//Human intercrine-alpha (hIRH) mRNA, complete cds.//1.9e-05:418:59//U19495
 15 F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55.//0.0035:226:65//
 AF016861
 F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5.//3.9e-11:121:85//D17047
 F-NT2RP2006071
 F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete sequence.//0.46:264:59//
 20 AF027207
 F-NT2RP2006100//Human Chromosome X, complete sequence.//3.2e-94:488:95//AC004073
 F-NT2RP2006103//HS_2254_A2_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2254 Col=4 Row=G, genomic survey sequence.//5.7e-27:156:96//AQ129602
 F-NT2RP2006106//Human Chromosome 11 pac pDJ1173a5, complete sequence.//11.2e-62:655:71//AC000378
 25 F-NT2RP2006141//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING
 DRAFT SEQUENCE.//1.2e-69:316:98//AL034405
 F-NT2RP2006166//Homo sapiens chromosome 4 clone B32I8, complete sequence.//3.1e-45:387:81//AC004063
 F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase Lec4A cell line point mutant mR-
 NA, complete cds.//0.99:111:73//U62587
 30 F-NT2RP2006186//Homo Sapiens mRNA for KIAA0654 protein, partial cds.//7.8e-113:567:96//AB014554
 F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence.//2.8e-28:718:62//AC005232
 F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66
 unordered pieces.//6.5e-83:239:94//AC006057
 F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.4e-116:618:93//X96484
 35 F-NT2RP2006237//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey se-
 quence.//2.0e-18:118:97//AQ012480
 F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//7.6e-102:635:86//
 U49055
 F-NT2RP2006258//RPCI11-9N9.TP RPCI-11 Homo sapiens genomic clone RPCI11-9N9, genomic survey se-
 40 quence.//8.6e-05:181:63//B71615
 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//0.44:111:71//X97630
 F-NT2RP2006275//Pseudorabies virus UL[5,6,7,8,8.5,9,10,11,12,13] genes.//2.0e-05:501:59//X97257
 F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.7e-138:679:97//AF035262
 F-NT2RP2006320//P.falciparum pfmdr1 gene.//0.00013:425:60//X56851
 45 F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.1e-19:545:62//
 AC003973
 F-NT2RP2006323//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745I14, WORKING
 DRAFT SEQUENCE.//8.9e-18:131:90//AL033532
 F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//6.2e-125:602:
 50 98//AC004893
 F-NT2RP2006334//Homo sapiens chromosome 19, cosmid R27139, complete sequence.//2.1e-06:241:65//
 AC005514
 F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic survey sequence.//7.8e-06:148:
 70//AL029590
 55 F-NT2RP2006393//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and
 pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//6.8e-06:167:70//AL022727
 F-NT2RP2006436//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING
 DRAFT SEQUENCE.//4.2e-92:363:84//AL023808

F-NT2RP2006441
F-NT2RP2006454//Sequence 8 from Patent WO9517522 //2.9e-06:180:66//A45338
F-NT2RP2006456
F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein //3.4e-148:545:98//AJ006266
5 F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons encoding ch1-ch4 and secretion domains, partial cds //0.061:201:66//U50149
F-NT2RP2006472
F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism,
10 complete sequence //8.8e-10:273:66//Z93929
F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene, exon 6 //0.71:174:59//U40965
F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds //6.6e-114:669:90//AF038966
F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone B2-1 //6.0e-26:
15 503:63//M20855
F-NT2RP2006573//Mollusca contagiosum virus subtype 1, complete genome //0.44:134:71//U60315
F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033 //5.0e-16:140:85//U50537
F-NT2RP3000002//***ALU WARNING: Human Alu-Sc subfamily consensus sequence //3.8e-32:214:89//U14571
F-NT2RP3000003//Homo sapiens mRNA for histone deacetylase-like protein (JM21) //5.8e-136:637:98//
20 AJ011972
F-NT2RP3000046//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds //5.4e-05:571:60//L14320
F-NT2RP3000047
F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9 //1.0e-67:626:74//
25 M27877
F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence //3.5e-10:394:64//AC001227
F-NT2RP3000068
F-NT2RP3000072//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence //1.0:301:61//AC004746
F-NT2RP3000080//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102D24, WORKING
30 DRAFT SEQUENCE //1.9e-44:297:79//AL021391
F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds //4.5e-33:528:65//U12536
F-NT2RP3000092//RPCI-11-22M5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22M5, genomic survey sequence //3.3e-27:157:97//B84237
35 F-NT2RP3000109//Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds //0.92:185:64//L29260
F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence //1.2e-112:286:89//AC005189
F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds //9.0e-181:849:98//AB011164
40 F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.264_B_14, complete sequence //4.2e-24:155:94//AC005884
F-NT2RP3000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 500L14, WORKING DRAFT SEQUENCE //7.2e-43:269:81//AL023583
F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9 //0.098:405:57//L39063
45 F-NT2RP3000207//Drosophila melanogaster DNA sequence (P1 DS00164 (D269)), complete sequence //0.96:608:55//AC004716
F-NT2RP3000220
F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds //2.0e-18:509:58//AF059569
50 F-NT2RP3000235//Mouse Cosmid ma53a016 from 14D1-D2, complete sequence //3.5e-05:224:65//AC004101
F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds //2.1e-109:691:86//D86972
F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence //0.20:119:68//Z70213
F-NT2RP3000252//Homo sapiens cosmid 1F1, complete sequence //9.8e-78:174:88//AF065393
F-NT2RP3000255
55 F-NT2RP3000267
F-NT2RP3000299//Mus musculus Crk-associated substrate (Cas-b) mRNA, complete cds //5.9e-48:374:82//U48853
F-NT2RP3000312//Fruit fly (D.melanogaster) Glued mRNA, complete cds //4.9e-22:583:63//J02932

- F-NT2RP3000320//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//4.4e-06:87:88//AQ047107
- F-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//5.5e-26:283:79//U78090
- 5 F-NT2RP3000333//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 973M2, WORKING DRAFT SEQUENCE.//1.0:309:60//AL033533
- F-NT2RP3000341//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//6.7e-42:465:74//Z97181
- F-NT2RP3000348
- 10 F-NT2RP3000350//Homo sapiens cosmid 1F1, complete sequence.//3.4e-79:174:88//AF065393
- F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//2.2e-127:816:85//M25757
- F-NT2RP3000361//Schizosaccharomyces pombe DNA for pre-mRNA splicing factor, complete cds.//0.0075:288:58//D83743
- 15 F-NT2RP3000366//Mus musculus ras-related protein (rab18) mRNA, complete cds.//7.1e-134:693:94//L04966
- F-NT2RP3000393//Rattus norvegicus mRNA for GABA-B R2 receptor.//0.049:308:60//AJ011318
- F-NT2RP3000397//S.cerevisiae chromosome VII reading frame ORF YGL120c.//0.00012:441:58//Z72642
- F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//5.0e-174:841:97//AF071185
- F-NT2RP3000418//Homo sapiens chromosome 17, clone hRPK.1053_B_8, complete sequence.//7.9e-53:817:68//AC006083
- 20 F-NT2RP3000433//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//6.1e-31:590:63//AL031681
- F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22aB10, genomic survey sequence.//4.0e-19:169:81//AL026471
- 25 F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//2.4e-41:459:65//Z84488
- F-NT2RP3000449//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//1.1e-100:365:87//AL031650
- F-NT2RP3000451//HS_2024_A1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2024 Col=19 Row=1, genomic survey sequence.//0.011:367:57//AQ229420
- 30 F-NT2RP3000456//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//1.5e-89:458:96//AQ055548
- F-NT2RP3000484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90L6, WORKING DRAFT SEQUENCE.//0.043:147:70//Z97353
- 35 F-NT2RP3000487//H.sapiens CpG island DNA genomic MseI fragment, clone 11b11, forward read cpg11b11.ft1a.//1.7e-11:96:92//Z64440
- F-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X16667
- F-NT2RP3000526//Homo sapiens full-length insert cDNA clone YZ38E04.//4.1e-30:283:76//AF086071
- F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966
- 40 F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//1.9e-14:220:70//AF061260
- F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//0.00019:361:60//AC002554
- F-NT2RP3000561//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//9.0e-171:827:98//AC006012
- 45 F-NT2RP3000562
- F-NT2RP3000578//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271
- F-NT2RP3000582//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//B73597
- 50 F-NT2RP3000584
- F-NT2RP3000590//H.sapiens CpG island DNA genomic MseI fragment, clone 170d7, forward read cpg170d7.ft1a.//3.0e-22:128:100//Z59723
- F-NT2RP3000592//CIT-HSP-2288J7.TR CIT-HSP Homo sapiens genomic clone 2288J7, genomic survey sequence.//2.2e-78:382:98//B98868
- 55 F-NT2RP3000596//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00076:143:67//AQ109305
- F-NT2RP3000599//Caenorhabditis elegans cosmid T19B10, complete sequence.//1.2e-13:295:66//Z74043

EP 1 074 617 A2

F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.37:520:57//L14320
F-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//8.8e-155:526:97//AC006128
5 F-NT2RP3000622//HS_3213_A2_D02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//4.1e-29:238:85//AQ175104
F-NT2RP3000624//Homo sapiens clone DJ0800G07, complete sequence.//0.47:75:80//AC004890
F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete
10 sequence.//0.078:393:58//AL031313
F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.4e-96:541:79//U71363
F-NT2RP3000644//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.2e-46:421:77//AC005089
F-NT2RP3000661
15 F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.//1.7e-11:292:65//AL022237
20 F-NT2RP3000685//H.sapiens mRNA for novel protein.//2.4e-80:460:92//X99961
F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10F6.//1.0:141:65//Z77872
F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds.//6.1e-20:127:96//D50930
F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//1.1e-46:622:67//AF015264
25 F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//4.7e-37:429:70//U16655
F-NT2RP3000753
F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//2.8e-38:519:69//Z99281
F-NT2RP3000815//HS_2237_A2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic survey sequence.//0.79:151:61//AQ067252
30 F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds.//0.36:378:58//L39387
F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds.//0.0025:291:62//U02513 F-NT2RP3000836//Mouse complement factor H-related protein mRNA, complete cds, clone 9C4.//0.69:563:57//M29009
35 F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs, polymorphic CA repeat, CpG island, CpG island genomic fragments.//2.1e-46:666:68//Z86062
F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequence.//3.4e-92:193:93//AC005581
40 F-NT2RP3000847//Human HepG2 3' region cDNA, clone hmd5d02.//3.4e-32:261:81//D16938
F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.1e-44:358:81//AC005082
F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome 1q24. Contains the LNHR (SELL) gene coding for Lymph Node Homing Receptor (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte surface antigen Leu-8, TQ1, GP90-MEL, LECAM1 Leukocyte-Endothelial Cell Adhesion Molecule 1, CD62L). Contains the SELE gene coding for E-Selectin precursor (CD62E, ELAM-1 Endothelial Leukocyte Adhesion Molecule 1, LECAM-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknown gene with homology to predicted yeast, plant and worm proteins. Contains ESTs and STSs, complete sequence.//4.4e-123:150:98//AL021940
45 F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, genomic survey sequence.//0.016:185:65//B60831
F-NT2RP3000865
F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//2.0e-29:766:60//U53445
50 F-NT2RP3000869//H.sapiens gene for plectin.//1.1e-12:700:60//Z54367
F-NT2RP3000875//HS_2236_B1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2236 Col=19 Row=N, genomic survey sequence.//0.98:153:68//AQ154007
F-NT2RP3000901//Human herpesvirus 2 glycoprotein B precursor (UL27) gene, complete cds.//0.44:213:65//

AF021340
 F-NT2RP3000904//Rat Na⁺ channel mRNA, 3' end.//3.6e-106:505:99//M27223
 F-NT2RP3000917//Mouse mRNA for Dhml protein, complete cds.//3.1e-132:691:93//D38517
 F-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//
 5 3.2e-97:585:88//AF015264
 F-NT2RP3000968//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//5.8e-70:181:
 89//U91326
 F-NT2RP3000980//R.norvegicus CYP3A1 gene, 5' flanking region.//6.1e-26:507:66//X98335
 F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone
 10 Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529
 F-NT2RP3001004//H.sapiens CpG island DNA genomic MseI fragment, clone 39c1, reverse read cpg39c1.r11a./
 15.9e-27:150:99//Z60925
 F-NT2RP3001007//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.11:
 610:57//AC006039
 F-NT2RP3001055//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORK-
 15 ING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653
 F-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//1.4e-49:437:77//X78927
 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//8.4e-50:534:74//
 AF060219
 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds.//1.2e-14:474:60//AB018325
 F-NT2RP3001096//CIT-HSP-2305P8.TF CIT-HSP Homo sapiens genomic clone 2305P8, genomic survey se-
 quence.//3.4e-37:222:93//AQ021278
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712:64//D86969
 F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma
 25 (polg) gene, complete sequence.//2.7e-116:186:99//AC005317
 F-NT2RP3001111
 F-NT2RP3001113//Human DNA sequence from cosmid U157D4, between markers DXS366 and DXS87 on chro-
 mosome X.//2.4e-05:702:58//Z68871
 F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.9e-170:821:98//
 30 AC005189
 F-NT2RP3001116//HS_3075_A1_F01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3075 Col=1 Row=K, genomic survey sequence.//7.3e-49:290:92//AQ120581
 F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from
 gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island,
 35 complete sequence.//1.4e-121:598:97//AL031864
 F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687:75//U09367
 F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39, UL40 and UL41.//6.8e-05:344:
 64//Z49078
 F-NT2RP3001133//Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds.//0.00021:529:60//
 40 AF027735
 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.6e-179:851:98//AB018305
 F-NT2RP3001147//RPCI11-3M16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-3M16, genomic survey se-
 quence.//2.1e-15:106:96//B48859
 F-NT2RP3001150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING
 45 DRAFT SEQUENCE.//2.0e-159:418:95//AL034379
 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:891:98//AJ006266
 F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.1-41 Contains GSS, com-
 plete sequence.//1.1e-69:207:97//AL034351
 F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING
 50 DRAFT SEQUENCE, 9 unordered pieces.//0.16:475:58//AC005507
 F-NT2RP3001216//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-
 05:561:56//AC004845
 F-NT2RP3001221
 F-NT2RP3001232//Mouse mRNA for serine protease PC6, complete cds.//1.0e-11:120:87//D12619
 55 F-NT2RP3001236
 F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule-associated protein.//3.9e-19:501:61//X51396
 F-NT2RP3001245//CITBI-E1-2505C1.TF.1 CITBI-E1 Homo sapiens genomic clone 2505C1, genomic survey se-
 quence.//8.5e-70:337:100//AQ242007

- F-NT2RP3001253//CITBI-E1-2505N14.TR CITBI-E1 Homo sapiens genomic clone 2505N14, genomic survey sequence.//0.83:235:60//AQ260430
- F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds.//3.8e-47:761:64//AB018269
- F-NT2RP3001268//Homo sapiens zinc finger protein (HZF6) mRNA, 5' UTR and partial cds.//2.3e-64:618:72//AF027513
- 5 F-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//2.6e-99:669:83//Y18101
- F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//0.99:400:58//U07561
- 10 F-NT2RP3001281//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence.//5.9e-39:304:70//AC005837
- F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds.//7.6e-47:544:69//D87457
- F-NT2RP3001307//Ambystoma tigrinum RPE65 protein mRNA, complete cds.//2.4e-27:547:63//AF047465
- F-NT2RP3001318//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00022:624:60//AC004709
- 15 F-NT2RP3001325//Caenorhabditis elegans cosmid F36H12.//0.25:523:59//AF078790
- F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds.//5.1e-29:345:73//D86966
- F-NT2RP3001339//Rattus norvegicus mytonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds.//1.2e-151:821:91//AF021935
- 20 F-NT2RP3001340//Homo sapiens HMGB box factor SOX-13 mRNA, complete cds.//5.3e-27:247:81//AF083105
- F-NT2RP3001355//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-16:130:76//AC000052
- F-NT2RP3001356
- F-NT2RP3001374
- 25 F-NT2RP3001383//Homo sapiens DNA sequence from PAC 140C12 on chromosome 6q26-q27.//0.00082:365:61//AL008628
- F-NT2RP3001384//Homo sapiens HRIHFB2018 mRNA, partial cds.//6.4e-157:743:98//AB015332
- F-NT2RP3001392//Human DNA sequence from PAC 302D9 on chromosome 22q11.2-qter. Contains STS, complete sequence.//0.045:359:61//Z82198
- 30 F-NT2RP3001396//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.3e-16:336:65//AC004296
- F-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.1e-100:711:82//U49046
- F-NT2RP3001399//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//5.4e-20:245:73//AC005521
- 35 F-NT2RP3001407//RPCI11-41A20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41A20, genomic survey sequence.//0.051:306:59//AQ029031
- F-NT2RP3001420//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.90:170:65//AL021327
- F-NT2RP3001426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//2.9e-89:138:98//AL031447
- 40 F-NT2RP3001427//CIT-HSP-2302H24.TF CIT-HSP Homo sapiens genomic clone 2302H24, genomic survey sequence.//8.1e-36:212:94//AQ020997
- F-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//8.5e-73:431:91//U69668
- 45 F-NT2RP3001432//HS_3032_B1_A03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=B, genomic survey sequence.//0.00024:111:76//AQ096619
- F-NT2RP3001447
- F-NT2RP3001449//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs,
- 50 complete sequence.//2.1e-105:223:99//AL031282
- 55 F-NT2RP3001453//Ralstonia sp. E2 positive phenol-degradative gene regulator (poxR), phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds.//0.75:349:59//AF026065

F-NT2RP3001457
 F-NT2RP3001459
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds//1.3e-08:168:70//
 AF072836
 5 F-NT2RP3001490
 F-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//1.0e-26:191:90//U13395
 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//
 8.5e-171:804:98//AF064801
 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete, cds//8.9e-140:743:
 10 91//U36499
 F-NT2RP3001529//Streptomyces griseus DNA for ribosoma protein L21, ribosomal protein L27, Obg, complete
 cds//2.1e-14:517:59//D87916
 F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic survey sequence//4.7e-05:217:
 63//AF078176
 15 F-NT2RP3001554//Rattus norvegicus microtubule-associated protein 1A MAP1A (Mtap-1) mRNA, complete cds//
 4.3e-17:332:67//M83196
 F-NT2RP3001580//RPC111-91E19.TV RPC111 Homo sapiens genomic clone R-91E19, genomic survey se-
 quence//4.2e-15:110:91//AQ281332
 F-NT2RP3001587//S.pombe chromosome II cosmid c16H5//6.6e-28:491:64//AL022104
 20 F-NT2RP3001589//RPC111-68M15.TK RPC111 Homo sapiens genomic clone R-68M15, genomic survey se-
 quence//8.7e-108:517:98//AQ237629
 F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete
 sequence//1.0e-09:257:65//AC004674
 F-NT2RP3001608//Methylococcus capsulatus methane monooxygenase component A alpha chain, methane mo-
 25 nooxygenase A beta chain and methane monooxygenase component C genes, complete cds//0.59:450:57//
 M90050
 F-NT2RP3001621//Human DNA sequence from clone 24c18 on chromosome 6p21.31-22.2 Contains zinc finger
 protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST,
 STS, GSS, complete sequence//1.8e-42:278:79//AL021808
 30 F-NT2RP3001629
 F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein//1.5e-63:276:97//AJ130978
 F-NT2RP3001642//Caenorhabditis elegans cosmid F45E6, complete sequence//0.018:127:66//Z68117
 F-NT2RP3001646
 F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.4e-171:816:98//AJ012449
 35 F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protein (Scm) mRNA, complete cds//1.6e-
 38:542:66//U49793
 F-NT2RP3001676//HS_3090_B1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3090 Col=7 Row=D, genomic survey sequence//3.1e-07:333:64//AQ123250
 F-NT2RP3001678//Drosophila melanogaster; Chromosome 3L; Region 63C5-63D3; P1 clone DS01859, WORK-
 40 ING DRAFT SEQUENCE, 6 unordered pieces//1.0:539:57//AC004358
 F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and
 non-small cell lung cancer, segment 3/11//2.8e-130:355:96//AB020860
 F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds//
 2.1e-37:512:70//AF059273
 45 F-NT2RP3001690//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey se-
 quence//2.8e-19:123:95//AQ012480
 F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds//9-4e-11:167:74//D31962
 F-NT2RP3001708//H.sapiens CpG island DNA genomic MseI fragment, clone 4g7, reverse read cpg4g7.rt1d//
 1.3e-17:113:97//Z61312
 50 F-NT2RP3001712//M.musculus mRNA for HP1-BP74 protein//2.2e-95:601:88//X99642
 F-NT2RP3001716
 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-159:
 565:97//AF054177
 F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2)-mRNA, partial cds//1.7e-132:786:
 88//AF008554
 55 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//3.9e-104:811:78//D50918
 F-NT2RP3001739//Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete se-
 quence//6.5e-07:178:69//AC000097

- F-NT2RP3001752//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence//5.2e-31:311:77//AL031311
- F-NT2RP3001753//Sequence 29 from patent US 5658882//0.11:513:58//I62381
- F-NT2RP3001764//Sequence 6 from Patent WO9706245//6.4e-47:673:66//A59888
- 5 F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10//0.078:290:63//U39644
- F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//2.8e-151:710:98//AB007928
- F-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds//1.2e-26:213:85//U13262
- F-NT2RP3001799//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE//8.4e-51:168:95//AL031284
- 10 F-NT2RP3001819//S.glaucescens genes strU, strX, strV and strW, for 5'-hydroxystreptomycin production and transport polypeptides//0.084:526:58//X89010
- F-NT2RP3001844//HS_3110_B1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=19 Row=J, genomic survey sequence//1.5e-40:232:82//AQ140433
- 15 F-NT2RP3001854//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces//0.14:452:58//AC005505
- F-NT2RP3001855//Mus musculus homeobox protein PKNOX1 (Pknx1) mRNA, complete cds//2.7e-39:575:67//AF061270
- F-NT2RP3001857//M.musculus tex292 mRNA (5'region)//8.7e-07:106:81//X80434
- 20 F-NT2RP3001896
- F-NT2RP3001898//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 163G9, WORKING DRAFT SEQUENCE//0.094:456:60//AL008733
- F-NT2RP3001915//Caenorhabditis elegans cosmid C12D8, complete sequence//0.58:482:56//Z73969
- F-NT2RP3001926//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE//0.42:401:58//AL034557
- 25 F-NT2RP3001929//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence//3.1e-28:263:77//AC004651
- F-NT2RP3001931
- F-NT2RP3001938//CIT-HSP-2165E8.TR CIT-HSP Homo sapiens genomic clone 2165E8, genomic survey sequence//3.6e-24:182:91//B95475
- 30 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//1.8e-165:815:96//AB014575
- F-NT2RP3001944
- F-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces//4.8e-62:304:89//AC005844
- 35 F-NT2RP3001989//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds//8.2e-10:564:60//AF030694
- F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs//2.5e-57:361:80//Z83822
- 40 F-NT2RP3002004//Sequence 3 from patent US 5798245//1.6e-26:104:100//AR025386
- F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence//0.0053:633:58//AC004137
- F-NT2RP3002014//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence//1.3e-32:334:68//AC004640
- 45 F-NT2RP3002033//H.sapiens DNA sequence//0.012:214:63//Z22493
- F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin//8.7e-116:713:86//X53773
- F-NT2RP3002054//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162//1.6e-12:613:60//AL021841
- 50 F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X//0.17:566:59//Z77249
- F-NT2RP3002057//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces//3.3e-24:167:82//AC005682
- F-NT2RP3002062
- F-NT2RP3002063//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4//0.24:508:58//AJ235272
- 55 F-NT2RP3002081//HS_2001_B1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence//9.7e-22:155:90//AQ218494
- F-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-

- plete sequence//9.6e-66:562:77//AC006210
 F-NT2RP3002102//CIT-HSP-2307B10.TR CIT-HSP Homo sapiens genomic clone 2307B10, genomic survey sequence//5.9e-16:214:74//AQ018040
 F-NT2RP3002108
 5 F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence//7.6e-29:414:68//AC004020
 F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (pltB) and polyketide synthase type I (pltC) genes, complete cds//0.96:434:60//AF003370
 F-NT2RP3002147//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329F2, WORKING
 10 DRAFT SEQUENCE//1.3e-63:380:91//AL031710
 F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence//9.9e-60:315:80//U95742
 F-NT2RP3002163
 F-NT2RP3002165//M.musculus HCNGP mRNA//1.4e-142:867:87//X68061
 15 F-NT2RP3002166//Homo sapiens chromosome X, clone hCIT.200_L_4, complete sequence//0.090:394:59//AC006121
 F-NT2RP3002173//HS_3062_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=9 Row=N, genomic survey sequence//3.3e-101:509:96//AQ193219
 F-NT2RP3002181//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence//4.5e-106:432:84//AL021808
 20 F-NT2RP3002244//Homo sapiens chromosome 19, cosmid R27377, complete sequence//0.63:353:60//AC005321
 F-NT2RP3002248//HS_3029_A1_D10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=19 Row=G, genomic survey sequence//3.5e-10:125:79//AQ094880
 F-NT2RP3002255//Bovine herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5' end//5.6e-09:629:59//L14321
 F-NT2RP3002273//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence//4.9e-35:366:74//B03004
 30 F-NT2RP3002276//B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex//0.023:326:60//X64898
 F-NT2RP3002303//Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome//3.8e-12:643:57//AE000810
 F-NT2RP3002304//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING
 35 DRAFT SEQUENCE, 3 unordered pieces//1.6e-09:490:60//AC005504
 F-NT2RP3002330//Human DNA sequence from cosmid L58b6, Huntington's Disease Region, chromosome 4p16.3, containing STS matches//1.9e-93:572:88//Z49862
 F-NT2RP3002343//HS_3010_A2_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=16 Row=C, genomic survey sequence//9.0e-75:373:97//AQ119068
 40 F-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15)//4.9e-64:588:75//X16396
 F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene, alternatively spliced form//1.3e-164:770:98//Y16355
 F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4e-190:911:98//AB018331
 45 F-NT2RP3002399
 F-NT2RP3002402//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds//7.2e-25:249:79//D89340
 F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.2e-138:649:99//AB014578
 F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP Homo sapiens genomic clone 367N3, genomic survey sequence//5.0e-18:115:96//B78927
 50 F-NT2RP3002501//Caenorhabditis elegans cosmid K01C8, complete sequence//0.00020:170:65//Z49068
 F-NT2RP3002512//Homo sapiens clone 664 unknown mRNA, partial sequence//1.6e-59:308:97//AF091088
 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//1.4e-144:763:93//U35246
 F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.8e-178:833:98//AB018272
 55 F-NT2RP3002549//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces//4.7e-26:123:72//AC004821
 F-NT2RP3002566//Streptomyces viridifaciens sigma factor (hrdD) gene, complete cds//0.76:459:59//U60418
 F-NT2RP3002587//Homo sapiens chromosome Y, clone 264.M.20, complete sequence//4.6e-13:199:76//

- AC004617
 F-NT2RP3002590//*Porphyra purpurea* chloroplast, complete genome.//0.88:284:60//U38804
 F-NT2RP3002602//CIT978SK-A-441H11-2.TPB CIT978SK Homo sapiens genomic clone A-441H11, genomic survey sequence.//2.0e-22:140:95//B68331
- 5 F-NT2RP3002603
 F-NT2RP3002628//*C.acetobutylicum* dnaJ and orfB genes.//2.0e-05:333:60//X69050
 F-NT2RP3002631
 F-NT2RP3002650//*Mus musculus* mRNA for cartilage-associated protein (CASP).//1.5e-20:641:62//AJ006469
 F-NT2RP3002659//Bovine herpesvirus type 1 UL22-35 genes.//5.2e-05:621:59//Z78205
- 10 F-NT2RP3002660//Homo sapiens PAC clone DJ1006K12 from 7q31.2-q31, complete sequence.//0.98:453:57//AC004946
 F-NT2RP3002663//Homo sapiens chromosome 19, cosmid F6697, complete sequence.//3.3e-22:407:67//AC006129
 F-NT2RP3002671//*S.pombe* chromosome III cosmid c553.//1.0e-12:336:66//AL023704
- 15 F-NT2RP3002682//*Caenorhabditis elegans* cosmid F17C11, complete sequence.//1.3e-21:448:64//Z72507
 F-NT2RP3002687//CIT978SK-A-789B1.TP CIT978SK Homo sapiens genomic clone A-789B1, genomic survey sequence.//2.5e-25:173:91//B51656
 F-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.2e-73:728:74//D17577
 F-NT2RP3002701//CITBI-E1-2507L14.TF CITBI-E1 Homo sapiens genomic clone 2507L14, genomic survey sequence.//0.0012:55:92//AQ263530
- 20 F-NT2RP3002713
 F-NT2RP3002763//*Caenorhabditis elegans* cosmid T20F10, complete sequence.//0.98:209:63//Z81594
 F-NT2RP3002770
 F-NT2RP3002785//Homo sapiens laminin beta-4 chain precursor (LAMB4) mRNA, alternatively spliced short variant, partial cds.//0.78:515:57//AF029325
- 25 F-NT2RP3002799//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//1.9e-21:167:79//AL022718
- 30 F-NT2RP3002810//Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.//0.32:187:66//AC005549
 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds.//6.9e-54:615:70//AF004715
 F-NT2RP3002861//*Caenorhabditis elegans* cosmid M03F4.//4.2e-05:226:65//U64601
 F-NT2RP3002869//*Mus musculus* semaphorin VIa mRNA, complete cds.//2.0e-93:638:83//AF030430
- 35 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds.//8.5e-89:557:88//AB001895
 F-NT2RP3002877//Homo sapiens chromosome 12p13.3 clone RPC11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//7.9e-12:160:78//AC006087
 F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//5.7e-180:853:98//AB018314
 F-NT2RP3002911//RPC11-24N15.TPC RPC1-11 Homo sapiens genomic clone RPC1-11-24N15, genomic survey sequence.//2.3e-13:442:61//B88815
- 40 F-NT2RP3002948//, complete sequence.//2.2e-110:637:91//AC005500
 F-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.7e-166:793:98//AC005754
 F-NT2RP3002955//Human HepG2 partial cDNA, clone hmd3c02m5.//0.00011:61:95//D17024
- 45 F-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.2e-128:808:85//D30666
 F-NT2RP3002972//H.sapiens (xs168) mRNA, 381bp.//1.5e-43:312:85//Z36820
 F-NT2RP3002978//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00044:527:57//AC005505
- 50 F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence.//0.92:341:60//AC001644
 F-NT2RP3002988//HIS_3015_A1_B07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=13 Row=C, genomic survey sequence.//4.4e-05:379:58//AQ091708
 F-NT2RP3003008//*Mus musculus* major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.4e-72:197:79//AF109905
- 55 F-NT2RP3003032//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 3-80, complete sequence.//1.6e-08:809:58//AL010153
 F-NT2RP3003059//*Rattus norvegicus* potassium channel regulator 1 mRNA, complete cds.//4.1e-111:804:81//U78090

- F-NT2RP3003061//Human mRNA for ankyrin (variant 2.1)//1.4e-12:633:59//X16609
 F-NT2RP3003068//Human BAC clone RG264L19 from 7p15-p21, complete sequence//0.034:282:60//AC002410
 F-NT2RP3003071//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read
 cpg13d12.r11c.//6.8e-15:95:100//Z64565
- 5 F-NT2RP3003078
 F-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds//8.1e-72:732:71//D88315
 F-NT2RP3003121
 F-NT2RP3003133//Homo sapiens chromosome 19, cosmid.R30385, complete sequence//3.5e-12:168:76//
 AC004510
- 10 F-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds//4.0e-148:908:87//
 D12646
 F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds//2.0e-31:658:63//
 U17995
 F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds//3.5e-22:430:63//AF017639
- 15 F-NT2RP3003150
 F-NT2RP3003157//HS_3055_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3055 Col=9 Row=N, genomic survey sequence//1.9e-92:493:94//AQ155489
 F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete
 cds//8.6e-06:228:65//AF064868
- 20 F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein//7.4e-73:737:71//X78933
 F-NT2RP3003197
 F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds//
 4.1e-48:640:67//AF015264
 F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence//0.0033:69:81//U31059
- 25 F-NT2RP3003210//Homo sapiens SYBL1 gene//1.1e-34:430:70//AJ004799
 F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds//6.3e-75:
 776:74//U20286
 F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein//1.8e-62:575:74//AJ006064
 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//3.7e-128:617:98//AF055460
- 30 F-NT2RP3003251//H.sapiens Staf50 mRNA//3.5e-67:651:76//X82200
 F-NT2RP3003264//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING
 DRAFT SEQUENCE, 8 unordered pieces//0.015:473:58//AC004153
 F-NT2RP3003278//H.sapiens CpG island DNA genomic MseI fragment, clone 28b4, forward read cpg28b4.ft1a.//
 4.0e-27:174:93//Z60555
- 35 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//1.3e-131:694:93//L36983
 F-NT2RP3003290//Homo sapiens nickel-specific induction protein (Cap43) mRNA, complete cds//1.7e-64:662:
 71//AF004162
 F-NT2RP3003301//Spinacia oleracea mRNA for ATP-dependent protease Lon, complete cds//4.9e-37:682:64//
 D85610
- 40 F-NT2RP3003302//Homo sapiens, clone hRPK.15_A_1, complete sequence//4.6e-95:680:82//AC006213
 F-NT2RP3003311//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete se-
 quence//1.0:191:62//AC004527
 F-NT2RP3003313//Streptomyces coelicolor cosmid 5A7.//0.0084:403:61//AL031107
 F-NT2RP3003327//H.sapiens Staf50 mRNA//2.5e-29:253:67//X82200
- 45 F-NT2RP3003330
 F-NT2RP3003344
 F-NT2RP3003346//Homo sapiens chromosome 17, clone hRPK.795_F_17, complete sequence//9.0e-41:296:
 84//AC005284
 F-NT2RP3003353//Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a
 BAC end-sequence (GSS).//0.047:404:60//AL021069
- 50 F-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces//
 8.3e-122:632:96//AC005519
 F-NT2RP3003384//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unor-
 dered pieces//0.0036:127:74//AC000360
- 55 F-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds//2.0e-110:843:79//U09874
 F-NT2RP3003403//Human Chromosome X, complete sequence//7.5e-21:647:61//AC002407
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//1.0e-20:430:
 63//U90653

F-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//4.2e-139:524:90//
 AF071317
 F-NT2RP3003427//HS-1051-A1-D03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone
 Plate=CT 773 Col=5 Row=G, genomic survey sequence.//8.8e-18:111:97//B40173
 5 F-NT2RP3003433//HS_2219_B2_A11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2219 Col=22 Row=B, genomic survey sequence.//1.2e-57:410:83//AQ145866
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.2e-181:853:98//
 AF004828
 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.6e-173:826:98//AB018268
 10 F-NT2RP3003491//CIT-HSP-2344O1.TR CIT-HSP Homo sapiens genomic clone 2344O1, genomic survey se-
 quence.//1.2e-39:213:97//AQ057124
 F-NT2RP3003500//HS_3000_B1_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.025:253:60//AQ090347
 F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (LANL), complete sequence.//0.95:279:
 15 60//AC004234
 F-NT2RP3003552//Homo sapiens clone UWGC:y54c222 from 6p21, complete sequence.//1.8e-88:166:84//
 AC006049
 F-NT2RP3003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING
 DRAFT SEQUENCE.//8.9e-17:245:72//AL031985
 20 F-NT2RP3003564//HS_3141_B1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3141 Col=19 Row=N, genomic survey sequence.//2.7e-79:442:93//AQ187798
 F-NT2RP3003572
 F-NT2RP3003576//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.8e-
 55:275:84//AC005632
 25 F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein.//1.1e-94:488:95//X56387
 F-NT2RP3003621//Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.//6.0e-88:
 463:84//AC004235
 F-NT2RP3003625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 390E6, WORKING
 DRAFT SEQUENCE.//0.98:307:60//AL031600
 30 F-NT2RP3003656
 F-NT2RP3003659//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//
 AL011271
 F-NT2RP3003665//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//0.011:279:65//
 AC002096
 35 F-NT2RP3003672
 F-NT2RP3003680//Drosophila melanogaster; Chromosome 2R; Region 39B1-39B3; P1 clone DS05527, WORK-
 ING DRAFT SEQUENCE, 9 unordered pieces.//3.4e-16:425:64//AC005811
 F-NT2RP3003686//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-27:153:98//AQ136993
 40 F-NT2RP3003701
 F-NT2RP3003716//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.6e-107:
 788:82//U42975
 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//2.3e-148:700:98//AB018300
 F-NT2RP3003746//CIT-HSP-2306A10.TF CIT-HSP Homo sapiens genomic clone 2306A10, genomic survey se-
 45 quence.//0.39:212:61//AQ015785
 F-NT2RP3003795//Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (pos-
 sibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene
 for Synaptogyrin 1A, 1B and 1C (SYNGR1A, SYBGR1B, SYNGR1C), both genes downstream of a putative CpG
 island. Contains ESTs, an STS, GSSs, genomic marker D22S1155 and a ca repeat polymorphism, complete se-
 50 quence.//4.2e-21:445:66//AL022326
 F-NT2RP3003799//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic
 sequence, complete sequence.//1.0:257:63//AF038458
 F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosine-specific protein kinase, com-
 plete cds.//1.2e-63:484:81//M17031
 55 F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//
 AC005321
 F-NT2RP3003809//Bovine herpesvirus 1 complete genome.//7.2e-12:615:60//AJ004801
 F-NT2RP3003819

F-NT2RP3003825
 F-NT2RP3003828//Human rRNA primary transcript internal transcribed spacer 2 (ITS2)//6.2e-16:543:62//X17626
 F-NT2RP3003831//RPCI11-50N15.TJ RPCI11 Homo sapiens genomic clone R-50N15, genomic survey sequence//1.1e-21:174:85//AQ082633
 5 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//8.0e-47:242:98//AF070611
 F-NT2RP3003842//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence//9.7e-25:143:97//AQ195884
 F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.2e-36:335:68//AB018268
 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//4.1e-174:805:99//AB018343
 10 F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds//2.7e-109:709:84//U19181
 F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds//8.9e-11:193:70//U20554
 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//2.6e-47:404:77//AF057358
 15 F-NT2RP3003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces//0.68:597:55//AC005504
 F-NT2RP3003989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404H4, WORKING DRAFT SEQUENCE//0.37:548:56//AL031661
 F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNCG2) mRNA, complete cds//0.021:433:58//U58837
 20 F-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein//1.4e-164:838:94//X84692
 F-NT2RP3004016//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018K9, WORKING DRAFT SEQUENCE//0.00042:356:62//AL031726
 F-NT2RP3004041//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 809F4, WORKING DRAFT SEQUENCE//6.8e-112:627:82//AL022400
 25 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//2.2e-61:774:67//AB002317
 F-NT2RP3004070//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence//7.9e-17:484:62//AL021939
 30 F-NT2RP3004078//M.musculus (BALB/c) MRFX2 mRNA//1.9e-102:684:83//X76089
 F-NT2RP3004093//F24P17-Sp6 IGF Arabidopsis thaliana genomic clone F24P17, genomic survey sequence//0.021:207:63//B09433
 F-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces//3.5e-25:272:77//AC005038
 35 F-NT2RP3004110//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence//8.6e-28:223:73//AC003973
 F-NT2RP3004125//Homo sapiens TTF-1 interacting peptide 20 mRNA, partial cds//2.2e-28:637:63//AF000560
 F-NT2RP3004145
 F-NT2RP3004148
 40 F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//6.5e-120:578:98//AF032900
 F-NT2RP3004189//M.musculus tex292 mRNA (5'region)//1.1e-06:102:82//X80434
 F-NT2RP3004206//D.melanogaster crn mRNA//7.3e-69:715:71//X58374
 F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds//4.8e-42:650:66//D64009
 45 F-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence//8.4e-55:184:84//D42052
 F-NT2RP3004215//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence//0.22:458:60//AC006084
 F-NT2RP3004242//Caenorhabditis elegans cosmid ZK632, complete sequence//1.6e-29:409:69//Z22181
 F-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence//3.6e-117:242:100//AC005385
 50 F-NT2RP3004253//H.sapiens 28S rRNA V8 region (LAN5-6)//2.6e-12:589:59//X69353
 F-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds//1.2e-88:489:91//AF013967
 F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//3.1e-153:733:98//AF088982
 F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//1.3e-24:597:61//AF007871
 55 F-NT2RP3004332
 F-NT2RP3004334//L.esculentum gene for fruit ripening polygalacturonase//0.23:501:57//X80908
 F-NT2RP3004341//Human DNA sequence from clone 503G16 on chromosome 6p23 Contains EST, CpG island, complete sequence//0.0014:198:66//Z93020

EP 1 074 617 A2

F-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877
F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-49:480:75//AC004025
F-NT2RP3004378//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORK-
5 ING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653
F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1.//7.2e-140:804:90//X97249
F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678
F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206
F-NT2RP3004451//RPCI11-51J15.TK RPCI11 Homo sapiens genomic clone R-51J15, genomic survey se-
10 quence.//8.8e-19:180:82//AQ052326
F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917
F-NT2RP3004466//HS_3038_B2_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458
F-NT2RP3004470//H.sapiens CpG island DNA genomic MseI fragment, clone 81a11, reverse read
15 cpg81a11.r11a.//7.0e-25:148:96//Z56029
F-NT2RP3004472//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//
1.6e-20:143:92//AQ052792
F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925
F-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.0e-119:679:90//
20 U47024
F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//7.1e-155:752:97//AB012851
F-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//
4.0e-67:265:84//AC006023
F-NT2RP3004503//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)
25 complete sequence.//1.2e-55:415:78//AC004673
F-NT2RP3004504//M.musculus mRNA for CPEB protein.//2.0e-110:618:91//Y08260
F-NT2RP3004507//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.3e-46:433:76//
AC005328
F-NT2RP3004527//Homo sapiens mRNA; transcriptional unit N144, 5' end.//1.1e-100:508:97//AJ002574
30 F-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.0e-93:442:84//L11316
F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//8.5e-145:679:98//AB014532
F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//2.8e-169:793:98//AB011126
F-NT2RP3004566//Mus musculus kruppel-related zinc finger protein (Emz1) mRNA, complete cds.//6.9e-18:433:
64//AF031955
35 F-NT2RP3004569//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey se-
quence.//5.3e-15:138:84//AQ280780
F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//1.0e-179:860:97//
AF026445
F-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//4.2e-150:711:98//AB007946
40 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//1.1e-158:796:95//AJ006266
F-NT2RP3004617//Homo sapiens clone DJ1152C17, WORKING DRAFT SEQUENCE, 1 unordered pieces.//9.3e-
14:360:65//AC004977
F-NT2RP3004618//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.9e-52:539:
73//AF005355
45 F-NT2RP3004669//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160
nt].//0.046:437:57//S69350
F-NT2RP3004670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING
DRAFT SEQUENCE.//1.9e-05:625:59//Z98882
F-NT2RP4000008//Homo sapiens chromosome X, clone hCIT.200_L_4, complete sequence.//1.5e-155:844:92//
50 AC006121
F-NT2RP4000023//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.//
0.012:417:59//AB012242
F-NT2RP4000035//Homo sapiens BAC clone NH0353P23 from 2, complete sequence.//8.0e-18:242:74//
AC005035
55 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds.//2.1e-81:556:85//AF029761
F-NT2RP4000051//Mus musculus mRNA for cartilage-associated protein (CASP).//1.6e-19:654:63//AJ006469
F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.5e-149:720:97//AJ012449
F-NT2RP4000102//Plasmodium falciparum MAL3P2, complete sequence.//0.28:336:57//AL034558

- F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//4.4e-166:774:99//AB011538
 F-NT2RP4000111//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.6e-137:678:91//X75931
 F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//3.3e-114:548:98//AB007952
 5 F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.2e-104:677:85//U35776
 F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//7.2e-54:327:74//L20681
 F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA, partial sequence.//2.2e-62:360:92//AF091088
 F-NT2RP4000159//RPC111-75N16.TJ RPC111 Homo sapiens genomic clone R-75N16, genomic survey sequence.//2.6e-19:119:98//AQ267551
 10 F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//3.3e-49:683:67//AC006210
 F-NT2RP4000185//Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.//1.1e-99:543:93//U92989
 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.9e-174:825:98//AB014600
 F-NT2RP4000212//, complete sequence.//4.0e-131:233:94//AC005300
 15 F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.8e-161:751:99//AC005261
 F-NT2RP4000218//RPC111-69B7.TJ RPC111 Homo sapiens genomic clone R-69B7, genomic survey sequence.//1.7e-84:413:98//AQ268504
 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470
 20 F-NT2RP4000246//Mus musculus neural variant mena+++ protein (Mena) mRNA, complete cds.//2.1e-120:707:87//U72523
 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//2.8e-128:604:99//AF091092
 F-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.27:124:69//AQ043515
 25 F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-32:619:63//Z71408
 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds.//4.7e-41:685:63//D63481
 F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//6.9e-05:756:59//U59322
 F-NT2RP4000323
 30 F-NT2RP4000355
 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.0e-140:654:99//AB018281
 F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//2.6e-135:649:97//AF044195
 F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//2.0e-23:524:62//AJ235272
 35 F-NT2RP4000376//Sequence 1 from patent US 5580968.//1.6e-115:716:87//I30536
 F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//4.3e-05:450:58//D63850
 F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//9.2e-37:336:69//AC006116
 40 F-NT2RP4000415//Caenorhabditis elegans cosmid C42D8.//0.30:222:60//U56966
 F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4.//1.8e-48:580:69//AL021086
 F-NT2RP4000424//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.6e-42:265:81//AC003101
 45 F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 2370F8, genomic survey sequence.//2.0e-56:287:98//AQ110194
 F-NT2RP4000449//CIT-HSP-2366N18.TR CIT-HSP Homo sapiens genomic clone 2366N18, genomic survey sequence.//2.4e-42:236:95//AQ076183
 F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0.17:158:67//AC003982
 50 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.00034:532:57//Z72499
 F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds.//0.0094:616:58//U10483
 F-NT2RP4000481
 F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150.//5.7e-24:633:60//Z38125
 55 F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//2.4e-62:667:73//X74904
 F-NT2RP4000515
 F-NT2RP4000517//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence.//1.6e-179:851:98//AC006238

- F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//6.7e-33:203:93//AJ010840
 F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk2/tyro3) gene, alternative 5' coding exon 2C.//0.26:162:61//U23720
 F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds.//1.2e-139:809:89//U32498
 5 F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12.//1.0e-06:404:59//AF003386
 F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 DS02109 (D53)), complete sequence.//1.3e-05:498:58//AC002443
 F-NT2RP4000556//Sequence 1 from Patent EP 0285405.//1.2e-18:586:61//I05465
 F-NT2RP4000560//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//2.5e-53:183:82//AF059580
 10 F-NT2RP4000588//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 414D7, WORKING DRAFT SEQUENCE.//0.00062:253:65//AL033543
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//3.2e-138:666:98//AF067730
 15 F-NT2RP4000638//HS_3042_B2_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.0e-06:78:89//AQ099333
 F-NT2RP4000648//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//1.9e-11:104:85//AB017335
 F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.//0.34:350:62//AF100904
 20 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856.//3.3e-167:785:99//AB004852
 F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cds.//3.7e-07:261:65//U61149
 F-NT2RP4000724//Human endogenous retrovirus env mRNA.//9.2e-136:474:89//X82272
 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds.//3.1e-41:350:71//AB011178
 25 F-NT2RP4000737//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//1.0:504:58//L19301
 F-NT2RP4000739//CIT-HSP-2010O22.TR CIT-HSP Homo sapiens genomic clone 2010O22, genomic survey sequence.//1.1e-24:161:93//B57903
 F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence.//0.052:493:58//AC004917
 30 F-NT2RP4000787//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//9.6e-18:259:68//U22818
 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//1.5e-174:816:98//AB007939
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.97:52:92//AC005189
 35 F-NT2RP4000837//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE.//2.1e-128:644:97//AL034420
 F-NT2RP4000839//RPC111-6D8.TP RPC1-11 Homo sapiens genomic clone RPC1-11-6D8, genomic survey sequence.//1.5e-44:281:91//B48216
 F-NT2RP4000855//Rattus norvegicus mRNA for aminopeptidase-B, complete cds.//9.5e-43:722:64//D87515
 40 F-NT2RP4000865//Human zinc finger protein ZNF136.//6.8e-95:415:78//U09367
 F-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//7.0e-87:646:80//AJ001616
 F-NT2RP4000879//N.tabaccum mRNA for ubiquitin activating enzyme E1.//9.0e-17:806:58//Y10804
 F-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//6.8e-153:934:86//D45913
 45 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein.//9.4e-79:584:78//AJ224901
 F-NT2RP4000918//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//2.0e-08:609:58//AC004290
 F-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//3.5e-64:415:87//U42975
 50 F-NT2RP4000927//H.sapiens genomic DNA (chromosome 3; clone NRL062R).//0.75:175:62//X87547
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//3.5e-163:781:97//AF069532
 F-NT2RP4000929//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.94:763:56//AC004688
 55 F-NT2RP4000955//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.0e-128:673:96//AC005519
 F-NT2RP4000973//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.6e-15:255:69//AL032657

EP 1 074 617 A2

F-NT2RP4000975//CIT-HSP-230716.TF CIT-HSP Homo sapiens genomic clone 230716, genomic survey sequence.//6.5e-31:317:79//AQ015742
 F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end.//0.88:54:90//M22942
 F-NT2RP4000984//Rhodobacter sphaeroides mRNA.//0.76:214:64//M83823
 5 F-NT2RP4000989//F.rubripes GSS sequence, clone 011A11aE12, genomic survey sequence.//1.0:149:65//AL010911
 F-NT2RP4000996//Penaeus setiferus microsatellite Pse017 repeat region.//3.3e-08:139:74//AF047358
 F-NT2RP4000997//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//3.6e-126:824:84//AF025424
 10 F-NT2RP4001004
 F-NT2RP4001006//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//1.4e-110:861:78//U83176
 F-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//2.0e-135:789:89//U67140
 15 F-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.7e-120:718:88//U20086
 F-NT2RP4001041//Schizosaccharomyces pombe mRNA, partial cds, clone: SY 0717.//4.1e-22:452:64//D89170
 F-NT2RP4001057
 F-NT2RP4001064//Mus musculus mRNA for cartilage-associated protein (CASP).//1.2e-20:639:62//AJ006469
 20 F-NT2RP4001078//Streptomyces coelicolor cosmid 1C2.//0.0025:474:59//AL031124
 F-NT2RP4001079//Rat alternatively spliced mRNA.//1.4e-141:832:88//M93018
 F-NT2RP4001080//H.sapiens PTB-4 gene for polypirimidine tract binding protein.//9.0e-64:628:70//X65372
 F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//4.7e-84:604:86//AB011164
 F-NT2RP4001095
 25 F-NT2RP4001100//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//9.4e-17:185:79//AQ263402
 F-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//1.0e-143:760:87//M96629
 F-NT2RP4001122
 F-NT2RP4001126//Homo sapiens shox gene, alternatively spliced products, complete cds.//4.2e-17:636:61//U82668
 30 F-NT2RP4001138//Homo sapiens PAC clone DJ1121E10 from 7q21.1-q2, complete sequence.//2.5e-23:408:60//AC004969
 F-NT2RP4001143//Sequence 5 from patent US 5753432.//1.8e-39:276:86//AR008079
 F-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.7e-116:684:89//AC005095
 35 F-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//3.0e-48:581:66//D67067
 F-NT2RP4001150//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.4e-25:193:67//AC004952
 40 F-NT2RP4001159//Human FMR1 gene, 5' end.//0.28:130:66//L19476
 F-NT2RP4001174//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//0.0014:187:67//S74494
 F-NT2RP4001206//Dictyostelium discoideum random slug cDNA19 protein (rscl9) mRNA, partial cds.//0.032:453:58//U82511
 45 F-NT2RP4001207//HS_2248_A1_C03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=5 Row=E, genomic survey sequence.//0.00018:58:94//AQ192358
 F-NT2RP4001210//Homo sapiens chromosome 10 clone CIT987SK:1019O18 map 10p11.2-10p12.1, complete sequence.//0.93:515:58//AC005877
 F-NT2RP4001213//Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant, complete cds.//3.6e-44:187:74//U37251
 50 F-NT2RP4001219//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.3e-15:288:67//AL032657
 F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.2e-26:855:60//AF059569
 F-NT2RP4001235//RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence.//2.7e-15:101:98//B88081
 55 F-NT2RP4001256//Amycolatopsis mediterranei 3-amino-5-hydroxy benzoic acid synthase (rifD) gene, complete cds.//1.0:459:59//U33061
 F-NT2RP4001260//Sequence 2 from Patent WO9601901.//0.0018:246:63//A48324

F-NT2RP4001274//Homo sapiens, complete sequence //2.5e-05:201:67//AC005854
 F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15, genomic survey se-
 quence //3.5e-18:138:92//AQ040728
 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding
 5 mitochondrial protein, complete cds //7.4e-30:535:65//AF043250
 F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5 //3.5e-145:795:91//AJ001119
 F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey se-
 quence //8.4e-16:109:94//B89870
 F-NT2RP4001339//HS_3205_B1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 10 nomic clone Plate=3205 Col=15 Row=J, genomic survey sequence //7.1e-24:305:73//AQ183725
 F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete sequence //1.9e-17:106:91//
 AC004918
 F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase //7.6e-40:631:66//X91011
 F-NT2RP4001351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 184J9, WORKING
 15 DRAFT SEQUENCE //2.7e-30:608:64//AL031428
 F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7 //0.23:540:57//AL031107
 F-NT2RP4001372//RPC111-49L11.TJ RPC111 Homo sapiens genomic clone R-49L11, genomic survey se-
 quence //8.5e-23:129:100//AQ051701
 F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1 //0.15:213:61//X78609
 20 F-NT2RP4001375
 F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311_F_12, complete sequence //7.3e-28:153:
 88//AC005722
 F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence //7.2e-47:518:73//
 AC004691
 25 F-NT2RP4001407//P.falciparum glutamic acid-rich protein gnen, complete cds //0.00079:686:57//J03998
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds //2.0e-76:818:71//D86957
 F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein //3.5e-87:839:73//X78933
 F-NT2RP4001442
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds //0.21:218:63//AB018326
 30 F-NT2RP4001474//Human NotI linking clone 924A058R, genomic survey sequence //7.6e-14:109:90//U49884
 F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds //2.5e-59:480:75//D10523
 F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds //9.7e-39:392:72//
 AF049612
 F-NT2RP4001502//H.sapiens (D8S135) DNA segment containing GT repeat //2.7e-24:147:96//X61693
 35 F-NT2RP4001507//Plasmid pSB24.2 (from S.cyanogenus) neomycin resistance protein gene, complete cds //
 0.87:583:58//M32513
 F-NT2RP4001524//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING
 DRAFT SEQUENCE, 5 unordered pieces //0.93:394:58//AC005308
 F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds //3.1e-143:820:89//
 40 U20086
 F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNR048w //2.2e-05:319:61//Z71663
 F-NT2RP4001551//S.pombe chromosome II p1 p8B7 //0.64:335:60//AL032684
 F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPC111-360E11 (RoSwell Park Cancer Institute Human BAC Li-
 brary) complete sequence //1.0:309:58//AC004806
 45 F-NT2RP4001567//HS_2166_B1_C07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2166 Col=13 Row=F, genomic survey sequence //0.99:188:59//AQ086290
 F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds //7.0e-53:566:72//D79989
 F-NT2RP4001571//RPC111-21F20.TP RPC111 Homo sapiens genomic clone RPC111-21F20, genomic survey
 sequence //2.8e-19:119:97//B85885
 50 F-NT2RP4001574//B.primigenius mRNA for coat protein gamma-cop //5.8e-129:813:85//X92987
 F-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein //3.4e-131:795:86//AJ223830
 F-NT2RP4001592//S.aureus gene for isoleucyl-tRNA synthetase //1.3e-14:663:59//X74219
 F-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore hu-
 man cosmid library) complete sequence //6.4e-10:135:73//AC002364
 55 F-NT2RP4001614//HS_3042_B2_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3042 Col=10 Row=H, genomic survey sequence //3.4e-06:78:89//AQ099333
 F-NT2RP4001634
 F-NT2RP4001638//cSRL-161F1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic

- clone cSRL-161F1, genomic survey sequence.//4.9e-12:144:76//B02870
 F-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//3.8e-69:437:86//Y11092
 F-NT2RP4001656//HS_2013_A1_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2013 Col=1 Row=G, genomic survey sequence.//2.0e-30:207:89//AQ224793
 5 F-NT2RP4001677//Hylobates lar huntingtin gene, partial exon.//0.23:105:71//L49362
 F-NT2RP4001679//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462O23, WORKING
 DRAFT SEQUENCE.//2.7e-45:351:84//AL031431
 F-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.8e-30:163:88//
 U96629
 10 F-NT2RP4001725//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.1e-
 13:402:63//AC004296
 F-NT2RP4001730//RPCI11-37M21.TK RPCI-11 Homo sapiens genomic clone RPCI-11-37M21, genomic survey
 sequence.//0.88:177:67//AQ029840
 F-NT2RP4001739
 15 F-NT2RP4001753//H.sapiens telomeric DNA sequence, clone 12QTEL023, read 12QTELOO023.seq.//4.9e-36:
 192:98//Z96232
 F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//2.3e-140:866:86//L11316
 F-NT2RP4001790//Homo sapiens clone NH0569I24, complete sequence.//1.4e-29:327:74//AC005678
 F-NT2RP4001803
 20 F-NT2RP4001822//Homo sapiens tetraspan TM4SF (TSPAN-4) mRNA, complete cds.//1.0e-16:576:60//
 AF054841
 F-NT2RP4001823//Human DNA sequence from clone 181C9 on chromosome 22q13.2-13.33. Contains a PHAPI2
 Leucine Rich Acidic Nuclear Protein pseudogene, part of a putative novel gene, ESTs, STSs and GSSs, complete
 sequence.//2.1e-08:601:59//Z98743
 25 F-NT2RP4001828
 F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds.//2.2e-53:555:73//D31888
 F-NT2RP4001841
 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds.//1.7e-55:813:65//AB014572
 F-NT2RP4001861//Human simple repeat polymorphism.//0.0014:145:66//M87691
 30 F-NT2RP4001889//HS_2052_B1_H06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2052 Col=11 Row=P, genomic survey sequence.//1.0e-23:187:86//AQ270425
 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//7.3e-76:178:95//
 AC005014
 F-NT2RP4001896//T3B4TFC TAMU Arabidopsis thaliana genomic clone T3B4, genomic survey sequence.//0.99:
 35 354:61//B26193
 F-NT2RP4001901//Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AlsA, Orf8, partial and complete cds.//
 0.031:409:60//AB011413
 F-NT2RP4001927//HS_2216_B1_D03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2216 Col=5 Row=H, genomic survey sequence.//4.9e-32:216:89//AQ184677
 40 F-NT2RP4001938//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.2e-83:709:79//U49046
 F-NT2RP4001946//HS_3021_B2_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3021 Col=20 Row=P, genomic survey sequence.//7.6e-09:120:76//AQ133185
 F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alterna-
 tively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin,
 45 subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs,
 complete sequence.//2.1e-18:421:65//AL022577
 F-NT2RP4001953//CIT-HSP-2294D14.TR CIT-HSP Homo sapiens genomic clone 2294D14, genomic survey se-
 quence.//0.030:358:61//AQ005028
 F-NT2RP4001966//Mus musculus DOC4 (Doc4) mRNA, complete cds.//2.5e-68:812:68//AF059485
 50 F-NT2RP4001975//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence.//1.9e-57:555:75//
 AC003976
 F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic
 clone cSRL-143G4, genomic survey sequence.//8.9e-21:123:98//B01950 F-NT2RP4002047//Saccharomyces
 cerevisiae chromosome XII cosmid 8003.//1.6e-29:520:64//U17243
 55 F-NT2RP4002052//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey se-
 quence.//2.8e-22:137:96//B80243
 F-NT2RP4002058//T20L11-T7 TAMU Arabidopsis thaliana genomic clone T20L11, genomic survey sequence.//
 0.019:141:65//AQ248640

- F-NT2RP4002071//CIT-HSP-2314J9.TF CIT-HSP Homo sapiens genomic clone 2314J9, genomic survey sequence//0.99:163:63//AQ027223
- F-NT2RP4002075//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE//0.15:506:59//Z92841
- 5 F-NT2RP4002078//RPC111-73M20.TJ RPC111 Homo sapiens genomic clone R-73M20, genomic survey sequence//4.8e-21:130:96//AQ269030
- F-NT2RP4002081//F.rubripes GSS sequence, clone 190O22bB9, genomic survey sequence//0.0024:350:60//Z92062
- F-NT2RP4002083//M.musculus tex27 mRNA//8.2e-77:456:89//X80437
- 10 F-NT2RP4002408//Caenorhabditis elegans serine/threonine kinase LET-502 (let-502) mRNA, complete cds//3.7e-18:541:62//U85515
- F-NT2RP4002791
- F-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence//4.7e-39:385:75//AC002383
- 15 F-NT2RP4002905//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence//6.5e-91:672:83//AC004662
- F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds//2.9e-37:193:99//M33197
- F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs//7.9e-51:300:80//Z82901
- 20 F-NT2RP5003477//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces//6.7e-77:150:100//AC000380
- F-NT2RP5003492
- F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSs and CpG island//1.7e-111:623:93//Z81365
- 25 F-NT2RP5003506//H.sapiens CpG island DNA genomic MseI fragment, clone 71h2, reverse read cpg71h2.rt1a//1.4e-49:283:93//Z62703
- F-NT2RP5003512//HS_3084_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence//7.7e-18:117:95//AQ186312
- F-NT2RP5003522//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces//3.8e-101:211:96//AC005236
- 30 F-NT2RP5003524//Homo sapiens beta-spectrin (HSpTB1) gene, exon 14 and partial cds//0.00056:650:57//AF013178
- F-NT2RP5003534//H.sapiens CpG island DNA genomic MseI fragment, clone 14c10, forward read cpg14c10.ft1b//0.00013:70:91//Z54631
- 35 F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//1.2e-67:373:94//AB007934
- F-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence//5.8e-93:518:81//AC005510
- F-OVARC1000006//Gallus gallus histone H2A (H2A-VIII) gene, complete cds//9.1e-56:392:84//U38933
- F-OVARC1000013
- 40 F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//5.6e-170:815:98//AF058922
- F-OVARC1000017//Streptomyces glaucescens tcm operon//0.37:347:60//M80674
- F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//6.8e-36:238:89//AF064603
- F-OVARC1000058
- F-OVARC1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cds//2.5e-36:192:98//U85625
- 45 F-OVARC1000068//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404K8, WORKING DRAFT SEQUENCE//0.14:554:57//AL023883
- F-OVARC1000071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 596C15, WORKING DRAFT SEQUENCE//5.3e-104:197:100//AL031387
- F-OVARC1000085//Human DNA sequence from clone 191N21 on chromosome 6q27 Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA factor (TFIID), proteasome subunit HC5, EST, STS, GSS, complete sequence//1.6e-116:588:96//AL031259
- 50 F-OVARC1000087//HS_2004_B2_E11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence//7.1e-11:94:94//AQ221037
- F-OVARC1000091//nbxb0020P17r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020P17r, genomic survey sequence//5.2e-05:238:64//AQ258489
- 55 F-OVARC1000092//Homo sapiens chromosome Y, clone 264.M.20, complete sequence//1.1e-10:720:58//AC004617
- F-OVARC1000106//HS_3212_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

EP 1 074 617 A2

nomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//9.9e-05:141:73//AQ175369
 F-OVARC1000109
 F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.6e-133:663:96//AF069250
 5 F-OVARC1000114//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1111N9, WORKING DRAFT SEQUENCE.//2.3e-51:547:70//AL022574
 F-OVARC1000133//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.62:349:61//AC005027
 F-OVARC1000139//Caenorhabditis elegans cosmid F09D1.//2.5e-18:314:64//AF040640
 10 F-OVARC1000145//HS_2257_B2_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=22 Row=H, genomic survey sequence.//5.8e-30:203:90//AQ304854
 F-OVARC1000148//CIT-HSP-2345A22.TR CIT-HSP Homo sapiens genomic clone 2345A22, genomic survey sequence.//1.1e-26:146:100//AQ056703
 F-OVARC1000151//Sequence 1 from patent US 5665588.//2.6e-61:677:70//I64695
 15 F-OVARC1000168//Homo sapiens chromosome 19, cosmid R31343, complete sequence.//4.9e-19:381:63//AC005764
 F-OVARC1000191//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//1.3e-06:745:57//AL034557
 F-OVARC1000198//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//6.4e-161:781:97//AC004604
 20 F-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//9.2e-33:511:65//AF068332
 F-OVARC1000212//F.rubripes GSS sequence, clone 185L11aC1, genomic survey sequence.//1.1e-13:139:79//AL019910
 25 F-OVARC1000240//Sequence 1 from patent US 5710024.//1.4e-129:623:98//I81226
 F-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-112:697:87//AF060194
 F-OVARC1000288 2.2e-22:181:83//J00345
 F-OVARC1000302//A-192A9.TP CIT978SK Homo sapiens genomic clone A-192A9, genomic survey sequence.//4.8e-18:110:99//B18003
 30 F-OVARC1000304//Mouse mRNA from Mov10 locus.//5.5e-100:631:85//X52574
 F-OVARC1000309
 F-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.1e-122:325:95//AC005236
 35 F-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.0e-46:339:84//U19614
 F-OVARC1000335//Caenorhabditis elegans cosmid F15B10.//0.020:545:57//AF036696
 F-OVARC1000347//Homo sapiens clone GS051M12, complete sequence.//0.71:252:59//AC005007
 F-OVARC1000384//Homo sapiens expanded SCA7 CAG repeat.//2.2e-09:276:64//AF020275
 40 F-OVARC1000408//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//0.61:343:59//AC003693
 F-OVARC1000411//S.cerevisiae chromosome XI reading frame ORF YKL202w.//0.075:242:60//Z28201
 F-OVARC1000414//Homo sapiens PAC clone DJ0905M06 from 7q31, complete sequence.//0.00088:285:62//AC005166
 45 F-OVARC1000420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 371H6, WORKING DRAFT SEQUENCE.//0.14:487:60//AL031718
 F-OVARC1000427//Homo sapiens clone UWGC:rg041a03 from 7p14-15, complete sequence.//4.9e-30:195:84//AC005826
 F-OVARC1000431//Plasmodium falciparum MAL3P2, complete sequence.//1.3e-05:651:59//AL034558
 50 F-OVARC1000437//Chicken tensin mRNA, complete cds.//9.6e-54:296:78//M74165
 F-OVARC1000440//Human PINCH protein mRNA, complete cds.//2.7e-19:116:99//U09284
 F-OVARC1000442//Human DNA sequence from clone 816K17 on chromosome 20p12.2-13 Contains TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANS-GLUTAMINASE 3), and another member of the Transglutaminase family, complete sequence.//1.0e-21:202:79//AL031678
 55 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.0e-138:566:99//AB014583
 F-OVARC1000461
 F-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//4.7e-

- 124:650:93//AF023451
 F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence//1.0e-15:510:59//AC004221
 F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomic survey sequence//2.5e-06:272:62//AJ227191
 5 F-OVARC1000479//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein)//1.1e-117:652:90//E12829
 F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceeded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs//1.7e-13:709:60//Z99297
 10 F-OVARC1000496//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE//6.0e-23:316:72//AL031733
 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//2.1e-113:539:99//AF051850
 15 F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces//8.0e-149:716:98//AC005024
 F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence//5.8e-137:545:97//AC004510
 F-OVARC1000543//HS_3055_A2_F10_MF CIT Approved Human Genomic_Sperm Library D Homo sapiens genomic clone Plate=3055 Col=20 Row=K, genomic survey sequence//0.19:104:71//AQ102820
 20 F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence//4.4e-136:670:97//AL022069
 F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence//1.3e-15:262:69//AC002985
 25 F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence//1.9e-41:476:70//AF046733
 F-OVARC1000573//HS_3241_B1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=5 Row=P, genomic survey sequence//2.2e-101:530:95//AQ211942
 F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE, 2 unordered pieces//9.7e-97:445:90//AC002414
 30 F-OVARC1000578//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence//9.1 e-27:354:72//AC003973
 F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence//0.97:276:62//AL023775
 35 F-OVARC1000605
 F-OVARC1000622//Homo sapiens (subclone 2_d8 from P1 H42) DNA sequence, complete sequence//7.2e-60:457:82//L81648
 F-OVARC1000640//Human BAC clone RG326K09 from 7q21, complete sequence//6.2e-58:499:80//AC002069
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds//5.1e-77:424:93//D43772
 40 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//4.8e-99:536:94//AB011162
 F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-29c7, genomic survey sequence//2.5e-57:336:91//B04244
 F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7//1.6e-81:291:84//AJ001713
 45 F-OVARC1000681//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE//8.2e-158:782:96//AL034424
 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//1.5e-151:549:99//AF027156
 F-OVARC1000689//nxbx0003aG01f CUGI Rice BAC Library Oryza sativa genomic clone nxbx0003M01f, genomic survey sequence//0.17:499:60//AQ050003
 50 F-OVARC1000700
 F-OVARC1000703//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds//3.5e-26:425:65//U34925
 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds//3.7e-109:451:91//AF038661
 55 F-OVARC1000730
 F-OVARC1000746
 F-OVARC1000769//HS_2056_B2_G06_T7 CIT Approved Human Genomic Sperm-Library D Homo sapiens genomic clone Plate=2056 Col=12 Row=N, genomic survey sequence//8.8e-19:147:86//AQ245905

- F-OVARC1000771//M.musculus mRNA for GTP-binding protein.//2.2e-62:305:78//X95403
 F-OVARC1000781//Sequence 5 from Patent WO9722695.//1.9e-89:705:78//A63552
 F-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.0e-131:631:98//AC004542
- 5 F-OVARC1000800//Human Chromosome 11q23 PAC clone pDJ254e13, complete sequence.//1.7e-32:295:80//AC003691
 F-OVARC1000802//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//3.2e-55:356:88//AC004469
 F-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//9.5e-27:163:94//Y17711
- 10 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds.//6.0e-150:432:100//AB014543
 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//1.0e-135:632:99//AF045584
 F-OVARC1000862//M.musculus mRNA for FT1.//2.6e-109:769:83//Z67963
 F-OVARC1000876//S.cerevisiae chromosome IX cosmid 9150.//7.4e-21:541:61//Z38125
 F-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.2e-08:98:88//U20086
- 15 F-OVARC1000885//B.subtilis 25 kb genomic DNA segment (from sspE to katA).//0.25:231:61//Z82044
 F-OVARC1000886//CIT-HSP-2171H6.TR CIT-HSP Homo sapiens genomic clone 2171H6, genomic survey sequence.//0.00035:139:69//B89721
 F-OVARC1000890
 F-OVARC1000891
- 20 F-OVARC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12.1-12.3. Contains part of a Homeobox domain containing gene and GSSs, complete sequence.//1.4e-18:473:64//AL024494
 F-OVARC1000912//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.9e-08:378:63//L14320
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds.//7.7e-85:440:95//AB011172
- 25 F-OVARC1000924//HS_2022_A1_C01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2022 Col=1 Row=E, genomic survey sequence.//5.7e-21:122:99//AQ269493
 F-OVARC1000936//Human PAC clone DJ0093I03 from Xq23, complete sequence.//1.2e-113:476:91//AC003983
 F-OVARC1000937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//0.00066:436:61//AL031848
- 30 F-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//5.0e-89:556:86//AB005549
 F-OVARC1000948//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:160:64//X95276
 F-OVARC1000959//CIT-HSP-2348O16.TR CIT-HSP Homo sapiens genomic clone 2348O16, genomic survey sequence.//0.99:270:59//AQ062850
- 35 F-OVARC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.9e-41:577:72//AL009181
 F-OVARC1000964//P.falciparum malaria antigen (M26-32-2) gene, partial cds.//0.19:83:73//M63270
 F-OVARC1000971//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//0.013:670:57//Z92841
- 40 F-OVARC1000984//Leishmania major chromosome 1, complete sequence.//0.80:345:58//AE001274
 F-OVARC1000996//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.6e-55:403:82//S51858
 F-OVARC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene, complete cds.//0.33:105:69//AF042785
- 45 F-OVARC1001000//HS_2247_A1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=O, genomic survey sequence.//3.1e-60:315:96//AQ153910
 F-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//3.1e-124:595:98//AC004190
 F-OVARC1001010//CIT-HSP-2034M3.TF CIT-HSP Homo sapiens genomic clone 2034M3, genomic survey sequence.//1.0:151:60//B74290
- 50 F-OVARC1001011//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//3.0e-08:149:79//Z78021
 F-OVARC1001032//Yeast (S.cerevisiae) mitochondrial Tyr-tRNA gene.//3.2e-13:667:60//M12451
 F-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//2.5e-119:737:86//AF001533
 F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//2.7e-150:733:97//AF099149
- 55 F-OVARC1001040//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.8e-29:277:76//AC005081
 F-OVARC1001044//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 36411, WORKING DRAFT SEQUENCE.//0.0017:387:6.1//AL031319

- F-OVARC1001051//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds//0.012:112:74//AF053768
- F-OVARC1001055//Sequence 1 from patent US 5580754.//3.3e-45:381:81//I30292
- 5 F-OVARC1001062//nxb0026H08r CUGI Rice BAC Library Oryza sativa genomic clone nxb0026H08r, genomic survey sequence.//0.018:344:59//AQ271878
- F-OVARC1001065//S.pombe chromosome I cosmid c29E6.//0.86:338:59//Z66525
- F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.0e-130:620:98//AF082657
- 10 F-OVARC1001072//Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions.//9.3e-24:285:65//AF003529
- F-OVARC1001074//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//2.0e-07:652:59//AL022153
- F-OVARC1001085//Homo sapiens c-syn protooncogene mRNA, complete cds.//5.0e-35:187:99//M14333
- 15 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.0e-74:289:95//AJ005897
- F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds.//3.6e-72:351:86//AF015913
- F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//6.4e-150:710:98//AF051782
- F-OVARC1001117//Homo sapiens chromosome 5, P1 clone 328E3 (LBNL H53), complete sequence.//0.99:148:67//AC005178
- 20 F-OVARC1001118//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.6e-35:302:74//AC000382
- F-OVARC1001129//CIT-HSP-647P20.TP CIT-HSP Homo sapiens genomic clone 647P20, genomic survey sequence.//0.94:106:66//B79052
- F-OVARC1001154//R.norvegicus mRNA for epithelin 1 and 2.//1.8e-95:462:79//X62322
- 25 F-OVARC1001161//Homo sapiens chromosome 4 clone B71M12 map.4q25, complete sequence.//2.9e-90:496:84//AC004069
- F-OVARC1001162
- F-OVARC1001167//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00090:219:64//AC004961
- 30 F-OVARC1001169//Borrelia burgdorferi (section 27 of 70) of the complete genome.//1.0:265:59//AE001141
- F-OVARC1001170//H.sapiens (xs170) mRNA, 350bp.//4.6e-58:355:90//Z36823
- F-OVARC1001171//CIT-HSP-2285E22.TF CIT-HSP Homo sapiens genomic clone 2285E22, genomic survey sequence.//1.5e-25:152:83//AQ002315
- F-OVARC1001173//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//0.0024:94:80//AL022323
- 35 F-OVARC1001176//Streptomyces plicatus B-N-acetylhexosaminidase (hex) gene, complete cds.//1.0:356:60//AF063001
- F-OVARC1001180//G.gallus DNA for polyubiquitin gene Ub II.//0.0062:275:60//X58195
- F-OVARC1001188//Homo sapiens full-length insert cDNA clone ZD93F03.//1.8e-32:180:97//AF086486
- 40 F-OVARC1001200
- F-OVARC1001232//Caenorhabditis elegans cosmid F10B5, complete sequence.//0.013:128:67//Z48334
- F-OVARC1001240//Human Chromosome 11 pac pDJ360p17, WORKING DRAFT SEQUENCE, 44 unordered pieces.//3.7e-131:811:87//AC001235
- F-OVARC1001243//Human BAC clone GS117O10 from 7q21-q22, complete sequence.//0.044:457:59//AC003078
- 45 F-OVARC1001244//Human homolog of Drosophila female sterile homeotic mRNA, complete cds.//8.4e-18:118:95//M80613
- F-OVARC1001261//Mus musculus putative membrane-associated guanylate kinase 1 (Magi-1) mRNA, alternatively spliced c form, partial cds.//1.4e-95:649:84//AF027505
- F-OVARC1001268//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//0.00051:72:83//U35776
- 50 F-OVARC1001270
- F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds.//2.1e-142:644:96//AB014543
- F-OVARC1001282//RPC111-60K8.TK RPC111 Homo sapiens genomic clone R-60K8, genomic survey sequence.//0.0089:285:58//AQ195857
- 55 F-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//3.0e-20:263:73//U97018
- F-OVARC1001306//nxb0002M13r CUGI Rice BAC Library Oryza sativa genomic clone nxb0002M13r, genomic survey sequence.//0.98:170:66//AQ156061

- F-OVARC1001329//Homo sapiens BAC clone RG370M10 from 7p15, complete sequence.//1.3e-05:432:61//AC003986
- F-OVARC1001330//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.027:444:59//AC005504
- 5 F-OVARC1001339//Homo sapiens chromosome 17, clone hCIT.124_H_2, complete sequence.//0.76:89:74//AC006071
- F-OVARC1001341//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//0.99:45:86//AQ263402
- F-OVARC1001342
- 10 F-OVARC1001344//HS-1059-A2-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=4 Row=O, genomic survey sequence.//1.5e-07:254:67//B44456
- F-OVARC1001357//Homo sapiens Xp22-149 BAC RPC11-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.83:376:61//AC005297
- F-OVARC1001360
- 15 F-OVARC1001369//Homo sapiens clone 162B15, complete sequence.//0.0066:99:76//AC004811
- F-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.7e-142:683:98//AF034801
- F-OVARC1001376//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//1.9e-52:382:73//AL031680
- F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//1.2e-147:683:99//AJ224819
- 20 F-OVARC1001391//S.coelicolor whiB gene.//0.018:454:59//X62287
- F-OVARC1001399//CIT-HSP-229118.TR CIT-HSP Homo sapiens genomic clone 229118, genomic survey sequence.//1.7e-11:104:87//AQ007611
- F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//3.9e-149:707:98//AB006651
- 25 F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.9e-48:586:69//U52426
- F-OVARC1001425//Human DNA sequence from clone 1048E9 on chromosome 22q11.2-12.2 Contains pseudo-gene similar to ribosomal protein S3A and part of a gene similar to C.elegans protein CE02118, ESTs, STS, GSS, complete sequence.//0.0019:96:78//Z99714
- F-OVARC1001436//Caenorhabditis elegans mitotic chromosome and X-chromosome associated MIX-1 protein (mix-1) mRNA, complete cds.//0.77:519:59//U96387
- 30 F-OVARC1001442//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING DRAFT SEQUENCE.//1.0:167:64//AL031687
- F-OVARC1001453//Human DNA sequence from PAC 453D15 on chromosome 6 contains STS.//4.4e-64:376:79//Z84482
- 35 F-OVARC1001476//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y24F12, WORKING DRAFT SEQUENCE.//0.20:107:71//AL022277
- F-OVARC1001480
- F-OVARC1001489//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.20:281:63//AC005140
- 40 F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//8.1e-85:479:92//AF016507
- F-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 -complete genomic sequence, complete sequence.//1.2e-98:503:83//AC002039
- F-OVARC1001525//Human beta-hexosaminidase alpha chain (HEXA) gene, exon 1.//1.7e-13:87:100//M16411
- F-OVARC1001542//H.sapiens polymorphic repeat associated with glutamate dehydrogenase pseudogene 5.//0.43:190:68//X69219
- 45 F-OVARC1001547//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.017:533:56//AC005140
- F-OVARC1001555//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.4e-159:416:99//AC005037
- 50 F-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//2.4e-115:540:99//AF031165
- F-OVARC1001600//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//5.5e-13:529:62//AF043945
- F-OVARC1001610//, complete sequence.//1.4e-12:152:77//AC005409
- 55 F-OVARC1001611
- F-OVARC1001615//Human DNA sequence from clone 873P14 on chromosome 20p12 Contains STS, GSS, complete sequence.//0.022:146:70//AL031682
- F-OVARC1001668//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.5e-109:358:96//AB005543

F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds.//1.8e-47:393:81//AB006867
 F-OVARC1001703//CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 2164L6, genomic survey sequence.//0.94:85:69//B92840
 F-OVARC1001711//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317C6, WORKING DRAFT SEQUENCE.//1.9e-06:489:61//Z97651
 5 F-OVARC1001713//Rattus norvegicus neuroligin 2 mRNA, complete cds.//1.0:262:59//U41662
 F-OVARC1001726//Human telomere associated repeat sequence, complete sequence.//7.5e-08:283:65//M57752
 F-OVARC1001731//Mus musculus gene for beta-tropomyosin.//2.6e-83:606:81//X12650
 F-OVARC1001745//HS_3007_B2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=18 Row=N, genomic survey sequence.//0.00020:269:60//AQ164522
 10 F-OVARC1001762//S.pombe chromosome III cosmid c338.//3.0e-17:624:61//AL023781
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//4.2e-149:706:98//U97670
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//3.0e-115:580:96//AB014575
 15 F-OVARC1001768
 F-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//5.7e-64:477:78//AC005066
 F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4q25, complete sequence.//6.5e-11:171:76//AC004704
 20 F-OVARC1001802//CITBI-E1-2502A17.TR CITBI-E1 Homo sapiens genomic clone 2502A17, genomic survey sequence.//0.98:214:61//AQ264481
 F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//9.5e-151:712:99//AL023694
 25 F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.7e-56:522:75//AF068748
 F-OVARC1001812//Homo sapiens chromosome 17, clone HCIT104N19, complete sequence.//1.7e-63:526:81//AC003662
 F-OVARC1001813//Human DNA sequence from cosmid U144A10, between markers DXS366 and DXS87 on chromosome X contains STS.//0.17:214:65//Z70224
 30 F-OVARC1001820//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 445N2, WORKING DRAFT SEQUENCE.//3.2e-55:379:82//AL031779
 F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//2.8e-17:509:62//AC005609
 35 F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DXS366 and DXS87 on chromosome X.//0.35:403:58//Z73361
 F-OVARC1001861//CIT-HSP-2165M3.TR CIT-HSP Homo sapiens genomic clone 2165M3, genomic survey sequence.//2.4e-25:148:96//B94622
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.2e-18:122:95//AF070611
 40 F-OVARC1001879//HS_3026_B1_F09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=17 Row=L, genomic survey sequence.//4.9e-29:204:87//AQ207748
 F-OVARC1001880//Human interferon regulatory factor 5 (Hmif5) mRNA, complete cds.//3.5e-05:489:60//U51127
 F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-29:350:74//AC005020
 45 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//8.6e-56:300:96//AF061749
 F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.3e-10:253:66//AL031904
 50 F-OVARC1001911//HS_2196_B2_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=22 Row=P, genomic survey sequence.//3.4e-09:123:78//AQ294069
 F-OVARC1001916//HS_3054_B1_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=F, genomic survey sequence.//1.2e-31:126:97//AQ099979
 F-OVARC1001928
 55 F-OVARC1001942//H.sapiens CpG island DNA genomic Mse1 fragment, clone 21d7, forward read cpg21d7.ft1a.//7.2e-12:83:98//Z60390
 F-OVARC1001943//Aplysia californica potassium channel modulatory factor mRNA, complete cds.//3.5e-50:535:69//AF059179

- F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds//1.7e-16:294:67//U37263
 F-OVARC1001950//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE//1.5e-20:261:68//AJ011929
 F-OVARC1001987//D.melanogaster G6PD gene, exons 2-4//0.99:447:57//Z19021
 5 F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces//2.9e-19:178:83//AC005995
 F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence//0.17:232:62//AL034559
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.1e-158:739:98//AB007934
 F-OVARC1002066//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15,
 10 WORKING DRAFT SEQUENCE//3.0e-17:781:59//AP000011
 F-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces//5.4e-136:683:96//AC006015
 F-OVARC1002107//Homo sapiens BAC clone RG276003 from 7q22-q31.1, complete sequence//1.0:220:61//AC004668
 15 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-115:557:98//AF041483
 F-OVARC1002127//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence//0.013:461:57//AC006241
 F-OVARC1002138//Caenorhabditis elegans cosmid F32D1//1.0e-29:545:64//AF016427
 F-OVARC1002143//CIT-HSP-2343H20.TR CIT-HSP Homo sapiens genomic clone 2343H20, genomic survey se-
 20 quence//2.3e-11:258:67//AQ055576
 F-OVARC1002156
 F-OVARC1002158//F17O7-T7 IGF Arabidopsis thaliana genomic clone F17O7, genomic survey sequence//1.8e-16:383:66//B11616
 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosinephosphatase//0.0041:300:64//X79568
 25 F-OVARC1002182//F.rubripes GSS sequence, clone 123123aA7, genomic survey sequence//1.4e-10:240:66//AL017241
 F-PLACE1000004//CIT-HSP-2294H13.TF CIT-HSP Homo sapiens genomic clone 2294H13, genomic survey se-
 quence//8.2e-10:158:75//AQ003859
 F-PLACE1000005//Mouse alpha-1 antitrypsin gene, segment 1//4.8e-15:89:93//M12585
 30 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.8e-51:550:72//AF022789
 F-PLACE1000014
 F-PLACE1000031//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.91:333:61//AC004821
 35 F-PLACE1000040//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island//2.6e-20:279:67//Z93023
 F-PLACE1000048//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence//3.6e-63:488:82//AC005177
 F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence//2.3e-10:141:75//U31508
 40 F-PLACE1000061//Human ribosomal protein L37a mRNA sequence//1.9e-30:190:94//L22154
 F-PLACE1000066//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence//6.0e-63:597:74//AC005521
 F-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6
 45 unordered pieces//5.2e-09:143:73//AC005848
 F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete se-
 quence//0.52:390:60//AC002389
 F-PLACE1000094
 F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and
 50 CpG Island, complete sequence//4.4e-129:731:92//AL023580
 F-PLACE1000142//H.sapiens AUH mRNA//6.4e-09:328:62//X79888
 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//7.7e-150:737:97//AF058291
 F-PLACE1000185//Sequence 15 from patent US 5691147//5.7e-106:558:94//I76211 F-PLACE1000213
 55 F-PLACE1000214//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING
 DRAFT SEQUENCE, 3 unordered pieces//1.8e-06:644:57//AC005504
 F-PLACE1000236//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695O20, WORKING
 DRAFT SEQUENCE//2.6e-39:191:83//AL032818

F-PLACE1000246//HS_2008_A2_D04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2008 Col=8 Row=G, genomic survey sequence.//0.96:153:61//AQ269813
 F-PLACE1000292//Drosophila melanogaster Oregon-R mitochondrial A+T region.//5.1e-12:571:60//U11584
 F-PLACE1000308//D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & amp; tRNA-Val.//0.00013:
 5 369:59//X54011
 F-PLACE1000332//HS_2016_B2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2016 Col=16 Row=H, genomic survey sequence.//7.5e-83:424:96//AQ232106
 F-PLACE1000347//CIT-HSP-2326A16.TV CIT-HSP Homo sapiens genomic clone 2326A16, genomic survey se-
 quence.//0.13:46:100//AQ047350
 10 F-PLACE1000374//Mus musculus putative CCAAT binding factor 1 (mCBF) mRNA, alternatively spliced transcript
 mCBF1, complete cds.//0.00048:84:83//U19891
 F-PLACE1000380//R.fubripes GSS sequence, clone 047P21aA10, genomic survey sequence.//0.43:198:62//
 Z88163
 F-PLACE1000383//Homo sapiens myotubularin related protein 1 (MTMR1) mRNA, partial cds.//8.7e-149:740:96//
 15 U58032
 F-PLACE1000401//Pinctada fucata mRNA for insoluble protein, complete cds.//0.22:484:56//D86074
 F-PLACE1000406//Human nuclear matrix protein 55 (nmt55) mRNA, complete cds.//3.3e-19:372:65//U89867
 F-PLACE1000420//Homo sapiens chromosome 17, clone hRPK.227_G_15, complete sequence.//1.6e-85:421:
 87//AC005899
 20 F-PLACE1000421//Human GT334 protein (GT334) gene, exons 16 and 17.//0.88:145:68//U61515
 F-PLACE1000424//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.076:196:66//
 AC005189
 F-PLACE1000435//HS_3217_A2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3217 Col=24 Row=A, genomic survey sequence.//2.2e-47:438:76//AQ181698
 25 F-PLACE1000444//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-
 61:616:71//AC004382
 F-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector
 pEMBLcos2, complete sequence.//5.8e-18:314:69//AF059580
 F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Cosmid Clone 94a In DGCR Region, complete se-
 30 quence.//1.1e-33:349:76//AC002491
 F-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//1.1e-34:256:83//
 U35245
 F-PLACE1000540//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.099:336:58//X95276
 F-PLACE1000547//Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds.//5.4e-
 35 11:279:63//AF076484
 F-PLACE1000562//, complete sequence.//1.7e-97:559:88//AC005409
 F-PLACE1000564
 F-PLACE1000583//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and-9.//3.3e-46:631:68//
 M27877
 40 F-PLACE1000588//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//7.3e-84:503:88//
 M55542
 F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.8e-164:798:97//AJ012449
 F-PLACE1000599//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.018:295:61//X95276
 F-PLACE1000610//HS_2056_A1_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 45 nomic clone Plate=2056 Col=19 Row=G, genomic survey sequence.//5.3e-24:188:87//AQ235967
 F-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.4e-47:687:66//
 AF044201
 F-PLACE1000636
 F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.5e-152:747:
 50 96//AF102265
 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and
 LLNLc110F1857Q7 (RZPD Berlin)).//2.3e-156:775:97//AJ005896
 F-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//8.0e-60:675:70//S78219
 F-PLACE1000712
 55 F-PLACE1800716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone
 Plate=CT 779 Col=5 Row=A, genomic survey sequence.//2.7e-42:266:82//B43026
 F-PLACE1000748//CIT-HSP-2372J8.TR CIT-HSP Homo sapiens genomic clone 2372J8, genomic survey se-
 quence.//0.023:157:68//AQ113109

- F-PLACE1000749//*Plasmodium falciparum* MAL3P7, complete sequence.//0.099:664:57//AL034559
 F-PLACE1000755//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00068:206:62//X76589
 F-PLACE1000769//RPCI11-3J18.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-3J18, genomic survey sequence.//6.5e-08:93:89//B63806
- 5 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//3.5e-138:663:98//AB014548
 F-PLACE1000786//*Drosophila melanogaster* cosmid 80H7.//1.4e-43:589:68//AL031027
 F-PLACE1000793//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpg13d12.rt1c.//4.6e-09:71:100//Z64565
 F-PLACE1000798//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//5.0e-14:235:72//AC002310
- 10 F-PLACE1000841//Homo sapiens clone NH0441G08, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.013:404:60//AC006158
 F-PLACE1000849//H.sapiens CpG island DNA genomic MseI fragment, clone 72a10, reverse read cpg72a10.rt1a.//3.3e-09:82:92//Z62712
- 15 F-PLACE1000856//*Hydra vulgaris* HT4 mRNA for collagen-like protein, partial cds.//1.0:317:59//AB008935
 F-PLACE1000863//H.sapiens CpG island DNA genomic MseI fragment, clone 53d2, forward read cpg53d2.ft1b.//7.3e-37:199:98//Z55621
 F-PLACE1000909//H.sapiens CpG island DNA genomic MseI fragment, clone 173f8, reverse read cpg173f8.rt1a.//1.5e-17:128:92//Z57391
- 20 F-PLACE1000931//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//8.1e-55:647:72//AL009181
 F-PLACE1000948
 F-PLACE1000972//RPCI11-61B1.TJ RPCI11 Homo sapiens genomic clone R-61B1, genomic survey sequence.//1.0e-26:148:99//AQ194348
- 25 F-PLACE1000977//Homo sapiens mRNA for KIAA0672 protein, complete cds.//6.1e-08:413:61//AB014572
 F-PLACE1000979//H.sapiens CpG island DNA genomic MseI fragment, clone 76e8, reverse read cpg76e8.rt1a.//2.7e-10:84:94//Z55963
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds.//8.0e-140:694:96//AB018267
 F-PLACE1001000//*Herpetomonas muscarum* muscarum kinetoplast 12S rRNA gene.//0.0056:443:58//U01011
- 30 F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sapiens genomic clone 2013L15, genomic survey sequence.//0.99:277:58//B58681
 F-PLACE1001010//Human cosmid g1572c101, complete sequence.//3.6e-55:294:88//AC000357
 F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 from 7p21, complete sequence.//7.2e-33:333:73//AC004741
- 35 F-PLACE1001024
 F-PLACE1001036//CIT-HSP-2373I10.TF CIT-HSP Homo sapiens genomic clone 2373I10, genomic survey sequence.//1.1e-80:393:98//AQ108662
 F-PLACE1001054//*Arabidopsis thaliana* genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence.//8.8e-40:483:66//AB013390
- 40 F-PLACE1001062//*Mus musculus* mRNA encoding lysine-ketoglutarate reductase/saccharopine dehydrogenase.//1.2e-23:224:80//AJ224761
 F-PLACE1001076//HS_2195_B1_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=9 Row=H, genomic survey sequence.//0.0014:168:66//AQ066659
 F-PLACE1001088
- 45 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//3.1e-95:489:96//AF065485
 F-PLACE1001104//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.0073:253:62//U81400
 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds.//2.5e-64:676:71//AF022158
- 50 F-PLACE1001136//Human amphiregulin (AR) gene, exon 5, clones lambda-ARH(6,12).//3.8e-26:174:93//M30702
 F-PLACE1001168
 F-PLACE1001171//Homo sapiens subtelomeric cosmid 11b-1, complete sequence.//7.6e-23:245:68//AC005603
 F-PLACE1001185//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker-CTX, the possibly alternatively spliced gene
- 55 for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.010:102:70//AL031177
 F-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//9.3e-82:684:

77//D14336
 F-PLACE1001241
 F-PLACE1001257//Caenorhabditis elegans cosmid R12E2.//1.1e-16:480:60//AF067219
 F-PLACE1001272//H.sapiens subunit of coatamer complex.//0.31:50:96//X70476
 5 F-PLACE1001279//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.054:352:60//AC005507
 F-PLACE1001280//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//1.0e-10:620:61//L14320
 F-PLACE1001294//M.musculus GEG-154 mRNA.//5.0e-107:826:80//X71642
 10 F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger protein ZFP-35.//1.2e-67:510:77//X17617
 F-PLACE1001311//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-47:491:73//AC005282
 F-PLACE1001323//HS-1007-A2-B10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 328 Col=20 Row=C, genomic survey sequence.//9.6e-26:142:100//B31181
 15 F-PLACE1001351
 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds.//8.6e-25:155:95//AB018342
 F-PLACE1001377//H.sapiens MADM gene (exon 1).//1.6e-43:393:79//Z48614
 F-PLACE1001383//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.5e-119:705:91//AL022324
 20 F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//5.7e-08:117:84//AJ001319
 F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58//I57340
 F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC genes for beta and beta-prime subunits of RNA polymerase (EC 2.7.7.6).//7.2e-11:620:60//X52177
 25 F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.0e-145:700:98//AC005412
 F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//2.0e-69:365:96//AF091087
 F-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//8.2e-121:608:97//AC006241
 30 F-PLACE1001440//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.3e-06:437:61//AC000384
 F-PLACE1001456//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//0.98:348:60//AC003106
 F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148
 35 F-PLACE1001484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL031660
 F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3) gene, exon I//0.00015:333:59//L78720
 F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//0.00016:161:66//AC004373
 40 F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//3.7e-22:260:76//AL021786
 F-PLACE1001534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031667
 45 F-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165_I_16, complete sequence.//2.7e-139:482:96//AC005669
 F-PLACE1001551//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.9e-116:681:89//AC005261
 F-PLACE1001570//HS_3105_A1_F06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, genomic survey sequence.//1.2e-10:137:79//AQ139817
 50 F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.8e-102:217:99//AB020860
 F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//3.7e-104:501:98//AF069984
 55 F-PLACE1001608//HS_2189_A1_G07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2189 Col=13 Row=M, genomic survey sequence.//2.9e-60:429:84//AQ221959
 F-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.4e-114:552:98//AC005037

F-PLACE1001611//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//0.93:131:71//AL031587

5 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.1e-74:702:75//AB018341

F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds.//1.2e-18:114:100//U17032

F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//7.7e-159:788:97//AC005971

10 F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//7.8e-36:365:73//AL022165

F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//9.1e-149:760:96//AC005921

15 F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//2.9e-57:643:71//M16200

F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958_E_11, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.9e-18:284:71//AC005883

F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds.//6.6e-68:369:73//D83776

20 F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3 In IGLC Region, complete sequence.//1.0:274:59//AC000051

F-PLACE1001729//Streptomyces coelicolor cosmid 1C2.//0.22:433:57//AL031124

F-PLACE1001739//Caenorhabditis elegans cosmid C18H7.//0.049:341:61//AF067607

F-PLACE1001740//Homo sapiens chromosome 5, P1 clone 1108H7 (LBNL H81), complete sequence.//4.8e-26:372:68//AC005221

25 F-PLACE1001745

F-PLACE1001746//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.018:472:57//AL031744

F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//8.8e-159:773:97//AF061243

30 F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPCI11-303E5, WORKING DRAFT SEQUENCE, 65 unordered pieces.//1.9e-54:274:81//AC005842

F-PLACE1001761//HS_3027_A1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, genomic survey sequence.//0.095:49:93//AQ130972

F-PLACE1001771//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//1.0e-146:709:97//AF080394

35 F-PLACE1001781 1.3e-08:238:65//AC005637

F-PLACE1001799//HS_3075_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, genomic survey sequence.//1.7e-09:166:69//AQ138474

F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence.//0.00035:196:66//AB020749

40 F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.1e-108:546:96//AF058953

F-PLACE1001821//RPCI11-35D17.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35D17, genomic survey sequence.//2.1e-55:300:97//AQ045286

45 F-PLACE1001844//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//2.8e-67:443:86//AC005177

F-PLACE1001845//Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence.//0.34:219:64//AC005850

50 F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rblK) and ribitol transporter (rblT) genes, complete cds.//7.1e-11:505:57//AF045244

F-PLACE1001897//RPCI11-46D15.TJ RPCI11 Homo sapiens genomic clone R-46D15, genomic survey sequence.//9.3e-08:383:63//AQ194408

F-PLACE1001912

F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//7.3e-156:753:98//AF099935

55 F-PLACE1001928//HS_2220_B2_G04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=8 Row=N, genomic survey sequence.//2.8e-43:233:97//AQ152361

F-PLACE1001983//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745C22, WORKING DRAFT SEQUENCE.//1.6e-07:396:62//AL031596

EP 1 074 617 A2

F-PLACE1001989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.0e-109:602:93//AL023755

F-PLACE1002004//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317E23, WORKING DRAFT SEQUENCE.//1.0e-69:475:87//AL020996

5 F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds.//7.2e-97:623:85//U58337

F-PLACE1002052//HS_2178_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=H, genomic survey sequence.//4.8e-22:140:95//AQ307908

F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.0063:371:60//U72284

10 F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A.//0.97:248:60//AF043195

F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds.//1.3e-37:635:64//AB011178

F-PLACE1002090//Homo sapiens full-length insert cDNA clone ZA85C09.//7.0e-122:583:98//AF086131

F-PLACE1002115//nbxb0038A20r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0038A20r, genomic survey sequence.//0.039:210:69//AQ291086

15 F-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds.//7.1e-61:540:77//AF079527

F-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-125:491:98//AL022162

20 F-PLACE1002150//Plasmodium falciparum MAL3P5, complete sequence.//0.12:408:61//AL034556

F-PLACE1002157//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.1e-44:515:71//AC005539

F-PLACE1002163//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.98:210:65//AE000662

25 F-PLACE1002170//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human BAC Library) complete sequence.//1.2e-06:283:60//AC004805

F-PLACE1002171//Mus musculus interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds.//1.0e-24:313:71//U06244

F-PLACE1002205//Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-05:428:60//AC005720

30 F-PLACE1002213//HS_3238_B1_G03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence.//2.2e-74:371:98//AQ206965

F-PLACE1002227//HS-1056-B1-C01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence.//2.1e-07:174:71//B42800

35 F-PLACE1002256//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-72, complete sequence.//0.022:458:59//AL010142

F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//3.5e-91:637:84//AL022324

40 F-PLACE1002319

F-PLACE1002342//Caenorhabditis elegans cosmid M03A1.//0.47:403:58//U49956

F-PLACE1002395//Homo sapiens chromosome 19, cosmid R28991, complete sequence.//1.9e-127:487:93//AC004623

F-PLACE1002399//Homo sapiens chromosome 17, clone hRPK_235_1_10, complete sequence.//5.6e-05:474:59//AC005922

45 F-PLACE1002433//Drosophila melanogaster lipidine gene, exons 1-7.//1.7e-11:613:58//AJ011928

F-PLACE1002437//M.musculus abc1 mRNA.//5.5e-62:452:85//X75926

F-PLACE1002438//Dictyostelium discoideum developmental protein DG1098 (DG1098) gene, partial cds.//0.013:372:59//AF081801

50 F-PLACE1002450//HS_3233_A1_G01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=1 Row=M, genomic survey sequence.//3.1e-07:449:59//AQ204769

F-PLACE1002465

F-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.5e-110:720:85//U69262

F-PLACE1002477//Homo sapiens Xp22-171-173 BAC GSHB-31214 (Genome Systems Human BAC Library) complete sequence.//3.9e-05:195:71//AC005926

55 F-PLACE1002493//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.020:301:60//AC006060

F-PLACE1002499

- F-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.1e-58:465:80//U50927
 F-PLACE1002514//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE.//3.7e-08:139:76//Z93930
 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//9.0e-143:583:95//AB018256
 5 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//0.00019:193:65//AC004774
 F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1). Contains GSSs, complete sequence.//4.7e-25:198:84//AL031575
 10 F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA, complete cds.//2.0e-13:400:60//L25314
 F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//3.5e-11:167:72//AC002523
 F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds.//4.2e-09:370:61//U31443
 F-PLACE1002591//H.sapiens mRNA for coronin.//7.2e-26:279:74//X89109
 15 F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.0013:375:64//AC005537
 F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence.//4.7e-05:556:59//D31785
 F-PLACE1002625
 F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.6e-128:229:92//AC005281
 20 F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//3.6e-107:706:84//AF079765
 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-186:804:97//AF068180
 25 F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:64//AF051726
 F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//I73723
 F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//0.0076:161:70//AL031273
 30 F-PLACE1002772//HS_3058_A1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=3 Row=G, genomic survey sequence.//0.0046:192:64//AQ134567
 F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//AF084259
 F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927
 35 F-PLACE1002794//CIT-HSP-2368A17.TR CIT-HSP Homo sapiens genomic clone 2368A17, genomic survey sequence.//1.3e-71:368:96//AQ075879
 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994
 F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR005295
 F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//1.3e-68:687:73//AF039691
 40 F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//9.3e-41:240:93//M27877
 F-PLACE1002839//Human BAC clone RG205G13 from 7q31, complete sequence.//0.00087:213:63//AC003045
 F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:66//AC005140
 45 F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.//0.032:275:62//M10126
 F-PLACE1002881//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.//4.7e-38:355:76//Z98200
 F-PLACE1002908//Gallus gallus beta-1,4-galactosyltransferase (CKII) mRNA, complete cds.//0.00012:200:64//U19889
 50 F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:241:70//AC000120
 F-PLACE1002962
 F-PLACE1002968//Plasmodium falciparum MAL3P2, complete sequence.//0.21:410:59//AL034558
 F-PLACE1002991//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//6.8e-121:605:93//AL023755
 55 F-PLACE1002993//CIT-HSP-2338I16.TF CIT-HSP Homo sapiens genomic clone 2338I16, genomic survey sequence.//1.9e-13:100:95//AQ054760
 F-PLACE1002996//Mouse U6 RNA gene.//2.0e-13:113:90//X06980

EP 1 074 617 A2

F-PLACE1003025//Plasmodium falciparum MAL3P6, complete sequence.//0.84:374:58//Z98551
 F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds.//6.1e-130:632:97//AB011088
 F-PLACE1003044//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829
 5 F-PLACE1003045//H.sapiens CpG island DNA genomic Mse1 fragment, clone 47g6, forward read cpg47g6.ft1a.//0.0064:52:96//Z61200
 F-PLACE1003092//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0031:249:63//B60158
 F-PLACE1003100//Human Hep27 protein mRNA, complete cds.//8.9e-65:650:73//U31875
 10 F-PLACE1003108
 F-PLACE1003136//Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.//6.3e-46:606:68//AC004219
 F-PLACE1003145
 F-PLACE1003153//RPCI11-13P16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13P16, genomic survey sequence.//2.7e-63:478:82//B76206
 15 F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
 F-PLACE1003176//HS_2255_A2_B01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey sequence.//6.3e-09:137:76//AQ131934
 20 F-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-138:791:901//AC005095
 F-PLACE1003200//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.7e-06:728:57//X95276
 F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence.//7.5e-05:249:63//AC002466
 F-PLACE1003238//HS_3239_A2_G02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey sequence.//0.36:64:87//AQ209954
 25 F-PLACE1003249
 F-PLACE1003256
 F-PLACE1003258//HS_3223_A1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey sequence.//1.4e-07:227:65//AQ190317
 30 F-PLACE1003296//CIT-HSP-2337F11.TF CIT-HSP Homo sapiens genomic clone 2337F11, genomic survey sequence.//1.1e-13:97:95//AQ057429
 F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//2.3e-92:485:95//M27877
 F-PLACE1003334
 35 F-PLACE1003342
 F-PLACE1003343//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.0e-20:179:84//AC004951
 F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//8.0e-143:773:92//U92715
 40 F-PLACE1003361//Human Cosmid g1248a143 from 7q31.3, complete sequence.//1.9e-30:402:70//AC004095
 F-PLACE1003366
 F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence.//7.6e-07:378:60//AL034558
 F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//6.0e-18:471:61//AC005247
 45 F-PLACE1003375
 F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer, segment 10/10.//2.3e-157:779:96//AB020878
 F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.//1.2e-104:596:91//M83680
 F-PLACE1003401//RPCI11-71J5.TJ RPCI11 Homo sapiens genomic clone R-71J5, genomic survey sequence.//0.85:140:65//AQ268588
 50 F-PLACE1003420//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3. WORKING DRAFT SEQUENCE.//0.0015:286:60//AL021388
 F-PLACE1003454//Plasmodium falciparum microsatellite pe63 sequence.//0.0084:219:61//AF015470
 F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) gene, complete cds.//1.3e-11:746:60//AF039401
 55 F-PLACE1003493
 F-PLACE1003516//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//8.2e-41:379:78//AC002994

- F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.2e-21:247:76//AF064859
- F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Contains two unknown genes and ESTs, STSs and a GSS.//4.4e-68:502:79//AL008729
- 5 F-PLACE1003528//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//1.0:323:58//AL022336
- F-PLACE1003537//Homo sapiens multispinning membrane protein mRNA, complete cds.//0.0054:322:59//U94831
- 10 F-PLACE1003553//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-78:267:88//AL031297
- F-PLACE1003566//Plasmodium falciparum MAL3P3, complete sequence.//0.00026:514:58//Z98547
- F-PLACE1003575//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.079:755:54//AC004688
- 15 F-PLACE1003583//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.1e-41:212:74//AL022324
- F-PLACE1003584//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-56, complete sequence.//0.0038:465:57//AL010230
- 20 F-PLACE1003592//Homo sapiens chromosome 17, clone 296K1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.72:111:71//AC002557
- F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.096:162:66//AC002476
- F-PLACE1003596//Mus musculus integral membrane protein 1 (Ihm1) mRNA, complete cds.//1.4e-54:685:68//L34260
- 25 F-PLACE1003602//Homo sapiens mRNA expressed in placenta.//1.1e-138:679:97//D83200
- F-PLACE1003605//Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.//0.0074:265:63//AC005356
- F-PLACE1003611//HS_2198_B1_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence.//2.1e-23:137:97//AQ184475
- 30 F-PLACE1003618//Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence.//3.0e-122:725:89//AC006226
- F-PLACE1003625//HS_2238_B2_D11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=22 Row=H, genomic survey sequence.//4.8e-12:92:94//AQ065662
- F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence.//0.043:264:63//AB011478
- 35 F-PLACE1003669
- F-PLACE1003704//RPC11-23H21.TKBF RPC1-11 Homo sapiens genomic clone RPC1-11-23H21, genomic survey sequence.//7.1e-31:199:91//AQ013830
- F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//4.3e-132:669:95//AF053305
- 40 F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//1.5e-31:166:99//AL021920
- F-PLACE1003723//HS_2231_A2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey sequence.//1.2e-12:114:90//AQ235672
- 45 F-PLACE1003738//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//5.9e-33:592:67//M58297
- F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//3.6e-11:92:93//AF054840
- F-PLACE1003762
- F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE.//4.8e-77:737:76//AP000014
- 50 F-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//2.1e-164:793:98//AC004160
- F-PLACE1003783//HS_2190_A2_C02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence.//1.1e-26:147:100//AQ218757
- 55 F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//4.5e-57:706:68//AC006210
- F-PLACE1003795//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyl-

- transferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene.//0.015:296:60//U52112
- F-PLACE1003833//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339
- 5 F-PLACE1003850//P.falciparum histidine-rich protein genes.//0.39:330:60//M17028
- F-PLACE1003858//Human DNA sequence from PAC 332O11 on chromosome 1q24-1q25. Contains ESTs and STSs.//4.8e-07:461:59//Z98043
- F-PLACE1003864//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.026:538:56//AC005139
- 10 F-PLACE1003870//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304
- F-PLACE1003885//Mus musculus poly(A) polymerase VI mRNA, complete cds.//9.4e-75:754:72//U58134
- F-PLACE1003886//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.7e-20:432:64//AC006030
- 15 F-PLACE1003888//Human mRNA for phospholipase C, complete cds.//2.6e-53:702:67//D42108
- F-PLACE1003892//RPCI11-24P17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759
- F-PLACE1003900//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240
- 20 F-PLACE1003903//Mus musculus CTP synthetase homolog (CTPsh) mRNA, complete cds.//2.7e-86:533:87//U49385
- F-PLACE1003915//Mus musculus clone OST1963, genomic survey sequence.//6.4e-29:251:80//AF046591
- F-PLACE1003923//Homo sapiens full-length insert cDNA clone ZD40A05.//2.8e-25:316:70//AF086251
- F-PLACE1003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//AC005505
- 25 F-PLACE1003936//CIT-HSP-2387C11.TR.1 CIT-HSP Homo sapiens genomic clone 2387C11, genomic survey sequence.//1.0:223:62//AQ239494
- F-PLACE1003968//Rattus norvegicus 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413
- 30 F-PLACE1004103//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//6.7e-29:241:84//AC005954
- F-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//3.0e-115:719:86//AF032666
- F-PLACE1004114//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000052
- 35 F-PLACE1004118//Pseudorabies virus with upstream and downstream sequences.//0.87:209:64//M34651
- F-PLACE1004128//M.musculus G protein beta-subunit mRNA, complete cds.//2.5e-62:437:84//M63658
- F-PLACE1004149//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//1.4e-16:342:65//AF005355
- F-PLACE1004156//Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p12.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, complete sequence.//1.2e-26:299:74//AL022099
- 40 F-PLACE1004161
- F-PLACE1004183//Homo sapiens for TOM1-like protein.//1.2e-146:731:96//AJ010071
- F-PLACE1004197
- F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//4.0e-144:695:98//AF069493
- 45 F-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.3e-151:772:95//AL021326
- F-PLACE1004256//HS_2010_B2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=8 Row=N, genomic survey sequence.//1.5e-44:372:79//AQ252434
- 50 F-PLACE1004257//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//0.00011:349:63//AC005034
- F-PLACE1004258//Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806
- 55 F-PLACE1004270//Human IgA C alpha 1 switch region (Sa1).//1.7e-08:622:61//L19121
- F-PLACE1004274//H.sapiens CpG island DNA genomic MseI fragment, clone 18g6, forward read cpg18g6.ft1b.//8.6e-37:196:98//Z57691
- F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//6.0e-156:756:

- 97//AF084830
 F-PLACE1004284//*Arabidopsis thaliana* genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence//
 0.0060:635:57//AB011480
 F-PLACE1004289//HS_3023_B1_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 5 nomic clone Plate=3023 Col=7 Row=J, genomic survey sequence//2.4e-12:86:98//AQ094451
 F-PLACE1004302//*Streptomyces coelicolor* cosmid 7H1 //0.26:297:64//AL021411
 F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//2.9e-150:797:94//Y11588
 F-PLACE1004336//*Drosophila melanogaster* DNA sequence (P1:DS07968 (D117)), complete sequence//0.87:
 206:59//AC004267
 10 F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//5.9e-139:
 688:97//AF100153
 F-PLACE1004376//*Mus musculus* clone OST20307, genomic survey sequence//4.1e-81:498:89//AF046631
 F-PLACE1004384//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1121J18, WORKING
 DRAFT SEQUENCE //3.6e-41:482:73//AL031653
 15 F-PLACE1004388//*Caenorhabditis elegans* cosmid K08F11 //8.6e-26:615:62//U070855
 F-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces//9.2e-
 150:749:96//AC005027
 F-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence//2.4e-08:129:76//
 AC005532
 20 F-PLACE1004428//*R.norvegicus* mRNA for Pristanoyl-CoA Oxidase//7.0e-17:549:61//X95188
 F-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene
 encoding mitochondrial protein, complete cds//3.1e-129:536:99//U49283
 F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region chromosome 13q12-13 con-
 tains BRCA2 exons 1-24, Interferon Induced 56Kd pseudogene and ESTs//4.8e-23:231:71//Z74739
 25 F-PLACE1004460//Homo sapiens PAC clone DJ1064B22 from 7q21, complete sequence//0.96:454:56//
 AC004954
 F-PLACE1004467//HS_2058_B1_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2058 Col=17 Row=F, genomic survey sequence//2.4e-87:433:98//AQ242700
 F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9//1.4e-74:665:70//
 30 M27877
 F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15; genomic survey se-
 quence//3.3e-20:140:92//B80243
 F-PLACE1004491//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING
 DRAFT SEQUENCE, 3 unordered pieces//9.9e-05:794:57//AC004709
 35 F-PLACE1004506//Human Gx-alpha gene//1.0e-05:231:63//D90150
 F-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds//3.2e-
 146:699:98//AF040701
 F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST//
 1.4e-33:367:71//Z86001
 40 F-PLACE1004518
 F-PLACE1004548//*Dictyostelium discoideum* MigA (migA) gene, complete cds//2.6e-05:318:62//U86962
 F-PLACE1004550//Human FMR1 gene, 5' end//0.0018:142:66//L19476
 F-PLACE1004564//*B.taurus* mRNA for cleavage and polyadenylation specificity factor//1.7e-114:513:85//X75931
 F-PLACE1004629//*Anolis carolinensis* Brain-1 gene, complete cds//0.00013:188:67//AB001868
 45 F-PLACE1004645//*Mycobacterium tuberculosis* H37Rv complete genome; segment 138/162//0.66:337:60//
 Z95120
 F-PLACE1004646//*Rattus norvegicus* retinal pigment epithelium-specific protein (Rpe65) mRNA, complete cds//
 1.1e-19:326:63//AF035673
 F-PLACE1004658//H.sapiens CpG island DNA genomic MseI fragment, clone 55h1, forward read cpG55h1.lt1a./
 50 12.4e-34:188:98//Z61632
 F-PLACE1004664//*Caenorhabditis elegans* cosmid W10G6, complete sequence//1.0:148:65//Z81140
 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene,
 complete cds//1.9e-101:182:95//U07561
 F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//4.3e-109:625:91//
 55 AF035606
 F-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and
 non-small cell lung cancer, segment 3/11//1.9e-152:759:96//AB020860
 F-PLACE1004686//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the

- SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//1.2e-34:320:71//Z95152
- 5 F-PLACE1004691//HS_3044_A1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey sequence.//0.018:191:63//AQ098323
- F-PLACE1004693//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.28:573:57//AL022577
- 10 F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence.//0.00081:428:59//Z98551
- F-PLACE1004722//HS_3052_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey sequence.//2.3e-05:104:75//AQ134959
- F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498
- 15 F-PLACE1004740//RPC111-58A7.TJ RPC111 Homo sapiens genomic clone R-58A7, genomic survey sequence.//8.6e-26:522:65//AQ195766
- F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//1.1e-112:711:86//AF061555
- F-PLACE1004751
- 20 F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//5.4e-171:828:97//AF084367
- F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//4.2e-134:763:90//AJ001713
- F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34), hypothetical protein EST, STS, GSS, complete sequence.//9.3e-132:759:90//AL022157
- 25 F-PLACE1004804
- F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.5e-06:403:58//AC004710
- F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//9.8e-39:207:99//AC005921
- 30 F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete sequence.//8.1e-15:203:73//AC004613
- F-PLACE1004824//G.gallus PB1 gene.//1.1e-103:759:80//X90849
- F-PLACE1004827//HS_2230_A2_A05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey sequence.//4.1e-38:330:81//AQ299313
- 35 F-PLACE1004836//H.sapiens nidogen gene (exon 8).//0.97:116:68//X84825
- F-PLACE1004838//HS_3241_A2_A04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence.//1.8e-87:425:98//AQ206740
- F-PLACE1004840//Sequence 2 from patent US 5728819.//6.7e-47:285:91//192819
- F-PLACE1004868
- 40 F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 9.//0.14:465:59//Z97344
- F-PLACE1004900
- F-PLACE1004902//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//3.6e-06:56:100//AQ261184
- F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.6e-151:770:91//AC005058
- 45 F-PLACE1004918//Mus musculus signaling molecule (ATTP) mRNA, complete cds.//2.6e-68:459:84//U97571
- F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//4.4e-106:545:95//AF070671
- F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//3.5e-45:226:84//AL020989
- 50 F-PLACE1004937
- F-PLACE1004969
- F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.//0.012:316:61//AC004843
- 55 F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.7e-39:394:77//AL031073
- F-PLACE1004982//Caenorhabditis elegans cosmid B0507.//0.16:167:65//U64833

EP 1 074 617 A2

F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence//8.8e-14:
 590:61//AE001373
 F-PLACE1005026
 F-PLACE1005027
 5 F-PLACE1005046
 F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SE-
 QUENCE, 35 unordered pieces//2.1e-135:675:97//AC005867
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.9e-159:761:98//AB011148
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//9.2e-10:757:56//
 10 AF059569
 F-PLACE1005077
 F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)
 complete sequence//6.9e-29:253:77//AC004673
 F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence//6.5e-52:446:78//
 15 AC002316
 F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces//2.0e-
 146:734:96//AC005225
 F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence//9.8e-83:254:95//
 AC004476
 20 F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence//0.46:179:64//AC003081
 F-PLACE1005111
 F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, com-
 plete cds//0.00051:287:63//L14320
 F-PLACE1005146//HS_3071_A1_E03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 25 nomic clone Plate=3071 Col=5 Row=I, genomic survey sequence//7.4e-38:299:82//AQ103361
 F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence//2.6e-44:346:82//
 AC002451
 F-PLACE1005176
 F-PLACE1005181//CIT-HSP-2340O5.TR CIT-HSP Homo sapiens genomic clone 2340O5, genomic survey se-
 30 quence//0.99:211:63//AQ054651
 F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 2358N6, genomic survey se-
 quence//2.7e-07:80:90//AQ074445
 F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence//0.98:216:61//AC000061
 F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces//
 35 0.70:245:63//AC004965
 F-PLACE1005243
 F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence//0.00041:254:61//Z47812
 F-PLACE1005266//H.sapiens mRNA (fetal brain cDNA a4_2g)//9.6e-33:177:98//Z70695
 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.6e-148:706:98//AB011182
 40 F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cds//2.8e-15:737:60//M69183
 F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds//3.8e-111:728:84//
 M25757
 F-PLACE1005308//Clethrionomys glareolus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Vole
 Cg14//1.0:128:67//AJ233621
 45 F-PLACE1005313//Caenorhabditis elegans cosmid D2092//8.8e-11:342:62//U88167
 F-PLACE1005327//HS_3080_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3080 Col=24 Row=B, genomic survey sequence//4.1e-25:147:96//AQ139116
 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence//1.4e-132:399:94//
 AC004794
 50 F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces//
 5.5e-114:237:92//AC000380
 F-PLACE1005373
 F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete sequence//0.20:305:58//
 AF017104
 55 F-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence//2.5e-148:760:95//AC003991
 F-PLACE1005453//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48A6,
 WORKING DRAFT SEQUENCE//0.00069:582:59//Z92854
 F-PLACE1005467//Rat mRNA//0.0014:131:70//M59859

- F-PLACE1005471//Human DNA sequence from clone 4514 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence//3.0e-23:530:67//AL023581
F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQUENCE//3.3e-131:814:88//Z82191
- 5 F-PLACE1005480//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D),TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS//7.0e-34:246:73//AL021878
F-PLACE1005481//RPCI11-74L17.TJ RPCI11 Homo sapiens genomic clone R-74L17, genomic survey sequence//0.37:403:57//AQ266885
- 10 F-PLACE1005494//Homo sapiens transient receptor potential protein 6 mRNA, complete cds//2.1e-67:325:99//AF080394
F-PLACE1005502//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence//0.015:403:61//AC005589
F-PLACE1005526//H.sapiens CpG island DNA genomic Mse1 fragment, clone 9f1, reverse read cpg9f1.r1a.//3.6e-27:159:96//Z66485
- 15 F-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE//2.6e-28:449:67//AP000038
F-PLACE1005530//Homo sapiens clone DJ0691L07, complete sequence//6.5e-18:234:72//AC004860
F-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH3, genomic survey sequence//1.2e-14:123:75//AL025925
- 20 F-PLACE1005554//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene//0.43:209:66//X02354
F-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence//9.3e-113:536:97//AC004707
F-PLACE1005574//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces//1.1e-10:514:59//AC005504
- 25 F-PLACE1005584//Homo sapiens mRNA for KIAA0617 protein, complete cds//0.00056:289:63//AB014517
F-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence//1.2e-111:262:89//AC004126
F-PLACE1005603
F-PLACE1005611//F16O5TFC IGF Arabidopsis thaliana genomic clone F16O5, genomic survey sequence//2.0e-10:209:66//B98589
F-PLACE1005623
F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces//1.2e-93:230:98//AC005840
- 35 F-PLACE1005639//HS_3095_B1_A03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=5 Row=B, genomic survey sequence//1.2e-05:220:63//AQ123022
F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//6.4e-150:721:98//AF083255
F-PLACE1005656//H.sapiens RR2 mRNA for small subunit ribonucleotide reductase//1.3e-51:480:74//X59618
- 40 F-PLACE1005666//RPCI11-78O15.TV RPCI11 Homo sapiens genomic clone R-78O15, genomic survey sequence//8.7e-05:243:62//AQ284667
F-PLACE1005698//Human membrane-associated lectin type-C mRNA//1.9e-63:374:85//M98457
F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence//0.69:633:57//AE001422
- 45 F-PLACE1005730//HS_2026_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence//2.0e-24:286:74//AQ231147
F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds//2.8e-55:621:71//U15635
F-PLACE1005755//HS_2213_A2_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=22 Row=O, genomic survey sequence//1.4e-25:290:75//AQ136844
- 50 F-PLACE1005763//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds//4.5e-40:297:70//M16200
F-PLACE1005799//R.norvegicus mRNA for mitochondrial isoform of cytochrome b5//0.91:287:63//Y12517
F-PLACE10058021//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence//5.0e-109:530:98//AC004827
- 55 F-PLACE1005803//HS_3092_B1_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=19 Row=B, genomic survey sequence//2.4e-08:76:96//AQ103695
F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//1.4e-126:636:96//AF027156
F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//2.6e-154:739:98//AF065482

- F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-37:355:77//AC004150
- F-PLACE1005834//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-105, complete sequence.//0.00080:663:58//AL010283
- 5 F-PLACE1005845//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00015:340:58//AC004153
- F-PLACE1005850//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//1.8e-46:278:85//AL031432
- F-PLACE1005851
- 10 F-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//5.0e-120:701:89//X75931
- F-PLACE1005884//CIT-HSP-2333O12.TR CIT-HSP Homo sapiens genomic clone 2333O12, genomic survey sequence.//4.6e-78:385:98//AQ039226
- F-PLACE1005890//Schizosaccharomyces pombe bem1/bud5 suppressor (Bem46+) mRNA, partial cds.//9.3e-16:638:57//U29892
- 15 F-PLACE1005898//Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds.//1.0:178:65//U67136
- F-PLACE1005921//M.musculus mRNA for immunity associated protein 38.//6.6e-17:614:59//Y08026
- F-PLACE1005923//RPCI11-33G19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-33G19, genomic survey sequence.//4.0e-10:535:57//AQ046151
- 20 F-PLACE1005925//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//0.17:159:65//AL034405
- F-PLACE1005932
- F-PLACE1005934//H.sapiens CpG island DNA genomic MseI fragment, clone 165g2, forward read cpg165g2.ft1a.//8.3e-43:247:93//Z57153
- 25 F-PLACE1005936//F.rubripes GSS sequence, clone 069K22aG2, genomic survey sequence.//0.91:116:68//AL014719
- F-PLACE1005951//Rhodobacter sphaeroides DMSO/TMAO-sensor kinase (dorS), DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds.//0.0022:495:59//AF016236
- 30 F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.9e-05:442:61//AC004081
- F-PLACE1005955//Caenorhabditis elegans cosmid F01F1.//4.3e-20:409:64//U13070
- F-PLACE1005966//P.falciparum aarp3 gene, exon.//0.0083:270:64//Y08925
- F-PLACE1005968
- 35 F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//1.0e-100:513:96//AC005866
- F-PLACE1006002//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//2.5e-54:444:77//Z86090
- F-PLACE1006003//HS-1059-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=2 Row=M, genomic survey sequence.//3.4e-05:214:64//B44442
- 40 F-PLACE1006011//Mus musculus poly-(ADPriboseyl)-transferase homolog PARP mRNA, complete cds.//4.3e-71:580:79//AF072521
- F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 -complete genomic sequence, complete sequence.//8.6e-32:177:83//AC002299
- 45 F-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//1.8e-34:269:83//U01139
- F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//3.4e-147:719:97//X99906
- F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs), complete sequence.//0.37:332:62//Z97200
- 50 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.3e-145:679:99//AF039023
- F-PLACE1006129
- F-PLACE1006139//Saccharomyces cerevisiae chromosome VI cosmid 9965.//4.8e-27:693:60//D44597
- F-PLACE1006143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//4.7e-46:435:77//Z93015
- 55 F-PLACE1006157//Saguinus oedipus mRNA for membrane cofactor protein CD46, complete cds, clone:B2.//0.048:290:60//D85750
- F-PLACE1006159//Homo sapiens chromosome 10 clone CIT987SK-1054O2 map 10q25, complete sequence.//3.2e-129:466:96//AC005661

- F-PLACE1006164//HS_3003_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=K, genomic survey sequence.//1.4e-70:388:93//AQ118200
F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//4.3e-78:385:86//AC005239
- 5 F-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.5e-91:630:84//X14972
F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//3.9e-149:694:99//AF091433
F-PLACE1006195//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//2.5e-16:283:70//AC003658
F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete
- 10 cds.//2.2e-94:648:84//L25125
F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence.//0.15:533:58//U75931
F-PLACE1006223//F24L20-T7 IGF Arabidopsis thaliana genomic clone F24L20, genomic survey sequence.//0.0068:175:64//B19803
F-PLACE1006225//CIT-HSP-2335123.TF CIT-HSP Homo sapiens genomic clone 2335123, genomic survey sequence.//2.1e-19:149:90//AQ039880
- 15 F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.//0.51:290:58//U91327
F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//7.4e-158:452:96//AC004142
F-PLACE1006246//RPC111-36123.TK RPC1-11 Homo sapiens genomic clone RPC1-11-36123, genomic survey sequence.//2.6e-31:176:97//AQ045400
F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.3e-166:791:98//AB014548
F-PLACE1006262//342E3.TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence.//1.0:228:63//B16447
- 25 F-PLACE1006288//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20N2, WORKING DRAFT SEQUENCE.//6.6e-172:809:99//AL031320
F-PLACE1006318
F-PLACE1006325//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.079:396:59//AC004454
F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VHSB32-D-JH2 region.//1.0:90:67//M55721
F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.16:445:56//AC005504
F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence.//6.1e-05:625:57//AL034559
- 35 F-PLACE1006368//X.laevis mRNA for KLP2 protein.//3.0e-25:376:68//X94082
F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//2.0e-146:711:97//AC004232
F-PLACE1006382
F-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-110:539:97//AF062085
- 40 F-PLACE1006412//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.3e-23:463:68//AC005029
F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds.//1.3e-109:525:98//AF069735
F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds.//6.9e-23:531:65//AB011129
F-PLACE1006445//HS_3071_A1_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence.//4.7e-74:392:95//AQ 103347
F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome.//1.1e-40:686:65//AF010496
F-PLACE1006470//T.brucei kinetoplast maxicircle variable region DNA.//0.99:250:59//Z15118
F-PLACE1006482//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE.//4.3e-120:328:98//AL021977
- 50 F-PLACE1006488//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//6.5e-86:478:91//X53744
F-PLACE1006492
F-PLACE1006506
F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//0.0010:547:58//AC005083
F-PLACE1006531//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-84:625:80//AF005355

- F-PLACE1006534//Caenorhabditis elegans cosmid Y40H7A, complete sequence.//0.00031:671:58//AL033510
 F-PLACE1006540
 F-PLACE1006552//P.falciparum glutamic acid-rich protein gnen, complete cds.//6.0e-10:636:59//J03998
 F-PLACE1006598//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//9.8e-25:170:77//AC006044
 5 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//6.7e-167:781:99//U97670
 F-PLACE1006617//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//0.98:514:59//AC004470
 10 F-PLACE1006626//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00079:206:62//X76589
 F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.0012:576:57//AC004015
 F-PLACE1006640//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0018:588:59//X95276
 15 F-PLACE1006673//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0028:469:58//AC004688
 F-PLACE1006678//Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase-I (b3GT1) gene, complete cds.//0.00011:184:64//AF029790
 F-PLACE1006704//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.0013:380:62//U67916
 20 F-PLACE1006731//Human DNA sequence from PAC 408N23 on chromosome 22q13. Contains HIP, HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN), ESTs and STS.//1.5e-78:520:86//Z98048
 F-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequencer.//1.9e-135:378:99//AC005626
 25 F-PLACE1006760//CIT-HSP-2336O13.TR CIT-HSP Homo sapiens genomic clone 2336O13, genomic survey sequence.//0.018:147:66//AQ039246
 F-PLACE1006779//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//2.6e-08:823:58//AE001426
 F-PLACE1006782//Homo sapiens clone NH0005N18, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.043:252:65//AC005487
 30 F-PLACE1006792//HS_3165_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3165 Col=1 Row=P, genomic survey sequence.//1.4e-11:249:67//AQ149559
 F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.//1.3e-12:155:80//M68513
 35 F-PLACE1006800//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-92, complete sequence.//6.7e-05:391:62//AL010272
 F-PLACE1006805//paramecium species 1,168 mt dna dimer: replication init. region.//9.1e-09:369:62//K00915
 F-PLACE1006815//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING DRAFT SEQUENCE.//0.89:465:58//AL031033
 40 F-PLACE1006819//Homo sapiens clone DJ1163L11, complete sequence.//1.5e-121:618:91//AC005230
 F-PLACE1006829//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.011:145:68//S69350
 F-PLACE1006860//Plasmodium falciparum MAL3P7, complete sequence.//2.2e-07:691:58//AL034559
 45 F-PLACE1006867//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 323M4, WORKING DRAFT SEQUENCE.//1.5e-132:643:98//AL033378
 F-PLACE1006878
 F-PLACE1006883//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.//1.0:236:62//Z95120
 F-PLACE1006901//Mus musculus t complex testis-specific protein (Tctex2) gene, t haplotype, promoter sequence.//2.7e-19:171:81//U21672
 50 F-PLACE1006904
 F-PLACE1006917//H.sapiens CpG island DNA genomic MseI fragment, clone 79g10, forward read cpg79g10.ft1a.//1.3e-21:131:98//Z63175
 F-PLACE1006932//Mus musculus FKBP65 binding protein mRNA, complete cds.//0.99:248:61//L07063
 55 F-PLACE1006935//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//0.85:161:63//AF029308
 F-PLACE1006956//Hylobates lar involucrin gene, complete cds.//0.077:355:61//M35447
 F-PLACE1006958//Mus musculus osmotic stress protein 94 (Osp94) mRNA, complete cds.//2.9e-89:483:86//

- U23921
 F-PLACE1006961//*Saccharomyces cerevisiae* mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//
 1.6e-06:651:58//AJ223323
 F-PLACE1006962//*H.sapiens* ir1B mRNA.//7.1e-15:202:71//X63417
- 5 F-PLACE1006966//*Caenorhabditis elegans* DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8,
 WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594
 F-PLACE1006989//cSRL-172A4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic
 clone cSRL-172A4, genomic survey sequence.//1.0:97:67//B03188
 F-PLACE1007014//*Rattus norvegicus* equilibrative nitrobenzylthioinosine-insensitive nucleoside transporter mR-
 NA, complete cds.//4.2e-07:592:58//AF015305
- 10 F-PLACE1007021//Homo sapiens chromosome 19, cosmid F16403; complete sequence.//5.1e-17:285:70//
 AC005777
 F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic
 CA repeat.//6.2e-131:775 :89//Z82899
- 15 F-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.7e-
 143:675:99//AC004895
 F-PLACE1007068//Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.//1.3e-131:652:
 97//AC005224
 F-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular
 Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane pro-
 tein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted
 tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//
 8.3e-158:768:97//AL021368
- 20 F-PLACE1007105//*Mus musculus* muskulin mRNA, complete cds.//4.1e-124:687:91//U72194
 F-PLACE1007111//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING
 DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:586:56//AC005139
 F-PLACE1007112//HS_2234_B2_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2234 Col=20 Row=N, genomic survey sequence.//0.26:200:62//AQ087801
 F-PLACE1007132//CIT978SK-A-211C6.TVB CIT978SK Homo sapiens genomic clone A-211C6, genomic survey
 sequence.//1.3e-40:255:92//B72112
- 30 F-PLACE1007140//QN1 orf [Coturnix coturnix, japonica, K2 neuroretinal cells, mRNA Partial, 3884 nt.//4.9e-15:
 386:62//S68151
 F-PLACE1007178//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING
 DRAFT SEQUENCE, 14 unordered pieces.//0.011:329:61//AC005140
- 35 F-PLACE1007226//Human lipocortin (LIP) 2 gene, upstream region.//0.0036:180:63//M62899
 F-PLACE1007238//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt.//2.8e-08:269:
 63//S74494
 F-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.3e-57:
 405:87//D50495
- 40 F-PLACE1007242//HS_3006_A1_B11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3006 Col=21 Row=C, genomic survey sequence.//0.088:191:59//AQ089443
 F-PLACE1007243//Human transporter protein (g17) mRNA, complete cds.//7.9e-12:245:66//U49082
 F-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//5.2e-144:677:98//Y15908
 F-PLACE1007274//HS_3003_A1_D08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3003 Col=15 Row=G, genomic survey sequence.//7.4e-49:345:85//AQ294154
- 45 F-PLACE1007276//*Fugu rubripes* GSS sequence, clone 014O10aG11, genomic survey sequence.//0.0052:228:
 62//AL024982
 F-PLACE1007282//*F.rubripes* GSS sequence, clone 019O07aB3, genomic survey sequence.//0.024:289:58//
 AL011743
- 50 F-PLACE1007286//Human Chromosome 16 BAC clone CIT987SK-A-256A9, complete sequence.//0.0048:185:
 69//AC002492
 F-PLACE1007301//*Dictyostelium discoideum* gene for TRFA, complete cds.//0.069:761:57//AB009080
 F-PLACE1007317
 F-PLACE1007342
- 55 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//5.4e-120:
 567:98//AF096870
 F-PLACE1007367//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-
 59:613:75//AC005077

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F-PLACE1007375//Caenorhabditis elegans cosmid D2092.//1.8e-12:193:70//U88167
F-PLACE1007386
F-PLACE1007402//HS_2170_A2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2170 Col=24 Row=G, genomic survey sequence.//5.6e-06:162:67//AQ125590
5 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 2 mRNA, complete sequence.//1.6e-25:165:93//AF093772
F-PLACE1007416
F-PLACE1007450//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.9e-34:764:62//AC003973
10 F-PLACE1007452//Mus musculus bet3 (Bet3) mRNA, complete cds.//4.1e-17:374:64//AF041433
F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment.//8.1e-52:317:93//L40391
F-PLACE1007460//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//0.0019:280:64//AL031117
F-PLACE1007478//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 -complete genomic sequence, complete sequence.//2.5e-24:362:71//AC002302
15 F-PLACE1007484
F-PLACE1007488//Danio rerio faciogenital dysplasia protein (fgd) mRNA, complete cds.//3.8e-14:293:63//AF017370
F-PLACE1007507//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//4.6e-10:152:75//AL031311
20 F-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//3.6e-139:477:98//AC004231
F-PLACE1007524//Plasmodium falciparum microsatellite 14C sequence.//0.0055:395:59//AF015461
F-PLACE1007525//Trypanoplasma borelli mitochondrion cytochrome oxidase subunit 1 (cox1), cytochrome oxidase subunit 2 (cox2), and apocytochrome b (cytb) genes, complete cds, and complete 9S rRNA gene and partial 12S rRNA gene.//0.0013:550:58//U11682 F-PLACE1007537//H.sapiens CpG island DNA genomic Mse1 fragment, clone 198g6, reverse read cpg198g6.rt1a.//0.98:121:67//Z60280
25 F-PLACE1007544//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508
F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds.//3.1e-69:733:71//AB014561
F-PLACE1007557//Drosophila yakuba mitochondrial DNA molecule.//0.022:393:61//X03240
F-PLACE1007583//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 545L17, WORKING DRAFT SEQUENCE.//3.6e-114:565:97//AL031665
F-PLACE1007598//CIT-HSP-2371G14.TF CIT-HSP Homo sapiens genomic clone 2371G14, genomic survey sequence.//2.0e-22:304:70//AQ111183
35 F-PLACE1007618//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence.//1.0:386:59//AC005245
F-PLACE1007621
F-PLACE1007632//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-88:276:96//AC006064
40 F-PLACE1007645//Bovine elastin mRNA, partial cds.//2.1e-07:110:79//M26132
F-PLACE1007649
F-PLACE1007677//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.2e-21:567:64//AL023755
45 F-PLACE1007688//Pseudorabies virus immediate-early gene.//2.2e-05:287:66//X15120
F-PLACE1007690//Caenorhabditis elegans cosmid R07G3.//0.40:122:70//U23452
F-PLACE1007697//Mus musculus LIM/homeobox (Lhx3) gene fragment.//0.85:117:71//L40483
F-PLACE1007705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//0.0035:75:88//AL031662
50 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-147:709:97//AF061243
F-PLACE1007725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence.//1.0:510:58//AB005231
F-PLACE1007729//Human endogenous retrovirus HML6 proviral clone HML6p, putative leader region, gag, pro and pol pseudogenes.//4.8e-136:516:89//U86698
55 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//7.9e-155:728:98//AB014585
F-PLACE1007737//Homo sapiens clone DJ0847O08, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.8e-22:806:60//AC005484
F-PLACE1007743//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING

DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504
 F-PLACE1007746//HS_2268_B1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2268 Col=19 Row=N, genomic survey sequence.//0.10:171:63//AQ124780
 F-PLACE1007791//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING
 5 DRAFT SEQUENCE.//0.63:241:58//AL031749
 F-PLACE1007807//Homo sapiens chromosome 17, clone hRPK.879_D_6, complete sequence.//1.0e-120:743:
 87//AC005273
 F-PLACE1007810//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete se-
 quence.//1.0e-113:739:86//AC003658
 10 F-PLACE1007829//CIT-HSP-2383J22.TR CIT-HSP Homo sapiens genomic clone 2383J22, genomic survey se-
 quence.//1.0e-47:254:97//AQ196438
 F-PLACE1007843//F.rubripes GSS sequence, clone 162K02bC12, genomic survey sequence.//1.6e-10:148:72//
 AL006903
 F-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15,
 15 WORKING DRAFT SEQUENCE.//3.4e-177:844:98//AP000010
 F-PLACE1007852//Mouse perlecan mRNA, complete cds.//8.5e-39:243:90//M77174
 F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//3.9e-189:894:98//AB018309
 F-PLACE1007866//CIT-HSP-2353D11.TF.1 CIT-HSP Homo sapiens genomic clone 2353D11, genomic survey se-
 quence.//0.015:279:61//AQ263271
 20 F-PLACE1007877
 F-PLACE1007897
 F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//2.3e-154:755:97//
 AB007956
 F-PLACE1007946//Human chromosome Y cosmid 56B5 genomic sequence, WORKING DRAFT SEQUENCE.//
 25 1.1e-59:310:81//AC003097
 F-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//2.1e-61:522:79//
 AC006157
 F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//2.7e-171:813:98//
 AF084530
 30 F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.5e-153:
 730:98//AF079529
 F-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//3.4e-32:383:74//
 U13262
 F-PLACE1007990//H.sapiens genomic DNA fragment (clone J31A212R).//6.6e-35:198:96//Z94758
 35 F-PLACE1008000//Mus musculus veli 3 mRNA, complete cds.//1.5e-118:706:88//AF087695
 F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.4e-
 163:786:98//AC005628
 F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//1.2e-95:625:
 84//L31840
 40 F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequence.//0.016:165:65//Z35719
 F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome
 4p16.3.//4.0e-07:251:64//Z68883
 F-PLACE1008095//RPCI11-21F19.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F19, genomic survey
 sequence.//1.5e-30:166:99//B85883
 45 F-PLACE1008111//Aphidius picipes NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial
 protein, partial cds.//7.5e-06:414:60//AF069163
 F-PLACE1008122//S.cerevisiae chromosome XV reading frame ORF YOL125w.//0.046:477:59//Z74867
 F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosid-
 ase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0068:446:57//AC004586
 50 F-PLACE1008132//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING
 DRAFT SEQUENCE.//3.6e-20:111:93//Z82199
 F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.5e-
 88:866:73//D14849
 F-PLACE1008181//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING
 55 DRAFT SEQUENCE.//0.0033:727:56//AL034397
 F-PLACE1008198//HS_3073_A1_C06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3073 Col=11 Row=E, genomic survey sequence.//2.3e-12:94:92//AQ171450
 F-PLACE1008201//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.5e-

162:791:97//AC005069
 F-PLACE1008209
 F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds.//0.65:174:66//M26332
 F-PLACE1008244//CIT-HSP-2337B4.TR CIT-HSP Homo sapiens genomic clone 2337B4, genomic survey se-
 5 quence.//6.7e-28:165:95//AQ039317
 F-PLACE1008273//B.primigenius mRNA for coat protein gamma-cop.//2.8e-71:709:71//X92987
 F-PLACE1008275//D.discoideum actin A-13 gene, 5' flank.//0.12:131:64//M29123
 F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library)
 complete sequence.//0.011:96:73//AC005913
 10 F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//8.2e-86:672:77//
 AF078779
 F-PLACE1008329//HS_2027_A1_C06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2027 Col=11 Row=E, genomic survey sequence.//8.7e-09:116:81//AQ244432
 F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//2.2e-141:670:98//
 15 AC005176
 F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-
 27:157:78//AC005000
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//1.1e-137:659:98//AB014579
 F-PLACE1008368//CIT-HSP-2311C9.TR CIT-HSP Homo sapiens genomic clone 2311C9, genomic survey se-
 20 quence.//7.1e-08:398:60//AQ016352
 F-PLACE1008369//HS_2251_B1_A02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2251 Col=3 Row=B, genomic survey sequence.//2.1e-35:217:93//AQ066512
 F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence.//1.4e-11:403:
 64//AC005856
 25 F-PLACE1008398//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING
 DRAFT SEQUENCE.//3.7e-144:681:99//AL034417
 F-PLACE1008401//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07;
 HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//2.8e-45:257:96//AC004604
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//4.3e-148:711:98//D86326
 30 F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING
 DRAFT SEQUENCE, 4 unordered pieces.//0.089:672:56//AC004688
 F-PLACE1008424
 F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and
 non-small cell lung cancer, segment 7/11.//1.0e-88:331:84//AB020864
 35 F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//0.55:530:58//
 U62317
 F-PLACE1008437//CIT-HSP-2376H4.TR CIT-HSP Homo sapiens genomic clone 2376H4, genomic survey se-
 quence.//3.3e-78:349:94//AQ112479
 F-PLACE1008455//HS_2064_B1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 40 nomic clone Plate=2064 Col=17 Row=J, genomic survey sequence.//4.7e-59:471:81//AQ246589
 F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//8.9e-43:307:
 73//AC004526
 F-PLACE1008465//CIT-HSP-2163F24.TR CIT-HSP Homo sapiens genomic clone 2163F24, genomic survey se-
 quence.//8.9e-41:210:99//B90014
 45 F-PLACE1008488//Mus musculus mRNA for testis-specific protein kinase 1, complete cds.//0.00013:516:58//
 AB003494
 F-PLACE1008524//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34B21, WORKING
 DRAFT SEQUENCE.//1.3e-161:778:98//AL031778
 F-PLACE1008531//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete
 50 cds.//1.1e-78:191:100//AF045555
 F-PLACE1008532//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING
 DRAFT SEQUENCE.//3.8e-24:257:70//Z93097
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//1.0e-13:215:
 71//AC004997
 55 F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//0.66:263:64//Z99571
 F-PLACE1008584//Homo sapiens cosmid clone U39B3 from Xp22.1-22.2, complete sequence.//1.1e-19:315:68//
 U73023
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-173:812:98//AB018334

EP 1 074 617 A2

F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces //3.9e-09:198:71//AC005077
 F-PLACE1008625//Homo sapiens chromosome 5, PAC clone 45L14 (LBNL H91), complete sequence //0.68:568:59//AC005373
 5 F-PLACE1008626//HS_3221_A2_F03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=K, genomic survey sequence //1.7e-13:147:82//AQ180967
 F-PLACE1008627//Cricetus griseus mRNA for Zn finger factor //9.7e-98:586:88//Y12836
 F-PLACE1008629//CIT-HSP-2012I4.TR CIT-HSP Homo sapiens genomic clone 2012I4, genomic survey sequence //0.00085:203:66//B53732
 10 F-PLACE1008630//Sequence 26 from Patent WO9517522 //9.7e-05:97:80//A45356
 F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP), complete cds //1.4e-23 :299:64//D38595
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds //1.1e-133:622:99//AF044333
 15 F-PLACE1008693//CIT-HSP-2346F2.TF CIT-HSP Homo sapiens genomic clone 2346F2, genomic survey sequence //0.24:89:76//AQ060732
 F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds //1.4e-94:420:97//AF038406
 F-PLACE1008715//CIT-HSP-2294K20.TR CIT-HSP Homo sapiens genomic clone 2294K20, genomic survey sequence //2.1e-70:349:98//AQ007199
 20 F-PLACE1008748//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence //0.14:347:59//AC004260
 F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence //7.9e-25 :244:71//AC003037
 25 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds //4.5e-120:503:97//AF060543
 F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence //0.00026:370:61//AF001549
 F-PLACE1008807//CIT-HSP-2334B19.TF CIT-HSP Homo sapiens genomic clone 2334B19, genomic survey sequence //3.3e-08:220:65//AQ036643
 30 F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds //1.7e-120:470:97//AF030933
 F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds //2.8e-87:504:89//AF032668
 F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence //4.0e-21:212:74//AL021920
 35 F-PLACE1008854
 F-PLACE1008867//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE //4.7e-77:477:84//Z82209
 F-PLACE1008887//Homo sapiens BAC clone NH0335J18' from 2, complete sequence //3.4e-53:699:70//AC005539
 40 F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds //2.1e-06:164:68//M63660
 F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds //6.4e-158:753:98//AB018308
 F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces //0.00013:400:63//AC002042
 45 F-PLACE1008934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE //7.4e-05:145:71//AL022312
 F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete cds //4.3e-41:282:87//L15309
 F-PLACE1008947//Pseudorabies virus with upstream and downstream sequences //5.9e-15:710:60//M34651
 50 F-PLACE1009020//HS_3051_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence //1.9e-21:167:86//AQ253727
 F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence //4.1e-152:763:97//AL031117
 F-PLACE1009039//HS_2034_A2_F08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, genomic survey sequence //0.17:252:59//AQ230137
 55 F-PLACE1009045//HS_3185_B2_B03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=6 Row=D, genomic survey sequence //1.9e-34:260:86//AQ172861
 F-PLACE1009048//Pig pituitary glycoprotein hormone alpha subunit gene, 5'flank and exon 1 //4.7e-70:463:80//D00766

- F-PLACE1009050//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence //0.63:280:61//AC004241
 F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting protein X), complete CDS //5.9e-113:725:85//AJ005073
- 5 F-PLACE1009090//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1045J21, WORKING DRAFT SEQUENCE //9.1e-27:222:84//AL021919
 F-PLACE1009091//Homo sapiens clone DJ0968116, complete sequence //0.027:630:58//AC006016
 F-PLACE1009094
 F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cds //2.1e-85:726:76//M36515
- 10 F-PLACE1009110
 F-PLACE1009111//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 138B7, WORKING DRAFT SEQUENCE //6.0e-12:362:64//Z98752
 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds //3.4e-138:671:97//AF035586
- 15 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds //3.6e-23:718:59//D25215
 F-PLACE1009150//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE //6.1e-142:684:98//AJ011929
 F-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE //4.3e-36:227:77//AP000031
- 20 F-PLACE1009158//H.sapiens genomic sequence for ERCC2 gene 3'region involved in DNA excision repair //1.0:173:60//X52222
 F-PLACE1009166
 F-PLACE1009172//Human BAC clone 7E17 from 12q, complete sequence //4.0e-35:257:85//AC002070
 F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human BAC Library) complete sequence //2.9e-19:288:72//AC004805
- 25 F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence //0.053:388:60//AB008266
 F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxC1) mRNA, complete cds //1.8e-50:317:89//AF061242
 F-PLACE1009190//RPCI11-81N5.TJ RPCI11 Homo sapiens genomic clone R-81N5, genomic survey sequence //0.91:114:67//AQ281881
- 30 F-PLACE1009200//CITBI-E1-2509J16.TF CITBI-E1 Homo sapiens genomic clone 2509J16, genomic survey sequence //2.8e-44:175:83//AQ262198
 F-PLACE1009230//H.sapiens gene for pregnancy specific beta-1 glycoprotein //1.1e-106:495:88//X63203
 F-PLACE1009246//HS_3058_B1_A06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=11 Row=B, genomic survey sequence //0.10:175:68//AQ185945
- 35 F-PLACE1009298//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds //1.8e-94:575:89//U47024
 F-PLACE1009308//Human clone mcag32 chromosome 7 CTG repeat region //0.0017:350:62//U23862
 F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds //3.0e-06:411:59//U83192
- 40 F-PLACE1009328//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191P20, WORKING DRAFT SEQUENCE //5.7e-138:830:86//AL034399
 F-PLACE1009335//Human (lambda) DNA for immunoglobulin light chain //0.071:253:62//D87015
 F-PLACE1009338//RPCI11-74N24 TV RPCI11 Homo sapiens genomic clone R-74N24, genomic survey sequence //2.4e-34:180:100//AQ268811
- 45 F-PLACE1009368
 F-PLACE1009375
 F-PLACE1009388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1014D13, WORKING DRAFT SEQUENCE //2.0e-37:288:84//AL022311
 F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cds //4.3e-78:730:74//M27878
- 50 F-PLACE1009404//SmD homolog [mice, liver, mRNA Partial, 199 nt] //0.16:95:71//S71494
 F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence //1.6e-150:701:99//AC005919
 F-PLACE1009434//Mus musculus clone OST431, genomic survey sequence //2.9e-73:442:88//AF046700
 F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162 //0.012:582:56//AL022022
- 55 F-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds //4.6e-21:146:93//AF012872
 F-PLACE1009459//Mus musculus clone OST9217, genomic survey sequence //2.9e-31:264:81//AF046660

EP 1 074 617 A2

F-PLACE1009468//Sequence 1 from patent US 5580968//1.9e-83:567:84//I30536
 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence//1.9e-142:704:97//AC004531
 F-PLACE1009477//Human 11p14.3 PAC clone pDJ939m16, complete sequence//2.2e-09:235:68//AC004601
 5 F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence//2.9e-83:171:92//U91321
 F-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence//3.8e-69:175:92//Z94160
 10 F-PLACE1009539//Mus musculus synaptojanin 2 isoform alpha mRNA, complete cds//7.0e-26:237:78//AF041862
 F-PLACE1009542//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence//3.1e-10:126:79//AL031587
 15 F-PLACE1009571//RPC111-60K12.TK RPC111 Homo sapiens genomic clone R-60K12, genomic survey sequence//1.4e-05:68:91//AQ195869
 F-PLACE1009581
 F-PLACE1009595//Homo sapiens chromosome 5, P1 clone 1029A7 (LBNL H15), complete sequence//6.6e-19:309:70//AC003959
 20 F-PLACE1009596//Rattus norvegicus platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta) gene, complete cds//9.0e-09:485:59//AF016049
 F-PLACE1009607//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE//4.9e-43:714:66//Z83824
 25 F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces//0.017:655:57//AC004157
 F-PLACE1009621
 F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 791.Col=16 Row=J, genomic survey sequence//2.7e-15:100:98//B33248
 30 F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.63:130:67//AC005308
 F-PLACE1009639//S.pombe chromosome II cosmid c24E9//0.86:509:58//AL021816
 F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//1.4e-171:816:98//AB011159
 F-PLACE1009665//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence//3.4e-67:437:87//AC005177
 35 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//2.5e-147:701:98//AF062534
 F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence//1.5e-98:228:100//AC006011
 F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence//2.2e-130:736:91//AC000109
 F-PLACE1009731//M.musculus mRNA for immunity associated protein 38//1.1e-13:311:64//Y08026
 40 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//4.2e-125:602:98//AF046024
 F-PLACE1009794
 F-PLACE1009798//Hnman DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence//1.3e-73:271:84//AL030996
 45 F-PLACE1009845
 F-PLACE1009861//B.tauris cathepsin B mRNA, 3' end//0.00023:147:65//M64620
 F-PLACE1009879//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE//4.9e-27:725:63//AL034397
 50 F-PLACE1009886//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE//8.2e-12:135:82//AL031427
 F-PLACE1009888//F14G3-T7 IGF Arabidopsis thaliana genomic clone F14G3, genomic survey sequence//0.0044:232:60//AQ251431
 55 F-PLACE1009908//S.pombe chromosome I cosmid c3F10//1.5e-19:559:59//Z69369
 F-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid//5.9e-48:304:87//M63005
 F-PLACE1009924//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-2011O4, WORKING DRAFT SE-

QUENCE, 4 unordered pieces//2.4e-51:481:78//AC004529
 F-PLACE1009925//nbxb0027C22r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0027C22r, genomic survey sequence//0.98:220:67//AQ272066
 F-PLACE1009935//Sequence 16 from patent US 5552281 //0.030:152:67//I25655
 5 F-PLACE1009947//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces//2.6e-12:322:67//AC006026
 F-PLACE1009971
 F-PLACE1009992//HS_3178_B1_F04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=7 Row=L, genomic survey sequence//4.9e-23:142:95//AQ150311
 10 F-PLACE1009995//Caenorhabditis elegans cosmid C01A2, complete sequence//0.00019:231:64//Z81029
 F-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds//7.9e-87:552:80//U48288
 F-PLACE1010023
 F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence//6.9e-101:181:98//AL031775
 15 F-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein//2.3e-136:689:95//X84692
 F-PLACE1010069//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SEQUENCE //0.0090:383:60//Z95114
 20 F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.8e-166:792:98//AF065482
 F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds//7.5e-13:203:77//D25540
 F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.0e-152:727:98//AB007925
 F-PLACE1010089//HS_3111_A1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3111 Col=15 Row=I, genomic survey sequence//4.8e-07:124:78//AQ101268
 25 F-PLACE1010096//R.norvegicus mRNA for 100 kDa protein//1.2e-108:700:85//X64411
 F-PLACE1010102//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces//2.1e-07:476:60//AC005506
 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.8e-25:728:60//AF059569
 30 F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome Xq22//6.5e-25:488:63//Z93928
 F-PLACE1010134//S.pombe chromosome I cosmid c29B12//1.9e-13:238:67//Z99164
 F-PLACE1010148//Homo sapiens partial human cDNA (660 bp)//4.8e-83:409:98//AJ222636
 F-PLACE1010152//CIT-HSP-2381F24.TF CIT-HSP Homo sapiens genomic clone 2381F24, genomic survey sequence//1.5e-28:163:98//AQ196757
 35 F-PLACE1010181//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence//2.4e-15:197:72//AC004973
 F-PLACE1010194//Ictalurus punctatus tumor suppressor p53 mRNA, complete cds//3.0e-14:181:74//AF074967
 F-PLACE1010202//Homo sapiens mRNA for MBNL protein//1.2e-27:509:66//Y13829
 40 F-PLACE1010231//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SEQUENCE //2.3e-101:194:95//AL033377
 F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//5.8e-145:693:97//AB007917
 F-PLACE1010270//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence; WORKING DRAFT SEQUENCE, 2 unordered pieces//2.1e-05:347:60//AC004710
 45 F-PLACE1010274//Caenorhabditis elegans cosmid C01A2, complete sequence//0.00040:231:64//Z81029
 F-PLACE1010293//Homo sapiens chromosome 2 PAC RPC13-417E16 (Roßwell Park Cancer Institute Human PAC library) complete sequence//6.5e-25:344:70//AC004464
 F-PLACE1010310//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence//3.5e-10:185:67//AL031005
 50 F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence//0.010:524:58//Z84468
 F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP Homo sapiens genomic clone 2335J21, genomic survey sequence//9.1e-90:448:97//AQ041837
 F-PLACE1010329//Apis mellifera ligustica complete mitochondrial genome//2.8e-08:384:64//L06178
 55 F-PLACE1010341//HS-1047-A2-C04-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=8 Row=E, genomic survey sequence//4.1e-21:141:92//B38252
 F-PLACE1010362//Mycobacterium tuberculosis H37Rv complete genome; segment 155/162//0.94:398:57//AL022121

- F-PLACE1010364//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y102G3, WORKING DRAFT SEQUENCE.//0.11:404:56//AL020985
 F-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186_H_2, complete sequence.//0.066:88:76//AC004675
- 5 F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP Homo sapiens genomic clone 2367K17, genomic survey sequence.//2.4e-71:454:88//AQ076825
 F-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//7.5e-134:722:93//AF003927
 F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//2.2e-150:702:99//AF039081
 F-PLACE1010492
- 10 F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq28.//0.022:405:60//U82695
 F-PLACE1010529//Sequence 1 from patent US 5776717.//2.9e-145:684:98//AR016417
 F-PLACE1010547//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.0:283:61//AL031677
 F-PLACE1010562//RPC111-65I16.TK RPC111 Homo sapiens genomic clone R-65I16, genomic survey sequence.//0.017:216:67//AQ200831
- 15 F-PLACE1010579//Homo sapiens full-length insert cDNA YI23D12.//3.9e-19:147:89//AF075014
 F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//6.4e-96:559:89//L25125
 F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds.//3.1e-146:707:97//AF045186
- 20 F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.045:454:59//AC005308
 F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence.//9.1e-07:378:60//AL034558
 F-PLACE1010624//Streptomyces coelicolor cosmid 5A7.//1.4e-05:518:61//AL031107
- 25 F-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.0e-137:675:97//AC004846
 F-PLACE1010629//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//2.5e-17:187:80//AC004682
 F-PLACE1010630//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence.//0.21:159:64//AB016872
- 30 F-PLACE1010631//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-144:720:97//AC005069
 F-PLACE1010661
 F-PLACE1010662//Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project).//0.90:257:61//AL021960
- 35 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds.//3.3e-73:697:74//U35376
 F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.010:447:59//AC004583
- 40 F-PLACE1010720//Mouse TPA-induced TIS11 mRNA.//2.0e-86:535:88//X14678
 F-PLACE1010739//HS_2013_B2_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=20 Row=D, genomic survey sequence.//5.7e-87:435:97//AQ235864
 F-PLACE1010743//R.norvegicus mRNA for myr5.//1.7e-87:582:85//X77609
- 45 F-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//4.7e-45:235:99//AC005921
 F-PLACE1010771//M.musculus HCNGP mRNA.//1.6e-135:801:88//X68061
 F-PLACE1010786//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-15, complete sequence.//0.35:334:60//AL010221
- 50 F-PLACE1010800//RPC111-79H17.TV RPC111 Homo sapiens genomic clone R-79H17, genomic survey sequence.//5.8e-18:168:82//AQ284252
 F-PLACE1010802//Human Chromosome X clone bWXD531, complete sequence.//1.6e-30:693:63//AC004384
 F-PLACE1010811//RPC111-51N5.TK RPC111 Homo sapiens genomic clone R-51N5, genomic survey sequence.//8.3e-11:142:78//AQ052380
- 55 F-PLACE1010833//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING DRAFT SEQUENCE.//7.3e-40:147:88//AL031283
 F-PLACE1010856//M.musculus mRNA for utrophin.//7.3e-17:150:86//Y12229
 F-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.4e-94:422:95//AB020868

EP 1 074 617 A2

F-PLACE1010870//M.musculus mRNA for ZT3 zinc finger factor.//1.3e-93:530:90//Z67747
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.1e-147:694:98//AB011182
 F-PLACE1010891
 F-PLACE1010896//Mouse BAC mbac20 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//3.9e-
 26:394:68//AC003997
 F-PLACE1010900
 F-PLACE1010916//HS_2242_A1_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2242 Col=7 Row=E, genomic survey sequence.//1.0e-78:391:97//AQ146687
 F-PLACE1010917
 F-PLACE1010925//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING
 DRAFT SEQUENCE, 4 unordered pieces.//0.11:629:56//AC004688
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.5e-138:653:98//AB011126
 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds.//5.6e-90:437:98//AF064243
 F-PLACE1010944//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-09:208:68//AF086247
 F-PLACE1010947
 F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP Homo sapiens genomic clone 2283D9, genomic survey se-
 quence.//2.1e-29:190:91//B98965
 F-PLACE1010960//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete
 sequence.//0.00074:421:60//AL010226
 F-PLACE1010965//CIT-HSP-2386K24.TF.1 CIT-HSP Homo sapiens genomic clone 2386K24, genomic survey se-
 quence.//1.8e-84:412:99//AQ240696
 F-PLACE1011026//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete
 sequence.//0.00037:257:64//AL008972
 F-PLACE1011032//Homo sapiens chromosome 5, BAC clone 118L13 (LBNL H176), complete sequence.//3.8e-
 06:315:65//AC005348
 F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds.//1.5e-56:286:98//U70669
 F-PLACE1011046//Rat phospholipase C-1 mRNA, complete cds.//1.3e-24:278:76//M20636
 F-PLACE1011054//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 981L23, WORKING
 DRAFT SEQUENCE.//3.8e-27:196:84//AL031686
 F-PLACE1011056//Ovis aries bactinecin 11 (Bac11) gene, exon 4; and complete cds.//5.4e-06:182:67//U77049
 F-PLACE1011057//protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA, 3255 nt].//3.2e-31:169:
 100//S75548
 F-PLACE1011090//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING
 DRAFT SEQUENCE.//5.1e-80:479:89//AL031687
 F-PLACE1011109//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//
 2.3e-24:192:84//L14684
 F-PLACE1011114//S.cerevisiae chromosome XI reading frame ORF YKR024c.//1.4e-14:346:60//Z28249
 F-PLACE1011133//T7E9-T7.1 TAMU Arabidopsis thaliana genomic clone T7E9, genomic survey sequence.//
 0.010:345:60//B19698
 F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey se-
 quence.//0.00013:95:76//AQ109305
 F-PLACE1011160//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.7e-111:692:
 87//AC004893
 F-PLACE1011165//H.sapiens galactokinase (GK2) mRNA, complete cds.//8.4e-31:194:92//M84443
 F-PLACE1011185//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-249B10, complete sequence.//3.1e-
 43:447:72//AC002288
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds.//
 3.3e-124:584:99//AF038664
 F-PLACE1011214//HS_2046_A2_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2046 Col=2 Row=C, genomic survey sequence.//2.0e-39:346:81//AQ305965
 F-PLACE1011219
 F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 Homo sapiens genomic clone 2513F18, genomic survey se-
 quence.//2.4e-20:119:100//AQ279801
 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds.//4.4e-146:675:99//AB011101
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.7e-42:212:84//
 AC005014
 F-PLACE1011273//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y37D8,
 WORKING DRAFT SEQUENCE.//1.0:214:60//Z92819

- F-PLACE1011291//RPCI11-16P9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-16P9, genomic survey sequence.//8.0e-08:66:98//B81770
 F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LANL), complete sequence.//0.027:135:67//AC004647
- 5 F-PLACE1011310//H.sapiens CpG island DNA genomic MseI fragment, clone 53c10, reverse read cpg53c10.r11b.//1.4e-05:57:100//Z61496
 F-PLACE1011325//Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds.//0.077:193:60//L02290
 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//3.1e-150:699:99//AF102265
- 10 F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388_F_14, complete sequence.//2.4e-38:186:83//AC005375
 F-PLACE1011371//Mus musculus PK-120 precursor (itih-4) mRNA, complete cds.//6.0e-35:689:63//AF023919
 F-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.0e-88:584:86//AJ010310
- 15 F-PLACE1011399//paramecium species 7,325 mt dna dimer: replication init. region.//0.00011:255:63//K00919
 F-PLACE1011419//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//0.067:337:62//AJ006996
 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.6e-157:743:98//AB011102
 F-PLACE1011452//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//1.1e-53:557:73//AJ011929
- 20 F-PLACE1011465//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//3.5e-71:498:80//AC004605
 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//4.8e-151:703:99//AB018255
 F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//5.2e-145:675:99//AF065482
 F-PLACE1011492//Ray (T.californica) acetylcholine receptor beta-subunit mRNA.//1.0:448:59//J00964
- 25 F-PLACE1011503
 F-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//3.8e-147:692:99//AC004968
 F-PLACE1011563//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//0.00036:296:61//X83546
 F-PLACE1011567//Homo sapiens PAC clone DJ1164K10 from 7p21-p22, complete sequence.//1.1e-38:315:82//AC004984
- 30 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds.//1.3e-65:268:86//AF054180
 F-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.0e-82:188:96//AC004477
- 35 F-PLACE1011635//Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.//1.8e-153:752:97//AC005224
 F-PLACE1011641//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//4.8e-05:190:67//AE000660
 F-PLACE1011643//Alcaligenes eutrophus phaP gene.//0.16:466:59//X85729
- 40 F-PLACE1011646//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1013A10, WORKING DRAFT SEQUENCE.//9.1e-19:156:76//AL033383
 F-PLACE1011649
 F-PLACE1011650//Homo sapiens retinol dehydrogenase gene, complete cds.//6.4e-09:172:74//AF037062
 F-PLACE1011664//D.melanogaster crn mRNA.//1.1e-52:650:68//X58374
- 45 F-PLACE1011675//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.11:443:58//AC005507
 F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//0.31:127:71//AL008719
 F-PLACE1011719//Human BAC clone RG369K23 from 7q31, complete sequence.//4.6e-52:461:77//AC002487
- 50 F-PLACE1011725
 F-PLACE1011729//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:320:62//AC004737
 F-PLACE1011749//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00031:544:59//AC004157
- 55 F-PLACE1011762//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-115:682:90//AC004003
 F-PLACE1011778//RPCI11-22D17.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22D17, genomic survey sequence.//2.7e-114:611:93//AQ008944

F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP Homo sapiens genomic clone 2317N1, genomic survey se-
 quence.//2.3e-17:120:94//AQ042330
 F-PLACE1011858//Gallus domesticus filamin mRNA, complete cds.//4.1e-24:565:64//U00147
 F-PLACE1011874//Homo Sapiens Chromosome X clone bWDX312, complete sequence.//2.5e-141:678:98//
 5 AC004478
 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds.//1.6e-108:526:98//AB011152
 F-PLACE1011891//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 439F8, WORKING
 DRAFT SEQUENCE.//0.0014:330:62//AL021392
 F-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//1.4e-89:678:82//U61969
 10 F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.069:246:
 61//U81400
 F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//1.2e-138:664:98//AF059617
 F-PLACE1011962//HS_3212_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//2.4e-07:154:74//AQ175369
 15 F-PLACE1011964//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 322P7, WORKING
 DRAFT SEQUENCE.//3.7e-22:369:69//AL023799
 F-PLACE1011982//HS-1041-A1-B01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone
 Plate=CT 823 Col=1 Row=C, genomic survey sequence.//0.44:309:58//B36529
 F-PLACE1011995//Homo sapiens Xq28 BAC RPC111-382P7 (Roswell Park Cancer Institute Human BAC Library)
 20 complete sequence.//8.8e-53:687:71//AC006054
 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.2e-146:690:98//AB018256
 F-PLACE2000003//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence.//1.7e-62:293:
 88//AC005837
 F-PLACE2000006//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE, 66
 25 unordered pieces.//1.4e-116:261:91//AC006057
 F-PLACE2000007
 F-PLACE2000011//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//5.2e-102:489:99//
 AC005578
 F-PLACE2000014//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1111N9, WORKING
 30 DRAFT SEQUENCE.//0.0095:307:62//AL022574
 F-PLACE2000015//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.0e-
 36:316:81//AC005069
 F-PLACE2000017//HS_3042_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3042 Col=15 Row=K, genomic survey sequence.//1.0:184:61//AQ098074
 35 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete
 cds.//4.6e-84:844:72//AF082556
 F-PLACE2000030//Human Chromosome 11 Cosmid cSRL16b6, complete sequence.//2.3e-22:233:77//U73638
 F-PLACE2000033//C.capitata mRNA for chorion protein s18.//0.0019:342:62//Y08913
 F-PLACE2000034//Rattus norvegicus transmembrane receptor Robo1 mRNA, complete cds.//2.8e-13:335:63//
 40 AF041082
 F-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//7.7e-84:
 489:90//L08505
 F-PLACE2000047//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and
 lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.0e-28:327:76//U95626
 45 F-PLACE2000050//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.1e-32:527:68//
 AC003101
 F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP Homo sapiens genomic clone 2346L20, genomic survey se-
 quence.//1.1e-05:89:83//AQ059010
 F-PLACE2000062//Human membrane-associated lectin type-C mRNA.//9.0e-113:662:86//M98457
 50 F-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//2.2e-133:631:98//AF027219
 F-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC11-189M20, WORKING DRAFT SE-
 QUENCE, 39 unordered pieces.//1.6e-16:119:93//AC005910
 F-PLACE2000100//HS_3184_A1_D06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3184 Col=11 Row=G, genomic survey sequence.//1.5e-80:409:97//AQ150004
 55 F-PLACE2000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING
 DRAFT SEQUENCE.//1.0e-172:830:98//AL031848
 F-PLACE2000111//Homo sapiens DNA, trinucleotide repeats region.//1.0:200:64//AB018491
 F-PLACE2000115

EP 1 074 617 A2

F-PLACE2000124//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence//6.2e-43:362:80//AC004531

F-PLACE2000132//RPCI11-79F15.TV RPCI11 Homo sapiens genomic clone R-79F15, genomic survey sequence//5.4e-35:206:94//AQ284166

5 F-PLACE2000136//Human BAC clone 7E17 from 12q, complete sequence//2.7e-12:814:59//AC002070

F-PLACE2000140//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE//3.6e-165:799:97//AL020995

F-PLACE2000164//Canine histamine H2 receptor gene, complete cds//0.10:392:56//M32701

F-PLACE2000170

10 F-PLACE2000172//Homo sapiens PAC clone DJ0811017 from 7q21-22, complete sequence//3.9e-91:552:88//AC006005

F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence//0.98:201:64//AC004032

F-PLACE2000187

15 F-PLACE2000216

F-PLACE2000223//RPCI11-12L17.TP RPCI-11 Homo sapiens genomic clone RPCI-11-12L17, genomic survey sequence//0.00039:325:58//B75888

F-PLACE2000235//Human Chromosome 16 BAC clone CIT987SK-254P9, complete sequence//7.5e-55:237:78//AC003003

20 F-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces//2.4e-92:236:94//AC005902

F-PLACE2000264//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudo-genes similar to ribosomal protein, ESTs, GSSs, complete sequence//1.4e-32:331:78//AL031577

F-PLACE2000274//Anthocidaris crassispina mRNA for B2HC, partial cds//8.5e-48:765:66//AB012308

25 F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds//8.3e-08:662:58//US2064

F-PLACE2000305//Homo sapiens clone DJ1129L24, WORKING DRAFT SEQUENCE, 5 unordered pieces//2.4e-08:95:81//AC006021

F-PLACE2000317//HS_3183_B2_F05_MR CIT Approved Human Genomic Sperm-Library D Homo sapiens genomic clone Plate=3183 Col=10 Row=L, genomic survey sequence//2.5e-71:346:99//AQ172747

30 F-PLACE2000335//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces//3.7e-14:402:65//AC004952

F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds//4.5e-77:555:82//AF026554

35 F-PLACE2000342//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial cds//1.8e-14:259:71//U66829

F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmids R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence//6.0e-34:376:74//AC003006

F-PLACE2000359//RPCI11-23J20.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23J20, genomic survey sequence//8.4e-21:288:69//AQ013849

40 F-PLACE2000366//Human Tigger1 transposable element, complete consensus sequence//5.0e-114:692:80//U49973

F-PLACE2000371//Homo sapiens 12p13.3 PAC RPCI1-29K11 (Roswell Park Cancer Institute Human PAC Library) complete sequence//0.38:356:58//AC005182

45 F-PLACE2000373//RPCI11-49C18.TJ RPCI11 Homo sapiens genomic clone R-49C18, genomic survey sequence//0.064:132:68//AQ051776

F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence//1.6e-130:776:88//AC003658

F-PLACE2000394//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence//5.4e-113:808:83//AC005909

50 F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosophila 'period' gene//0.87:286:63//X06967

F-PLACE2000399

F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence//2.9e-59:532:68//Z36238

55 F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds//0.44:553:56//U89984

F-PLACE2000419//Human adenosine deaminase (ADA) gene, complete cds//1.4e-56:303:86//M13792

F-PLACE2000425//HS_3047_A1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

EP 1 074 617 A2

nomic clone Plate=3047 Col=9 Row=O, genomic survey sequence.//2.8e-42:224:97//AQ126949
 F-PLACE2000427
 F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//1.1e-19:363:67//AC005821
 5 F-PLACE2000435//HS_3036_B1_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=L, genomic survey sequence.//3.1e-06:184:66//AQ096999
 F-PLACE2000438//Caenorhabditis elegans cosmid Y45F10D, complete sequence.//4.6e-23:550:62//AL021492
 F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//1.0e-78:604:80//AC006025
 10 F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//8.2e-05:330:63//AC002300
 F-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.7e-168:816:97//AC005740
 F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//4.3e-33:296:79//AC002037
 15 F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//3.4e-59:598:74//AC005057
 F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds.//7.6e-49:361:84//U81602
 F-PLACE3000009//Human placenta (Diff48) mRNA, complete cds.//3.0e-58:713:69//U49187
 20 F-PLACE3000020//R. norvegicus type III adenylyl cyclase mRNA, complete cds.//6.1e-103:600:89//M55075
 F-PLACE3000029
 F-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//4.4e-115:718:86//Y17267
 F-PLACE3000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.8e-17:250:74//AC005368
 25 F-PLACE3000103//Caenorhabditis elegans cosmid C13F10.//4.6e-07:408:61//U97006
 F-PLACE3000119//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.5e-58:291:86//AC004670
 F-PLACE3000121//Rattus norvegicus rsec15 mRNA, complete cds.//8.1e-81:837:71//AF032668
 F-PLACE3000124//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//1.8e-48:330:79//AC005695
 30 F-PLACE3000136
 F-PLACE3000142//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//0.011:294:62//AL033520
 F-PLACE3000145//Gallus gallus tensin mRNA, 3' end.//6.9e-52:659:68//L06662
 35 F-PLACE3000147//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//5.1e-37:305:81//AL031053
 F-PLACE3000148//Homo sapiens chromosome Y, clone 47511, complete sequence.//4.7e-32:766:63//AC004474
 F-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//7.4e-173:822:98//AC005277
 40 F-PLACE3000156//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-81:783:74//AC003682
 F-PLACE3000157
 F-PLACE3000158//, complete sequence.//1.0e-180:845:97//AC005500
 F-PLACE3000160//CIT978SK-152K7.TV CIT978SK Homo sapiens genomic clone 152K7, genomic survey sequence.//0.080:259:59//B50878
 45 F-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//9.8e-158:749:98//AC006130
 F-PLACE3000194
 F-PLACE3000197//F.rubripes GSS sequence, clone 075N04bB7, genomic survey sequence.//1.4e-08:164:68//AL003352
 50 F-PLACE3000199//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//0.0019:277:58//Z82207
 F-PLACE3000207//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//6.6e-21:312:67//AC005013
 55 F-PLACE3000208//Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds.//1.0:279:61//L23982
 F-PLACE3000218//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//9.3e-43:383:79//AC004086

- F-PLACE3000220//RPCI11-54B4.TV RPCI11 Homo sapiens genomic clone R-54B4, genomic survey sequence.//2.4e-36:381:76//AQ082056
- F-PLACE3000221//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-135:721:91//AC005231
- 5 F-PLACE3000226
- F-PLACE3000230//Homo sapiens c1cr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//3.3e-80:498:78//U95626
- F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.6e-54:254:92//Z98046
- 10 F-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.4e-139:850:86//X80169
- F-PLACE3000254//Ateline herpesvirus 3 complete genome.//1.3e-10:399:61//AF083424
- F-PLACE3000271//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//1.8e-21:350:68//AF001548
- 15 F-PLACE3000276//HS_2026_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//5.7e-45:376:81//AQ231147
- F-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//1.6e-138:650:99//AC005328
- 20 F-PLACE3000310
- F-PLACE3000320//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-41:379:77//AL034379
- F-PLACE3000322//Homo sapiens chromosome 17, clone hRPK:209_U_20, complete sequence.//3.3e-35:419:68//AC005822
- 25 F-PLACE3000331//CIT-HSP-2347D24.TR CIT-HSP Homo sapiens genomic clone 2347D24, genomic survey sequence.//2.7e-20:119:99//AQ061543
- F-PLACE3000339//Rhodobacter sphaeroides magnesium chelatase subunits Bchl (bchl) and BchD (bchD) genes, complete cds; and BchO (bchO) gene, partial cds.//0.99:310:58//AF017642
- F-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//7.5e-159:752:98//AC006055
- 30 F-PLACE3000350//Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds.//2.3e-107:592:92//AF084205
- F-PLACE3000352//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//2.1e-37:480:70//Z83732
- 35 F-PLACE3000353
- F-PLACE3000362//Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence.//0.00011:373:60//AC005969
- F-PLACE3000363
- F-PLACE3000365//Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.//0.074:279:61//Z81007
- 40 F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-118:653:92//Z92545
- F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//2.2e-25:288:71//AC005154
- 45 F-PLACE3000399//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING DRAFT SEQUENCE.//2.3e-69:303:86//Z97630
- F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence.//0.0063:435:58//Z93239
- F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.8e-25:292:73//AC006023
- 50 F-PLACE3000402//RPCI11-20D6.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-20D6, genomic survey sequence.//1.1e-10:154:74//AQ008761
- F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//2.9e-41:515:72//AC005701
- 55 F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone cSRL-179E11, genomic survey sequence.//2.8e-91:540:89//B03443
- F-PLACE3000413
- F-PLACE3000416//F19L8-Sp6 IGF Arabidopsis thaliana genomic clone F19L8, genomic survey sequence.//

0.0018:664:55//B11305
 F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence//1.1e-16:284:70//AL022719
 F-PLACE3000455//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE//3.6e-146:732:96//AL031284
 5 F-PLACE3000475//HS_2164_A2_H10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=20 Row=O, genomic survey sequence//1.5e-07:159:71//AQ132983
 F-PLACE3000477//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs//2.9e-11:213:70//Z83843
 10 F-PLACE4000009//Sequence 93 from patent US 5616500//9.9e-08 :692:60//I39845
 F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//1.1e-116:331:100//AB018352
 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence//5.0e-05:244:63//AC004131
 F-PLACE4000049//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence//1.2e-37:385:74//AC005926
 15 F-PLACE4000052//M.musculus abcl mRNA//1.5e-110:671:88//X75926
 F-PLACE4000063
 F-PLACE4000089//M.musculus BOX DNA for regulatory element and promoter region related to EC cell differentiation//3.7e-12:114:85//X74311
 20 F-PLACE4000093//CIT-HSP Homo sapiens genomic clone 2380K5, genomic survey sequence//0.11:245:60//AQ108342
 F-PLACE4000100//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE//2.9e-19:384:65//AL031848
 F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.2e-145:684:99//AB007931
 25 F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds//3.7e-62:541:78//AF091234
 F-PLACE4000129
 F-PLACE4000131//HS_3139_B2_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence//2.3e-14:221:70//AQ183207
 F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.2-23. Contains part of the COL4A5 gene for Collagen Alpha 5(IV) Chain Precursor. Contains GSSs, complete sequence//0.28:412:58//AL031622
 30 F-PLACE4000156//Human zinc finger protein ZNF136//7.2e-88:764:76//U09367
 F-PLACE4000192
 F-PLACE4000211
 35 F-PLACE4000222//344J1.TVB CIT978SKA1 Homo sapiens genomic clone A-344J01, genomic survey sequence//1.2e-14:177:76//B17158
 F-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds//9.8e-116:662:89//AF030430
 F-PLACE4000233//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence//5.2e-54:363:70//AC003973
 40 F-PLACE4000247
 F-PLACE4000250//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence//0.0053:229:65//AC004673
 F-PLACE4000252
 F-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein//2.0e-25:191:87//Z70200
 45 F-PLACE4000261//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds//2.6e-23:314:71//AF084259
 F-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds//5.5e-122:734:88//AF032667
 F-PLACE4000270
 F-PLACE4000300
 50 F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete cds//1.4e-21:135:96//L34075
 F-PLACE4000323//HS_2165_B1_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence//4.3e-08:170:71//AQ125036
 F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2//2.8e-06:311:63//M10296
 55 F-PLACE4000344//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence//0.014:252:60//AE001401
 F-PLACE4000367

EP 1 074 617 A2

F-PLACE4000369
 F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 2350B9, genomic survey sequence.//9.2e-46:282:86//AQ062661
 F-PLACE4000387//CIT-HSP-2382F11.TR CIT-HSP Homo sapiens genomic clone 2382F11, genomic survey sequence.//0.96:102:70//AQ080649
 5 F-PLACE4000392//Rattus norvegicus polymorphic marker D20UIA1 sequence.//1.2e-05:222:68//AF054088
 F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds.//9.6e-46:605:71//AB014540
 F-PLACE4000411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984
 10 F-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//4.0e-44:263:92//Z70200
 F-PLACE4000445//HS-1053-B1-D02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=3 Row=H, genomic survey sequence.//0.070:47:100//B41346
 F-PLACE4000450
 F-PLACE4000465//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//2.3e-07:273:65//AC005065
 15 F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//4.1e-34:351:70//AC005821
 F-PLACE4000489//HS_3012_B1_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3012 Col=9 Row=N, genomic survey sequence.//2.0e-36:220:92//AQ095537
 20 F-PLACE4000494//Homo sapiens 12p13.3 PAC RPC15-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC005865
 F-PLACE4000521//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE.//1.6e-163:770:98//AJ011929
 F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch2-C, partial cds.//4.0e-124:686:90//U47645
 25 F-PLACE4000548
 F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:435:59//X12747
 F-PLACE4000581
 F-PLACE4000590//Homo sapiens chromosome Y, clone 475I1, complete sequence.//3.6e-20:747:59//AC004474
 30 F-PLACE4000593//Caenorhabditis elegans cosmid F25D7, complete sequence.//5.6e-16:326:65//Z78418
 F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.7e-163:785:97//AC005281
 F-PLACE4000638//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.7e-74:707:74//AC006039
 35 F-PLACE4000650
 F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267
 F-PLACE4000670//Sequence 13 from patent US 5712381.//1.0:311:59//I82816
 F-SKNMC1000011//Gallus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577
 F-SKNMC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59//M25312
 40 F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.6e-147:706:98//AB014554
 F-SKNMC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//AR020616
 F-SKNMC1000091//Human NK homeobox protein (Nkx6.1) gene, exon 1.//0.0018:375:60//U66797
 F-THYRO1000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//6.6e-97:542:84//U91561
 45 F-THYRO1000026//Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence.//3.5e-46:353:82//AL008637
 F-THYRO1000034//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353
 50 F-THYRO1000035//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:303:83//AC004383
 F-THYRO1000040
 F-THYRO1000070//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//1.3e-05:613:58//AC005383
 F-THYRO1000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.7e-84:722:77//AB014557
 55 F-THYRO1000085
 F-THYRO1000092//CIT-HSP-2013L16.TFB CIT-HSP Homo sapiens genomic clone 2013L16, genomic survey sequence.//0.31:186:61//B60606
 F-THYRO1000107

- F-THYRO1000111//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:690:87//Z93403
- F-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//1.4e-127:816:85//U49055
- 5 F-THYRO1000124//H.sapiens CpG island DNA genomic MseI fragment, clone 72a7, forward read cpg72a7.ft1a.//9.5e-26:169:94//Z62724
- F-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e-154:732:98//AF087142
- F-THYRO1000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//3.7e-39:315:82//AC002096
- 10 F-THYRO1000156//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.2e-21:335:71//AL023574
- F-THYRO1000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7, complete sequence.//8.4e-52:301:88//AC002331
- F-THYRO1000173//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//4.0e-89:821:74//M62419
- 15 F-THYRO1000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207
- F-THYRO1000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57//X06214
- F-THYRO1000190//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//0.38:184:64//AC005746
- 20 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.5e-174:805:99//AJ005698
- F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.2e-86:616:84//AB014552
- F-THYRO1000206//HS_3047_A1_A05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.51:331:63//AQ099134
- F-THYRO1000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING
- 25 DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC004157
- F-THYRO1000241//Gallus gallus genome fragment with pentamer tandem repeats.//0.43:191:62//X00186
- F-THYRO1000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156
- F-THYRO1000253//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//AC006055
- 30 F-THYRO1000270
- F-THYRO1000279//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664
- F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179:848:98//AB016068
- F-THYRO1000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complete cds.//1.0e-44:331:83//AF036894
- 35 F-THYRO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//5.7e-112:641:91//L35233
- F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.2e-162:763:98//AB018333
- F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//2.2e-32:177:84//U29091
- 40 F-THYRO1000368//Caenorhabditis elegans cosmid W09G3, complete sequence.//0.97:206:60//Z82080
- F-THYRO1000381//Arthrobacter sp. glcI gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668
- F-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:98//AC006019
- F-THYRO1000394//HS_2061_A2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey sequence.//1.6e-29:202:91//AQ247672
- 45 F-THYRO1000395//Drosophila melanogaster ring canal protein and ORF2 mRNA, complete cds.//4.3e-15:512:59//L08483
- F-THYRO1000401 3.2e-116:504:80//AF051908
- F-THYRO1000438//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING
- 50 DRAFT SEQUENCE, 5 unordered pieces.//3.4e-09:539:59//AC005308
- F-THYRO1000452//RPCI11-1C19.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1C19, genomic survey sequence.//0.27:132:64//B49573
- F-THYRO1000471//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.3e-38:332:81//AC005229
- 55 F-THYRO1000484//Homo sapiens BAC378, complete sequence.//2.2e-37:254:76//U85196
- F-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//6.3e-130:327:97//AC005740
- F-THYRO1000501//H.sapiens Staf50 mRNA.//9.8e-74:615:77//X82200

- F-THYRO1000502//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.076:380:59//Z94056
F-THYRO 1000505
- 5 F-THYRO1000558//Human PAC clone 127H14 from 12q, complete sequence.//2.4e-27:412:69//AC002563
F-THYRO1000569//HS_2178_B2_E03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=6 Row=J, genomic survey sequence.//1.9e-27:326:74//AQ307499
F-THYRO1000570
F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//7.4e-167:808:97//
10 AF075587
F-THYRO1000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//0.99:280:61//U91323
F-THYRO1000602//HS_3037_B2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence.//1.2e-05:109:75//AQ097057
15 F-THYRO1000605//Homo sapiens map 2p11.2; 83cM from GATA85A06 repeat region, complete sequence.//1.0:84:70//AF067777
F-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//3.4e-174:820:98//AC005546
F-THYRO1000637//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//3.6e-38:289:84//AL024474
20 F-THYRO1000641//Plasmodium falciparum MAL3P7, complete sequence.//6.8e-07:540:56//AL034559
F-THYRO1000658//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//1.1e-68:468:84//AC005696
F-THYRO1000662//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0072:141:70//AB016874
25 F-THYRO1000666//Mus musculus mRNA for motor domain of KIF9, partial cds.//4.7e-58:367:87//AB001437
F-THYRO1000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//1.2e-36:396:71//AC005778
F-THYRO1000684//Fugu rubripes cosmid 165K09 DNA for GRM7, TRIP, Sand, PRGFR3 genes.//6.6e-13:236:69//AJ010317
30 F-THYRO1000699//RPC11-50D4.TK RPC11 Homo sapiens genomic clone R-50D4, genomic survey sequence.//2.7e-09:135:78//AQ052641
F-THYRO1000712//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//5.2e-17:290:67//AC005053
35 F-THYRO1000715//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.6e-08:517:60//L14320
F-THYRO1000734//HS_3233_B1_B04_T7 CIT Approved Human Genomic Sperm Library D-Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence.//6.0e-72:463:89//AQ182143
F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds.//9.7e-34:339:74//AB007871
40 F-THYRO1000756//M.musculus mRNA for Gal beta1, 3GalNAc alpha2,3-sialyltransferase.//0.00034:349:60//X73523
F-THYRO1000777//S.griseus strO gene and sts gene cluster.//8.2e-05:625:59//Y08763
F-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//4.0e-70:860:69//U37373
45 F-THYRO1000787//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 366D1, WORKING DRAFT SEQUENCE.//5.3e-09:221:66//Z97986
F-THYRO1000793
F-THYRO1000796//Cristatella mucedo clone 5.9 microsatellite sequence.//0.34:173:63//AF085422
F-THYRO1000805//Homo sapiens Xp21 PAC RPC11-37A12 containing exons 10 to 16 of the Duchenne Muscular
50 Dystrophy gene, complete sequence.//7.8e-43:677:66//AC004468
F-THYRO1000815//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//5.5e-43:405:77//AC005914
F-THYRO1000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence.//2.0e-20:159:88//AQ240053
55 F-THYRO1000843
F-THYRO1000852//Homo sapiens chromosome 19, cosmid R31855, complete sequence.//1.8e-33:445:72//AC005782
F-THYRO1000855//Mus musculus potassium channel alpha subunit (Kv9.1) mRNA, complete cds.//0.038:208:

- 64//AF008573
 F-THYRO1000865//Homo sapiens PAC clone DJ0283M22 from 14, complete sequence.//1.9e-30:286:74//AC005477
 F-THYRO1000895//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 385E7, WORKING DRAFT SEQUENCE.//2.8e-18:186:80//AL031720
 5 F-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-78:432:93//AC006015
 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.2e-178:839:98//AF079529
 10 F-THYRO1000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:759:63//M77836
 F-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229
 F-THYRO1000952
 F-THYRO1000974//HS_3238_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//12.4e-26:154:96//AQ219846
 15 F-THYRO1000975//Plasmodium falciparum TopoII gene.//0.32:491:58//X79345
 F-THYRO1000983//Mvwl9A3 exon amplification products from BACs in Mvwl region Mus musculus genomic, genomic survey sequence.//7.0e-16:112:94//AQ010457
 F-THYRO1000984//CIT-HSP-2167O17.TR CIT-HSP Homo sapiens genomic clone 2167O17, genomic survey sequence.//0.00015:186:66//B91313
 20 F-THYRO1000988//Human Chromosome 11q12.2 PAC clone pDJ756b9 containing human ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.024:267:63//AC004588
 F-THYRO1001003
 F-THYRO1001031//Homo sapiens chromosome 17, clone hRPC.859_O_20, complete sequence.//1.1e-55:543:72//AC003695
 25 F-THYRO1001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328 (section 5 of 148) of the complete genome.//0.94:445:58//AE000799
 F-THYRO1001062//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320
 30 F-THYRO1001093//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//4.9e-34:353:76//AC006241
 F-THYRO1001100//Human DNA-binding protein mRNA, 3'end.//1.1e-72:742:74//L14787
 F-THYRO1001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522
 35 F-THYRO1001121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 671O14, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595
 F-THYRO1001133//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//4.0e-35:349:76//AC004996
 F-THYRO1001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486
 40 F-THYRO1001142//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178
 F-THYRO1001173
 F-THYRO1001177//Human pigment epithelium-derived factor gene, complete cds.//1.9e-42:250:86//U29953
 45 F-THYRO1001189//HS_3171_B2_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=20 Row=L, genomic survey sequence.//1.8e-28:246:83//AQ302330
 F-THYRO1001204//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//4.9e-39:657:64//U34925
 F-THYRO1001213//, complete sequence.//1.7e-45:257:84//AC005300
 50 F-THYRO1001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.5e-40:274:87//AP000036
 F-THYRO1001271//Streptomyces coelicolor cosmid 1A6.//0.033:364:61//AL023496
 F-THYRO1001287//Drosophila melanogaster cosmid clone 86E4.119.6e-49:586:69//AL021086
 F-THYRO1001290//HS_2045_B1_H09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2045 Col=17 Row=P, genomic survey sequence.//4.4e-13:156:78//AQ248237
 55 F-THYRO1001313//S. lavendulae bla gene for beta-lactamase, complete cds.//1.0:229:64//D12693
 F-THYRO1001320//Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 In BCRL2-GGT Region, complete sequence.//1.1e-88:672:82//AC002472

F-THYRO1001321//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.2e-115:740:87//AC000114
 F-THYRO1001322//HS_3205_B2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3205 Col=24 Row=F, genomic survey sequence.//0.00031:285:61//AQ304025
 F-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//2.2e-43:638:64//AB018288
 5 F-THYRO1001363//Homo sapiens PAC clone DJ0845121 from 7q11.21-q11.23, complete sequence.//1.0e-09:189:
 74//AC004905
 F-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map-10q25, complete sequence.//
 7.6e-168:821:97//AC005660
 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//2.3e-155:740:97//AB014607
 10 F-THYRO1001401//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//3.2e-07:138:73//
 AC005239
 F-THYRO1001403//Homo sapiens chromosome 12p13.3 clone RPC13-454B23, WORKING DRAFT SEQUENCE,
 48 unordered pieces.//3.6e-70:360:86//AC005845
 F-THYRO1001405//Bos taurus mRNA for NDP52, complete cds.//2.6e-14:559:63//AB008852
 15 F-THYRO1001406//Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.//1.0e-91:631:
 82//AF064635
 F-THYRO1001411//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//5.5e-42:509:71//
 AC006126
 F-THYRO1001426//*** SEQUENCING IN PROGRESS *** Homo sapiens genomic DNA (PAC 1118i22) from chro-
 some 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.7e-31:172:81//AJ002553
 20 F-THYRO1001434//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered piec-
 es.//1.0:98:70//AC000384
 F-THYRO1001458//Bos taurus non-muscle myosin heavy chain mRNA, partial cds.//1.9e-58:653:71//U87265
 F-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//
 7.5e-42:357:80//AC006001
 25 F-THYRO1001487//H.sapiens DNA sequence.//0.92:160:64//Z22449
 F-THYRO1001534//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3
 unordered pieces.//4.8e-47:266:80//AC004666
 F-THYRO1001537//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING
 30 DRAFT SEQUENCE.//1.3e-79:479:89//AL031687
 F-THYRO1001541//Human DNA sequence from clone 399M14 on chromosome Xq26.1-26.3. Contains ESTs, an
 STS and GSSs, complete sequence.//0.0034:106:77//Z96074
 F-THYRO1001559//Rattus norvegicus simple sequence repeat D18Mco6.//1.6e-09:351:63//AF006056
 F-THYRO1001570//RPC111-49B23.TJ RPC111 Homo sapiens genomic clone R-49B23, genomic survey se-
 35 quence.//1.4e-65:384:91//AQ052105
 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA.//8.2e-104:546:95//AF070572
 F-THYRO1001584//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey se-
 quence.//1.3e-24:180:88//AQ080498
 F-THYRO1001595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING
 40 DRAFT SEQUENCE.//8.7e-145:779:93//AL023808
 F-THYRO1001602//Homo sapiens chromosome 17, clone hRPK:786_O_4, complete sequence.//2.9e-26:393:68//
 AC005863
 F-THYRO1001605//Dictyostelium discoideum filopodin (ItaA) gene, complete cds.//0.0012:436:58//U14576
 F-THYRO1001617//Homo sapiens full-length insert cDNA clone ZD69D05.//8.6e-43:342:82//AF086381
 45 F-THYRO1001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10 unordered pieces.//
 6.2e-15:318:66//AC004950
 F-THYRO1001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.5e-05:147:68//
 AC004827
 F-THYRO1001661
 50 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//2.5e-164:780:98//
 AJ225089
 F-THYRO1001673//Homo sapiens clone RG161A02, complete sequence.//4.4e-40:770:64//AC005071
 F-THYRO1001703//S.coelicolor plasmid SCP2 transfer region DNA.//0.14:414:59//X72857
 F-THYRO1001706//Homo sapiens BAC clone RG281B09 from 7q21.1-q31.1, complete sequence.//2.6e-43:308:
 55 75//AC004745
 F-THYRO1001721//, complete sequence.//9.9e-134:770:91//AC005500
 F-THYRO1001738//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 355C18, WORKING
 DRAFT SEQUENCE.//0.99:163:61//AL022327

F-THYRO1001745
 F-THYRO1001746
 F-THYRO1001772//HS_3069_B1_C05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3069 Col=9 Row=F, genomic survey sequence.//1.5e-61:360:91//AQ171021
 5 F-THYRO1001793//B.taurus mRNA for beta-subunit of rod photoreceptor CNG-channel.//0.028:446:58//X89626
 F-THYRO 1001809
 F-THYRO1001828//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 110F11, WORKING
 DRAFT SEQUENCE.//1.3e-175:841:98//AL033526
 F-THYRO1001854//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.9e-07:445:59//
 10 AC003664
 F-THYRO1001895
 4.4e-13:248:68//AB012576
 F-THYRO1001907//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.9e-15:144:77//
 AC005058
 15 F-VESEN1000122//HS_3075_B1_C09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3075 Col=17 Row=F, genomic survey sequence.//1.1e-16:130:90//AQ143749
 F-Y79AA1000013
 F-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//2.9e-95:300:94//
 AC006027
 20 F-Y79AA1000037//Human prot-oncogene (BMI-1) mRNA, complete cds.//2.4e-19:230:66//L13689
 F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds.//2.2e-38:629:64//U78521
 F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers DXS6791 and DXS8038 on
 chromosome X contains EST.//5.3e-10:117:83//Z72005
 F-Y79AA1000131//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//7.6e-10:381:64//U92893
 25 F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from
 gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island,
 complete sequence.//1.4e-165:732:99//AL031864
 F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.//9.1e-
 20:339:65//AC005115
 30 F-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//
 3.7e-72:397:93//AC004854
 F-Y79AA1000230
 F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cds.//8.5e-151:833:90//AF053232
 F-Y79AA1000258//Leishmania donovani histidine secretory acid phosphatase (SACP-1) gene, complete cds.//
 35 0.0099:547:58//U78522
 F-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//4.0e-11:424:62//AF035207
 F-Y79AA1000313
 F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey se-
 quence.//5.9e-07:173:69//B55085
 40 F-Y79AA1000342//RPC111-57J6.TK.1 RPC111 Homo sapiens genomic clone R-57J6, genomic survey sequence.//
 5.2e-27:151:99//AQ115511
 F-Y79AA1000346//B.primigenius mRNA for coat protein gamma-cop.//5.7e-69:694:71//X92987
 F-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//1.8e-98:535:92//X84692
 F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-
 45 21:129:85//AC005484
 F-Y79AA1000368//H.sapiens CpG island DNA genomic MseI fragment, clone 12f1, reverse read cpg12f1.rt1c.//
 0.00016:53:98//Z56610
 F-Y79AA1000405//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P4, WORKING
 DRAFT SEQUENCE.//0.069:366:59//AL031747
 50 F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome X.//1.0e-25:235:80//Z86061
 F-Y79AA1000420//H.sapiens CpG island DNA genomic MseI fragment, clone 82c3, forward read cpg82c3.ft1a.//
 2.0e-36:194:98//Z63378
 F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete
 cds.//8.5e-121:696:89//U41736
 55 F-Y79AA1000480//HS_2175_A2_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2175 Col=22 Row=O, genomic survey sequence.//2.5e-26:178:89//AQ307693
 F-Y79AA1000538//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//
 0.67:111:72//AC004980

F-Y79AA1000539//HS_2237_B2_F10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, genomic survey sequence//1.2e-14:168:77//AQ153503
 F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUENCE, 8 unordered pieces//0.94:127:67//AC005193
 5 F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C)//1.7e-114:776:84//X14972
 F-Y79AA1000574//M.musculus tex23 mRNA (5'region)//1.8e-23:291:75//X80424
 F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//8.6e-153:755:97//AF091080
 F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//5.2e-135:644:98//AF060503
 F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1//6.9e-148:902:86//X69942
 10 F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assembly factor, complete cds//4.8e-180:850:98//AB018080
 F-Y79AA1000748//Caenorhabditis elegans cosmid F25B5//0.00019:308:60//U23172
 F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein//1.7e-40:513:68//AJ003023
 F-Y79AA1000774
 15 F-Y79AA1000782
 F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//3.5e-177:847:97//AF098799
 F-Y79AA1000794//H.sapiens CpG island DNA genomic Mse1 fragment, clone 45a4, forward read cpG45a4.ft1a.//2.5e-13:104:92//Z61120
 F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.98:244:60//AF056085
 20 F-Y79AA1000802
 F-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence//9.3e-76:528:85//U73642
 F-Y79AA1000824//RPCI11-26B4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-26B4, genomic survey sequence//4.4e-14:99:95//B84538
 F-Y79AA1000827//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING
 25 DRAFT SEQUENCE//1.5e-08:249:69//AL022315
 F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin//1.8e-103:603:89//X04757
 F-Y79AA1000850
 F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat//0.038:468:59//Z82203
 30 F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds//9.7e-150:865:89//AF071314
 F-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds//6.4e-122:717:88//U38253
 F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence//1.0:155:63//AC002397
 35 F-Y79AA1000976//Caenorhabditis elegans cosmid F54C1//4.3e-06:130:73//U88165
 F-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds//2.4e-44:428:77//U05823
 F-Y79AA1001023
 F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//2.3e-13:90:100//U63329
 40 F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds//2.6e-28:772:60//D43682
 F-Y79AA1001061//Homo sapiens chromosome 4 clone B331M8 map 4q25, complete sequence//9.4e-36:292:82//AC004701
 F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [Streptomyces lividans, Genomic, 1146 nt]//0.17:537:59//S64314
 45 F-Y79AA1001077//Zea mays mRNA for aldehyde oxidase-2, complete cds//0.17:231:64//D88452
 F-Y79AA1001078
 F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete cds//3.1e-63:529:77//D26173
 F-Y79AA1001145//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces//1.3e-23:228:76//AC005015
 50 F-Y79AA1001167
 F-Y79AA1001177//M.musculus mRNA for NfiX1-protein//4.0e-10:398:64//Y07688
 F-Y79AA1001185//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 16915, WORKING
 DRAFT SEQUENCE//1.1e-113:666:90//Z93015
 55 F-Y79AA1001211//HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence//5.5e-12:87:96//AQ187492
 F-Y79AA1001216
 F-Y79AA1001228//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162//0.028:188:67//

- AL021841
F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogenase mRNA, complete cds //3.5e-24:731:60//M36263
- 5 F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLC1101133Q7 (RZPD Berlin))//1.2e-133:441:97//AJ005892
- F-Y79AA1001281//HS_2241_B2_F09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2241 Col=18 Row=L, genomic survey sequence //5.0e-27:169:94//AQ217497
- F-Y79AA1001299//Human Ini1 mRNA, complete cds //6.7e-115:323:93//U04847
- 10 F-Y79AA1001312
- F-Y79AA1001323
- F-Y79AA1001384
- F-Y79AA1001391//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds //5.8e-42:245:74//U59322
- F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequence //7.8e-18:636:58//Z48583
- 15 F-Y79AA1001402//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence //1.2e-110:738:85//AC005924
- F-Y79AA1001493//H.sapiens DNA sequence //2.0e-27:254:82//Z22497
- F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence //1.1e-158:804:95//AL034430
- 20 F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds //1.7e-100:820:78//D14336
- F-Y79AA1001541//HS_3197_A2_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence //5.1e-28:218:86//AQ150183
- F-Y79AA1001548//Homo sapiens chromosome 19, cosmid: R28738, complete sequence //5.4e-21:167:86//AC004151
- 25 F-Y79AA1001555//R.norvegicus mRNA for drebrin A //0.88:463:59//X59267
- F-Y79AA1001581//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt] //0.00051:252:65//S74494
- F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds //7.2e-33:375:76//M26434
- 30 F-Y79AA1001594
- F-Y79AA1001603//Homo sapiens PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence //4.2e-06:338:66//AF064861
- F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds //0.024:520:57//AB014583
- 35 F-Y79AA1001647//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53F4, WORKING DRAFT SEQUENCE //0.014:331:61//Z92860
- F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence //0.99:273:63//Z84468
- F-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds //1.2e-97:682:81//M22743
- 40 F-Y79AA1001692//Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1292 nt, segment 1 of 4] //5.6e-05:426:59//S37712
- F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polyprotein (containing putative helicase and putative RNA-dependent RNA polymerase domains), complete cds //1.0:437:60//D32136
- F-Y79AA1001705//M.musculus fkh-5 gene //0.18:153:64//X71943
- 45 F-Y79AA1001711//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE //5.4e-76:191:98//AL022240
- F-Y79AA1001781//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15, WORKING DRAFT SEQUENCE //0.99:227:63//AP000017
- F-Y79AA1001805//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpg13d12.r1c //2.6e-13:88:100//Z64565
- 50 F-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds //3.7e-130:775:88//U74297
- F-Y79AA1001846//CIT-HSP-2300M6.TR CIT-HSP Homo sapiens genomic clone 2300M6, genomic survey sequence //8.3e-17:218:76//AQ012369
- F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds //4.2e-10:378:62//AB002388
- 55 F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (rKr1) mRNA, complete cds //6.9e-41:441:71//U41164
- F-Y79AA1001874//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds //0.00017:412:62//AF029779

EP 1 074 617 A2

F-Y79AA1001875//CTT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271:67//AQ042654
F-Y79AA1001923//H.sapiens CpG island DNA genomic MseI fragment, clone 193c12, forward read cpg193c12.ft1a.//0.0031:108:75//Z60186
5 F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184
F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340
F-Y79AA1002083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 526114, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214
10 F-Y79AA1002089
F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 mRNA, partial cds.//1.2e-112:678:88//U43548
F-Y79AA1002103//HS_3052_B1_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014
15 F-Y79AA1002115
F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693
F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358
20 F-Y79AA1002204//HS_2235_B2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260
F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397
F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719
25 F-Y79AA1002210//Homo sapiens chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615
F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043
F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738
30 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045
F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.3e-174:821:98//AB014592
F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.50:470:60//AC005015
35 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6.8e-159:748:98//AB014555
F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds.//0.036:278:62//U10886
F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.4e-129:622:97//AB014534
F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877
F-Y79AA1002351//S.clavuligerus pah and cas genes.//1.0:369:58//X84101
40 F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//5.4e-105:762:80//Y18208
F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.0e-159:411:100//AC005920
F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//1.1e-118:609:84//AC004662
45 F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsh) mRNA, complete cds.//4.4e-90:529:88//U49385
F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, complete cds.//1.0:166:66//U36196
F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917
50 F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.9e-13:242:69//AC006116
F-Y79AA1002482//Homo sapiens full-length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022
F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677

55 Homology Search Result Data 3.

[0303] The result of the homology search of the GenBank using the clone sequence of 3'-end except EST and STS.

[0304] Data include

the name of clone,
 definition of the top hit data,
 the P-value: the length of the compared sequence: identity (%), and
 the Accession No. of the top hit data, as in the order separated by ///.

5

[0305] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0306] Data are not shown for the clones in which the P-value was higher than 1.

10

R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.6e-60:504:78//L16953

R-HEMBA1000030//F.rubripes GSS sequence, clone 063K10bD3, genomic survey sequence.//0.28:117:68//Z88864

R-HEMBA1000042//RPC11-77G23.TV RPC11 Homo sapiens genomic clone R-77G23, genomic survey sequence.//1.3e-56:292:97//AQ268240

R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence.//9.8e-56:401:82//U82696

15

R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455.//0.0010:175:68//L31948

R-HEMBA1000076//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.9e-41:364:79//AC005520

R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//4.7e-30:229:84//AC003684

20

R-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//2.4e-93:503:93//AC003104

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//6.5e-99:514:94//AB018340

R-HEMBA1000150//Homo sapiens clone RG086D03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.7e-37:289:83//AC005060

25

R-nnnnnnnnnnnnn//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64//L43631

R-HEMBA1000158

R-nnnnnnnnnnnnn

R-HEMBA1000180//Plasmodium falciparum encoding PfG27/25.//0.073:292:56//X84904

30

R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.3e-40:286:85//AC006146

R-HEMBA1000193

R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y17126

R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF100655

35

R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//2.5e-31:269:79//AF001548

R-nnnnnnnnnnnnn

R-HEMBA1000231//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//4.3e-24:400:68//AL009181

40

R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.3e-19:319:69//AC004526

R-HEMBA1000244

R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds; transfer RNA-His gene; 16S ribosomal RNA gene; ND3 gene, complete cds; cytochrome b (cytb) gene, 5' end of cds.//0.16:338:60//L76262

45

R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012

R-nnnnnnnnnnnnn//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//3.5e-10:238:70//AC003037

R-HEMBA1000282//Arabidopsis thaliana BAC IG002P16.//0.71:344:60//AF007270

50

R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//4.8e-33:267:82//AC003046

R-HEMBA1000290//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//2.2e-15:249:69//AC004223

R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP Homo sapiens genomic clone 2173N10, genomic survey sequence.//1.0:215:61//B95105

55

R-nnnnnnnnnnnnn//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//1.0e-77:551:82//AF030131

R-nnnnnnnnnnnnn//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//2.0e-96:546:90//U16802

- R-HEMBA1000307//Mus musculus mRNA for CDV-1 protein//3.8e-36:315:68//Y10496
 R-nnnnnnnnnnn//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces//0.078:379:59//AC005505
 R-HEMBA1000338//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE//2.0e-33:399:72//AL031667
 5 R-HEMBA1000351//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease//1.7e-39:272:87//AJ003147
 R-HEMBA1000355//Human primary Alu transcript//0.0045:67:85//U67829
 R-HEMBA1000357//Homo sapiens (subclone 9_h8 from PI H16) DNA sequence//8.7e-93:426:88//L42086
 10 R-HEMBA1000366//Homo sapiens PAC clone DJ094216 from 7q11, complete sequence//1.7e-12:130:83//AC006012
 R-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence//1.9e-69:355:97//AL031587
 15 R-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence//3.7e-66:410:89//AC006116
 R-HEMBA1000387//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces//2.0e-43:363:81//AC002993
 R-HEMBA1000390//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence//4.6e-23:417:69//AC005053
 20 R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence//6.2e-05:174:68//AC004582
 R-HEMBA1000396//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein//1.4e-62:564:77//AL022575
 25 R-HEMBA1000411
 R-HEMBA1000418//Liverwort Marchantia polymorpha chloroplast genome DNA//0.94:210:60//X04465
 R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP Homo sapiens genomic clone 2382A6, genomic survey sequence//4.4e-12:98:92//AQ078233
 R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence//2.0e-93:526:90//Z95400
 30 R-HEMBA1000434//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces//2.7e-07:452:60//AC004826
 R-HEMBA1000442//E.caballus microsatellite DNA, clone HMB4//0.39:135:62//Y07733
 R-HEMBA1000456//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete sequence//2.6e-05:174:70//AL010226
 35 R-HEMBA1000459//Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), putative acyl-coA dehydrogenase (AtG6), and calcium dependent protein kinase genes, complete cds; and unknown genes//0.013:212:63//AF049236
 40 R-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence//8.6e-114:556:98//AC004839
 R-HEMBA1000464//Caenorhabditis elegans cosmid C34B7, complete sequence//0.086:334:61//Z83220
 R-HEMBA1000469//Homo sapiens BAC clone RG442F18 from 2, complete sequence//1.8e-52:472:79//AC005104
 45 R-HEMBA1000488//, complete sequence//3.3e-68:200:99//AC005500
 R-HEMBA1000490//Caenorhabditis elegans cosmid Y53C12B, complete sequence//0.97:233:61//Z99278
 R-HEMBA1000491
 R-HEMBA1000504//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-64, complete sequence//1.7e-08:440:60//AL009014
 50 R-HEMBA1000505//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11//0.37:189:62//AB020858
 R-HEMBA1000508//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X//1.1e-25:248:80//Z70280
 R-HEMBA1000518//RPCI11-6022.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6022, genomic survey sequence//0.0035:293:61//B49544
 55 R-HEMBA1000519
 R-HEMBA1000520//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence//0.30:255:63//AC006232

- R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds.//1.2e-53:203:92//U15782
- R-HEMBA1000531//CIT-HSP-388J17.TR CIT-HSP Homo sapiens genomic clone 388J17, genomic survey sequence.//2.7e-24:137:99//B55638
- 5 R-HEMBA1000540//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044
- R-HEMBA1000545//Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.//6.9e-87:552:87//AC004103
- 10 R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//5.7e-45:307:87//AC004381
- R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence.//1.3e-43:279:90//AF046762
- R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//3.8e-05:506:56//AE001368
- 15 R-HEMBA1000568//RPC11-49P8.TK.1 RPC11 Homo sapiens genomic clone R-49P8, genomic survey sequence.//1.7e-101:498:97//AQ116293
- R-HEMBA1000575//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 754E20, WORKING DRAFT SEQUENCE.//1.3e-47:458:75//AL022335
- 20 R-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.9e-62:447:81//AF045573
- R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.2e-111:591:9411AJ007509
- R-HEMBA1000592//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-10, complete sequence.//3.5e-09:421:60//AL010216
- 25 R-HEMBA1000594//Homo sapiens clone RG004N09, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-15:421:66//AC005044
- R-HEMBA1000604//HS_2220_A1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=19 Row=M, genomic survey sequence.//1.0e-51:306:92//AQ151991
- 30 R-HEMBA1000608
- R-HEMBA1000622//H.sapiens CpG island DNA genomic MseI fragment, clone 155e4, reverse read cpg155e4.r11a.//4.5e-16:105:98//Z56962
- R-HEMBA1000636//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//4.8e-62:421:86//AP000008
- 35 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.2e-97:443:97//AB014590
- R-HEMBA1000655//Homo sapiens chromosome 19, cosmid R26349, complete sequence.//9.8e-61:311:90//AC005953
- R-HEMBA1000657
- R-HEMBA1000662
- 40 R-HEMBA1000673//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//1.0e-13:351:63//Z97196
- R-HEMBA1000682//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-50:298:79//AC005377
- R-HEMBA1000686//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00048:210:62//AQ093513
- 45 R-HEMBA1000702//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.7e-54:317:88//AC005000
- R-HEMBA1000705//Glossonotus uhivittatus 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//0.080:138:65//U77850
- 50 R-HEMBA1000719//Rattus norvegicus mRNA for TESK1, complete cds.//0.96:291:58//D50864
- R-HEMBA1000722
- R-HEMBA1000726//Homo sapiens PAC clone DJ0701016 from 7q33-q36, complete sequence.//4.4e-26:284:77//AC005531
- R-HEMBA1000727//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//9.1e-05:351:60//AL010266
- 55 R-HEMBA1000747//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.5e-16:123:93//AL021326

- R-HEMBA1000749//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//2.8e-32:298:79//AC003108
- R-HEMBA1000752//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-90:542:90//Z92545
- 5 R-HEMBA1000769//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-36:405:75//AC005031
- R-HEMBA1000773//HS_3050_A2_B08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=16 Row=C, genomic survey sequence.//0.00053:268:60//AQ105619
- 10 R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//4.7e-46:338:85//AC004690
- R-HEMBA1000791//**ALU WARNING: Human Alu-Sc subfamily consensus sequence.//5.3e-47:279:91//U14571
- R-HEMBA10008177//Sequence 1 from Patent WO 8904839.//0.86:148:67//I09339
- R-HEMBA1000822//T.brucei kinetoplast maxicircle variable region DNA.//0.00061:246:61//Z15118
- 15 R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds.//6.9e-43:228:98//AF048977
- R-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.7e-41:319:84//AL022394
- 20 R-HEMBA1000851//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.40:168:67//AC004260
- R-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPC14-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.5e-112:572:96//AC005295
- 25 R-HEMBA1000867//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//0.11:121:71//AC004938
- R-HEMBA1000869//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-22:186:76//AC002042
- 30 R-HEMBA1000870//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//0.0060:283:63//AC002528
- R-HEMBA1000872//Rattus norvegicus polymorphic satellite repetitive elements.//3.8e-05:269:61//M98801
- R-HEMBA1000876//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-38:327:77//AC006057
- 35 R-HEMBA1000908//CIT-HSP-2373I4.TR CIT-HSP Homo sapiens genomic clone 2373I4, genomic survey sequence.//5.0e-34:221:90//AQ108658
- R-HEMBA1000910//T.pigmentosa UM1060 macronuclear rDNA telomeric region 3' term.//0.19:280:61//X04205
- R-HEMBA1000918//RPC111-68E14.TK RPC111 Homo sapiens genomic clone R-68E14, genomic survey sequence.//1.3e-32:172:100//AQ267293
- 40 R-HEMBA1000919
- R-HEMBA1000934//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.6e-18:284:71//AL021997
- R-HEMBA1000942//Homo sapiens clone RG350L10, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.4e-17:217:76//AC005098
- 45 R-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//9.0e-113:586:95//AC005324
- R-HEMBA1000946//T5N8TFB TAMU Arabidopsis thaliana genomic clone T5N8, genomic survey sequence.//0.030:369:59//B26224
- 50 R-HEMBA1000960//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-52:494:77//AC005096
- R-HEMBA1000968//Homo sapiens P1 clone 797a11 containing MHC class II DQ-beta (HLA-DQB) and MHC class II DC-alpha (HLA-DCA) genes, complete cds.//3.5e-77:568:83//U92032
- R-HEMBA1000971//RPC111-54D1.TJ RPC111 Homo sapiens genomic clone R-54D1, genomic survey sequence.//2.3e-27:153:98//AQ081552
- 55 R-HEMBA1000972//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//7.3e-43:375:79//AL023876
- R-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//2.8e-104:521:97//AC004817

- R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//8.0e-22:352:68//AL031311
- R-HEMBA1000985//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-05:306:63//AC004888
- 5 R-HEMBA1000986//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.7e-37:296:83//AC005632
- R-HEMBA1000991//RPCI11-22017.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22017, genomic survey sequence.//6.5e-44:162:90//AQ008952
- R-HEMBA1001007
- 10 R-HEMBA1001008//Homo sapiens chromosome 16, P1 clone 79-2A (LANL), complete sequence.//0.082:313:60//AC005365
- R-HEMBA1001009//O.sativa osr40g2 gene.//0.99:203:62//Y08987
- R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//1.0e-113:587:95//AB007937
- R-HEMBA1001019//Bos taurus cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, complete cds.//7.4e-24:215:82//L26547
- 15 R-HEMBA1001020//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//2.8e-18:449:64//AL008722
- R-HEMBA1001022
- R-HEMBA1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//6.6e-48:536:74//AF070717
- 20 R-HEMBA1001026//T33H14TF TAMU Arabidopsis thaliana genomic clone T33H14, genomic survey sequence.//0.013:180:66//B97363
- R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region.//2.4e-24:279:74//X04751
- R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.3e-38:188:89//AC004217
- 25 R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region.//2.4e-24:279:74//X04751
- R-HEMBA1001060//HS_2056_B1_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence.//4.1e-14:137:83//AQ245004
- R-HEMBA1001071//M.musculus COL3A1 gene for collagen alpha-1.//6.9e-38:513:70//X52046
- 30 R-HEMBA1001077//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//1.9e-22:507:61//AL022318
- R-HEMBA1001080
- R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase Iix genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.2e-43:317:83//AC004586
- 35 R-HEMBA1001088//Caenorhabditis elegans cosmid C18H7.//0.46:301:60//AF067607
- R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//5.3e-98:501:96//AC005105
- R-HEMBA1001099
- R-HEMBA1001109//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE.//3.1e-39:335:80//AL033527
- 40 R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2.//9.8e-11:122:81//U81833
- R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence.//0.0024:284:63//Z98551
- R-HEMBA1001123//Human NFE genomic fragment.//3.6e-26:318:72//M98511
- R-HEMBA1001133
- R-HEMBA1001137//Homo sapiens full-length insert cDNA clone ZD29F04.//4.2e-88:426:98//AF086241
- 45 R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-41:304:84//AC005077
- R-HEMBA1001172//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//3.7e-36:261:85//Z98304
- R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.0:219:58//AE001398
- 50 R-HEMBA1001197
- R-HEMBA1001208//HS_2233_A1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey sequence.//0.083:174:68//AQ170789
- R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-59:553:75//AC005377
- 55 R-HEMBA1001235//RPCI11-50E6.TJ RPCI11 Homo sapiens genomic clone R-50E6, genomic survey sequence.//2.6e-08:97:76//AQ052666
- R-HEMBA1001247//Caenorhabditis elegans cosmid C01F1.//2.4e-05:319:63//U58761

- R-HEMBA1001257//Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.//1.5e-24:439:66//U89905
- R-HEMBA1001265//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//9.9e-21:537:63//AC004491
- 5 R-nnnnnnnnnnnn//Homo sapiens chromosome 17, clone HCIT75G16, complete sequence.//0.022:169:65//AC003042
- R-HEMBA1001286
- R-HEMBA1001289
- R-HEMBA1001294//HS_3219_A2_G01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=2 Row=M, genomic survey sequence.//0.24:251:63//AQ189882
- 10 R-HEMBA1001299//Homo sapiens, clone hRPK.12_A_1, complete sequence.//1.3e-38:381:76//AC006222
- R-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//4.1e-28:114:92//E12258
- R-HEMBA1001303//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.00011:382:58//AL031744
- 15 R-HEMBA1001310
- R-HEMBA1001319//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-09:491:58//AC005504
- R-HEMBA1001323//Drosophila yakuba mitochondrial DNA molecule.//8.3e-06:485:60//X03240
- 20 R-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//2.2e-14:277:69//AL021368
- R-HEMBA1001327//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.15:360:61//AL024509
- R-HEMBA1001330//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-27:481:67//AC004216
- 30 R-HEMBA1001351//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence.//7.1e-45:252:94//AC006238
- R-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//1.4e-113:569:97//AC006241
- R-HEMBA1001375//Homo sapiens full-length insert cDNA clone ZE09H03.//2.8e-89:428:99//AF086542
- 35 R-HEMBA1001377//Homo sapiens PAC clone DJ0728D04, complete sequence.//2.3e-32:324:77//AC004865
- R-HEMBA1001383
- R-HEMBA1001387
- R-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//8.9e-06:108:83//AC005073
- 40 R-HEMBA1001391//Yeast mitochondrial aapl gene for ATPase subunit 8.//7.3e-08:500:59//X00960
- R-HEMBA1001398//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//2.3e-48:315:88//AP000050
- R-HEMBA1001405//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//5.5e-35:464:68//AL034380
- 45 R-HEMBA1001407
- R-HEMBA1001411//Yeast (S.cerevisiae) mitochondria Ser-tRNA-UCN gene and flanks.//0.00029:301:62//K01981
- R-HEMBA1001413
- R-HEMBA1001415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41018, WORKING DRAFT SEQUENCE.//5.6e-101:512:96//AL031732
- 50 R-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.3e-37:302:81//AC006146
- R-HEMBA1001433//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.9e-32:242:79//Z97054
- 55 R-HEMBA1001435//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//5.7e-59:457:82//AC004527
- R-HEMBA1001442//Human DNA sequence from PAC 507115 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//0.051:276:63//Z98950

EP 1 074 617 A2

R-HEMBA1001446//HS_3207_A1_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey sequence.//8.9e-06:119:73//AQ175385
R-HEMBA1001450//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//0.0043:266:63//AC005065
5 R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from 7q31, complete sequence.//7.1e-25:210:82//AC004855
R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//2.7e-08:316:62//AC005324
R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064_E_11, complete sequence.//0.57:219:60//AC005208
10 R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//9.3e-50:252:80//AC004840
R-HEMBA1001478
R-HEMBA1001497
15 R-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//3.5e-41:282:86//U89337
R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//1.9e-79:529:86//Z98753
R-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//4.3e-18:335:71//AC004549
20 R-HEMBA1001522
R-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//5.6e-08:265:67//Z98258
R-HEMBA1001533//Human DNA sequence from PAC 179M20 on chromosome 20q12-13.1. Contains adenosine deaminase (ADA), placental protein Diff33, CA repeat, ESTs, STS.//7.8e-16:235:72//Z97053
25 R-HEMBA1001557
R-HEMBA1001566//Human Chromosome X clone bWXD187, complete sequence.//2.2e-44:416:78//AC004383
R-HEMBA1001569//Sequence 15 from patent US 5693476.//1.8e-59:389:88//I77040
R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//1.1e-44:316:87//AC004453
30 R-HEMBA1001579//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0047:437:60//AC005506
R-HEMBA1001581//P.falciparum complete gene map of plastid-like DNA (IR-B).//2.3e-07:491:58//X95276
R-HEMBA1001585//Caenorhabditis elegans cosmid C06A6.//0.68:224:62//U41012
35 R-HEMBA1001589
R-HEMBA1001595//CIT-HSP-2349G19. TF CIT-HSP Homo sapiens genomic clone 2349G19, genomic survey sequence.//8.0e-69:337:99//AQ060483
R-HEMBA1001608//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//9.5e-59:514:78//AC005177
40 R-HEMBA1001620//S.polyrrhiza mRNA for D-myo-inositol-3-phosphate synthase.//4.5e-12:289:65//Z11693
R-nnnnnnnnnnnn//HS_2195_A1_E09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=17 Row=I, genomic survey sequence.//5.8e-09:358:58//AQ292688
R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA, complete cds.//0.77:225:59//U04270
45 R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 6p21. Contains ETS related protein TEL like and GS2 like genes, ESTs and an STS.//6.0e-49:404:79//Z84484
R-nnnnnnnnnnnn
R-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.1e-103:532:95//AC005368
50 R-HEMBA1001658//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.0:197:64//AL023808
R-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.5e-100:457:93//AC005740
R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//1.2e-90:496:91//AF072247
55 R-HEMBA1001675
R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds.//1.3e-101:534:94//AF038962

- R-HEMBA1001681//CIT-HSP-2345M7.TF CIT-HSP Homo sapiens genomic clone 2345M7, genomic survey sequence.//0.21:124:68//AQ056593
- R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//8.3e-06:279:63//AC004801
- 5 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds.//1.9e-96:483:96//AB014598
- R-HEMBA1001711//Human HepG2 3' region cDNA, clone hmd2b02.//2.3e-31:169:100//D16886
- R-HEMBA1001712//HS-1015-B1-E01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 790 Col=1 Row=J, genomic survey sequence.//0.0025:200:65/B32577
- 10 R-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//6.6e-27:316:75//U12250
- R-HEMBA1001718//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//3.1e-41:167:87//B89781
- R-HEMBA1001723//Rattus norvegicus EH domain binding protein, Epsin mRNA, complete cds.//0.53:275:61//AF018261
- 15 R-HEMBA1001731//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 322P7, WORKING DRAFT SEQUENCE.//2.9e-48:292:84//AL023799
- R-HEMBA1001734//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-33:290:81//AC005959
- 20 R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21 Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs, GSSs and retroviral sequence, complete sequence.//0.98:203:62//AL022067
- R-HEMBA1001745//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//0.00019:312:59//AC005084
- 25 R-HEMBA1001746//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.045:457:61//AC004153
- R-HEMBA1001761//Homo sapiens chromosome X, clone hCIT.200_L_4, complete sequence.//3.8e-39:331:80//AC006121
- R-HEMBA1001781//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//0.0062:245:60//AC004554
- 30 R-HEMBA1001784//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.1e-22:370:63//AC005740
- R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-50:408:80//AL023575
- 35 R-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//9.0e-37:335:77//AQ009222
- R-HEMBA1001803//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.86:536:56//AC005506
- R-nnnnnnnnnnnn//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//2.9e-93:553:89//M21977
- 40 R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//2.8e-112:548:98//AB007969
- R-HEMBA1001809
- R-HEMBA1001815//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//2.6e-48:363:84//AC004025
- 45 R-HEMBA1001819//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 1577, WORKING DRAFT SEQUENCE.//1.1e-15:275:68//AJ009612
- R-HEMBA1001820//HS_3022_B1_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=17 Row=B, genomic survey sequence.//0.00054:335:59//AQ165107
- R-nnnnnnnnnnnn//Xenopus laevis intersectin mRNA, complete cds.//1.4e-19:533:63//AF032118
- 50 R-HEMBA1001824//S.clavuligerus linear plasmid pSCL (complete sequence).//0.62:189:65//X54107
- R-HEMBA1001835//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.//1.0:450:60//AL024507
- R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene, complete cds.//1.6e-07:170:68//U50871
- R-HEMBA1001847
- 55 R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//3.3e-108:553:96//AB014517
- R-HEMBA1001864//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463
- R-HEMBA1001866//HS_2258_B2_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=H, genomic survey sequence.//2.8e-39:397:75//AQ221138

EP 1 074 617 A2

R-nnnnnnnnnnnnn/Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//5.9e-56:303:94//AC005065

R-HEMBA1001888//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.7e-43:281:88//AC006210

5 R-HEMBA1001896

R-HEMBA1001910

R-HEMBA1001912//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.10:307:61//AC004775

R-HEMBA1001913

10 R-HEMBA1001915//HS_2037_A1_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=23 Row=I, genomic survey sequence.//0.071:206:64//AQ233106

R-HEMBA1001918//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.97:449:59//AC004775

R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.0e-105:534:96//AF000145

15 R-HEMBA1001939//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508115, WORKING DRAFT SEQUENCE.//4.6e-13:120:82//AL021707

R-HEMBA1001940//Homo sapiens clone DJ1093116, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-36:301:81//AC005629

20 R-HEMBA1001942//Human PAC clone DJ0205E24 from Xq23, complete sequence.//1.9e-10:208:68//AC003013

R-HEMBA1001945//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//1.2e-06:393:60//AE001433

R-HEMBA1001950//R.prowazekii genomic DNA fragment (clone A437R).//0.33:122:66//Z82646

R-HEMBA1001960//Borrelia afzelii VS461 outer surface protein D (ospD) gene, complete cds.//0.0086:427:59//U05329

25 R-HEMBA1001962//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//4.5e-07:176:70//AC004069

R-HEMBA1001964//HS_2215_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2215 Col=1 Row=P, genomic survey sequence.//7.3e-25:215:74//AQ151931

30 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//1.7e-51:209:95//AL031178

R-HEMBA1001979//CIT-HSP-2387112.TF.1 CIT-HSP Homo sapiens genomic clone 2387112, genomic survey sequence.//4.9e-06:153:71//AQ240461

35 R-HEMBA1001987//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//3.1e-46:437:77//AL033521

R-HEMBA1001991//Human DNA sequence from PAC 42616 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-48:446:78//AL020997

R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta).//5.1e-90:448:97//AJ005801

40 R-HEMBA1002008//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.2e-42:317:84//Z97181

R-HEMBA1002018//HS_3006_B1_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=19 Row=H, genomic survey sequence.//1.0:63:74//AQ089717

R-HEMBA1002022//Homo sapiens chromosome 18, clone hRPK.453_M_1, complete sequence.//0.93:339:59//AC006203

45 R-HEMBA1002035//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.4e-11:285:67//AC003694

R-HEMBA1002039

R-HEMBA1002049//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING DRAFT SEQUENCE.//5.3e-52:266:84//AL022315

50 R-HEMBA1002084//CIT-HSP-2357L11.TR CIT-HSP Homo sapiens genomic clone 2357L11, genomic survey sequence.//0.0013:185:66//AQ063078

R-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//2.7e-70:479:86//U92703

55 R-HEMBA1002100//Homo sapiens thyroid receptor interactor (TRIP7) mRNA, 3' end of cds.//8.5e-32:206:91//L40357

R-HEMBA1002102//Homo sapiens Chromosome 15q26.1 PAC clone pDJ427d15, complete sequence.//4.3e-42:302:85//AC005800

- R-HEMBA1002113//Human chromosome 12p13 sequence, complete sequence.//1.6e-64:550:80//U47924
 R-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.2e-92:435:92//AC000378
 R-HEMBA1002125
 R-HEMBA1002139//Human nebulin mRNA, partial cds.//0.056:68:88//U35637
 5 R-HEMBA1002144//Homo sapiens Chromosome 11p14.3 PAC clone 6-130a9 containing tryptophan hydroxylase gene, complete sequence.//2.0e-26:323:70//AC005728
 R-HEMBA1002150//Human DNA sequence from clone 742C19 on chromosome 22q12.3-13.1. Contains a pseudogene similar to Cytochrome C Oxidase Polypeptide VB and (parts of) up to four novel genes, two with homology to Phorbolins genes and one a novel Chromobox protein gene. Contains ESTs, an STS, GSSs and putative CpG islands, complete sequence.//1.0:371:61//AL031846
 10 R-HEMBA1002151
 R-HEMBA1002153//Human BAC 367D17 from chromosome 18, complete sequence.//2.4e-21:322:70//AC003971
 R-HEMBA1002160//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of *S.cerevisiae*, DNA binding protein similar to URE-B1, ESTs and STS.//2.5e-38:216:84//Z97054
 15 R-HEMBA1002161//CIT-HSP-2163F10.TF CIT-HSP Homo sapiens genomic clone 2163F10, genomic survey sequence.//3.1e-58:284:80//B89969
 R-HEMBA1002162//Caenorhabditis elegans cosmid F48C11, complete sequence.//0.0079:286:57//Z80789
 R-HEMBA1002166//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//5.9e-53:326:80//AC002980
 20 R-HEMBA1002177
 R-HEMBA1002185//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745I14, WORKING DRAFT SEQUENCE.//9.5e-37:356:76//AL033532
 R-HEMBA1002189//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.4e-43:244:77//AC003684
 25 R-HEMBA1002191//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.3e-37:323:78//AC005077
 R-HEMBA1002199//Human Cosmid g5129g124 from 7q31.3, complete sequence.//1.4e-89:564:87//AC002498
 R-HEMBA1002204//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.5e-31:313:71//AC000053
 30 R-HEMBA1002212//K.lactis mitochondrial COX1 and A8 genes for cytochrome oxidase subunit I and ATPase subunit 8.//0.0023:346:60//X57546
 R-HEMBA1002215//M.musculus mRNA for testin.//4.7e-61:414:84//X78989
 R-HEMBA1002226//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.//4.6e-46:375:77//AL033529
 35 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.6e-46:238:98//AF089814
 R-HEMBA1002237//Homo sapiens 12q13 PAC RPC11-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.3e-26:469:67//AC004242
 40 R-HEMBA1002253//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//5.1e-23:162:82//AC005016
 R-HEMBA1002257
 R-HEMBA1002267//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//4.6e-44:300:88//AF03 8127
 45 R-HEMBA1002270//Human BAC clone RG067M09 from 7q21-7q22, complete sequence.//1.9e-19:176:85//AC000057
 R-HEMBA1002321
 R-HEMBA1002328//HS_3061_A1_D06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=11 Row=G, genomic survey sequence.//1.0:151:65//AQ127617
 50 R-HEMBA1002337//Saccharomyces cerevisiae RNA polymerase II holoenzyme component (SRB7) gene, complete cds.//3.7e-07:328:63//U23811
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-128:642:96//AB018314
 R-HEMBA1002348//Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence.//3.7e-07:587:58//AL031256
 55 R-HEMBA1002349//Leishmania tarentolae maxicircle DNA fragment.//0.018:341:58//X02438
 R-HEMBA1002350//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//1.2e-121:661:93//AF092563
 R-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and

- non-small cell lung cancer, segment 11/11 //1.1e-70:559:79//AB020868
 R-HEMBA1002389//HS_3218_B2_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3218 Col=16 Row=J, genomic survey sequence //0.0011:122:72//AQ213602
 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784, complete sequence //4.2e-81:232:97//
 5 AC005954
 R-HEMBA1002419//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence //0.50:231:64//
 AC004848
 R-HEMBA1002430//P.falciparum complete gene map of plastid-like DNA (IR-B) //0.0023:604:56//X95276
 R-HEMBA1002439//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces //3.4e-
 10 23:183:80//AC006026
 R-HEMBA1002458//Human DNA sequence from clone 146H21 on chromosome Xq22 Contains cleavage stimu-
 lation factor, 64 KD subunit, gene similar to CYTOCHROME B-245 HEAVY CHAIN, pseudogene similar to hnRNP
 A1 protein and ESTs, complete sequence //7.7e-32:161:83//Z83819
 R-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence //2.6e-100:305:100//AC005378
 15 R-HEMBA1002462//Sequence 43 from patent US 5708157 //2.0e-10:131:77//I80068
 R-nnnnnnnnnnnnn
 R-HEMBA1002477//Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence //6.6e-33:279:
 80//AC004841
 R-HEMBA1002486//***ALU WARNING: Human Alu-Sq subfamily consensus sequence //2.1e-50:290:92//U14573
 20 R-HEMBA1002495//CITBI-E1-2515J10.TR CITBI-E1 Homo sapiens genomic clone 2515J10, genomic survey se-
 quence //1.0:122:68//AQ261762
 R-HEMBA1002498//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces //2.8e-22:210:78//AC004963
 R-HEMBA1002503//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence //2.7e-17:435:58//
 25 AC003043
 R-HEMBA1002508//Homo sapiens, clone hRPK.15_A_1, complete sequence //3.7e-09:408:61//AC006213
 R-nnnnnnnnnnnnn/Homo sapiens mRNA for histone deacetylase-like protein (JM21) //7.1e-112:456:92//AJ011972
 R-HEMBA1002515
 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds //1.6e-104:564:93//AB007923
 30 R-HEMBA1002542//HS_3197_B2_B10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3197 Col=20 Row=D, genomic survey sequence //2.8e-25:186:86//AQ188792
 R-HEMBA1002547//Mus musculus agrin gene, exon 36 //0.0095:93:75//M92658
 R-HEMBA1002552//Homo sapiens clone DJ1137M13, complete sequence //4.0e-49:308:90//AC005378
 R-HEMBA1002555//Homo sapiens full-length insert cDNA clone YR87G10 //8.3e-65:318:99//AF085957
 35 R-HEMBA1002558//, complete sequence //2.3e-38:264:89//AC005409
 R-HEMBA1002561//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS,
 GSS, complete sequence //7.1e-44:192:80//AL008634
 R-nnnnnnnnnnnnn/Homo sapiens protein associated with Myc mRNA, complete cds //4.5e-119:587:97//AF075587
 R-HEMBA1002583
 40 R-HEMBA1002590//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains
 the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein
 CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete se-
 quence //9.4e-42:248:88//Z95152
 R-HEMBA1002592//Homo sapiens chromosome 19, cosmid R30385, complete sequence //2.6e-56:302:84//
 45 AC004510
 R-HEMBA1002621
 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds //6.7e-76:380:97//AB018351
 R-HEMBA1002628//P.falciparum complete gene map of plastid-like DNA (IR-A) //8.8e-05:327:60//X95275
 R-HEMBA1002629//Mus musculus clone OST16705, genomic survey sequence //4.3e-06:205:66//AF046247
 50 R-HEMBA1002645//***ALU WARNING: Human Alu-J subfamily consensus sequence //7.1e-39:281:84//U14567
 R-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence //1.1e-104:500:95//
 AC004839
 R-HEMBA1002659//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs
 and GSSs, complete sequence //1.2e-61:280:92//AL022323
 55 R-HEMBA1002661//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 225E12, WORKING
 DRAFT SEQUENCE //3.2e-41:325:81//AL031772
 R-HEMBA1002666//Homo sapiens full-length insert cDNA clone YY74A07 //0.00037:79:84//AF088008
 R-HEMBA1002678//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1137F22, WORK-

ING DRAFT SEQUENCE//2.3e-107:561:94//AL034421
 R-nnnnnnnnnnn/CIT-HSP-2287E8.TF CIT-HSP Homo sapiens genomic clone 2287E8, genomic survey se-
 quence//5.4e-17:137:88//B99281
 R-HEMBA1002688//Homo sapiens chromosome 5, P1 clone 1354A7 (LBNL H47), complete sequence//0.033:
 5 146:70//AC004503
 R-HEMBA1002696
 R-HEMBA1002712//Homo sapiens PAC clone 166H1 from 12q, complete sequence//6.2e-44:302:87//AC003982
 R-HEMBA1002716//Mus musculus mRNA for ELM1, complete cds//1.1e-31:332:76//AB004873
 R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//1.2e-35:287:81//AB014521
 10 R-HEMBA1002730//D.discoideum actin M6 gene, 5' flank//0.018:233:66//M29109
 R-HEMBA1002742//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108H3, WORKING
 DRAFT SEQUENCE//2.6e-13:419:62//AL033525
 R-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence//0.019:202:65//
 AC003694
 15 R-HEMBA1002748//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404K8, WORKING
 DRAFT SEQUENCE//0.046:263:60//AL023883
 R-HEMBA1002750//Human DNA sequence from PAC 452H17 on chromosome X contains sodium-and chloride-
 dependent glycine transporter 1 (GLYT-1) like, ESTs//0.052:421:58//Z96810
 R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.2e-104:545:95//AB011126
 20 R-HEMBA1002770//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING
 DRAFT SEQUENCE, 14 unordered pieces//3.0e-07:523:59//AC005140
 R-HEMBA1002777
 R-HEMBA1002779//Human HepG2 3' region MboI cDNA, clone hmd1e03m3//9.4e-25:158:93//D17139
 R-HEMBA1002780//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORK-
 25 ING DRAFT SEQUENCE//1.6e-42:463:75//AL022344
 R-HEMBA1002794//Plasmodium falciparum MAL3P8, complete sequence//2.2e-05:417:59//AL034560
 R-HEMBA1002801//Meloidogyne javanica mitochondrial transfer RNA^{His}, 16S ribosomal RNA (16S rRNA) genes,
 ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS//0.00055:444:59//L76261
 R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//4.4e-115:559:97//AF071185
 30 R-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces//
 4.3e-88:329:94//AC005043
 R-HEMBA1002826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SE-
 QUENCE//1.9e-22:262:67//AP000041
 R-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence//1.3e-79:396:
 35 97//AC004707
 R-HEMBA1002850//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING
 DRAFT SEQUENCE, 7 unordered pieces//0.013:393:61//AC005506
 R-HEMBA1002863//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence//4.1e-73:489:
 85//AC005562
 40 R-HEMBA1002876//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORK-
 ING DRAFT SEQUENCE//0.21:549:55//AL034557
 R-HEMBA1002886//CIT-HSP-2013C4.TR CIT-HSP Homo sapiens genomic clone 2013C4, genomic survey se-
 quence//0.30:431:56//B53836
 R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//3.9e-106:541:95//
 45 AF037261
 R-HEMBA1002921
 R-HEMBA1002924//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10//
 4.6e-19:139:78//AB020875
 R-HEMBA1002934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING
 50 DRAFT SEQUENCE//7.5e-45:282:89//AL031681
 R-HEMBA1002935//CIT-HSP-2282P14.TFB CIT-HSP Homo sapiens genomic clone 2282P14, genomic survey
 sequence//1.5e-102:514:97//AQ008584
 R-HEMBA1002937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745114, WORKING
 DRAFT SEQUENCE//3.3e-87:444:97//AL033532
 55 R-HEMBA1002939
 R-HEMBA1002944//HS_3107_A1_C05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3107 Col=9 Row=E, genomic survey sequence//6.3e-21:250:73//AQ103952
 R-HEMBA1002951//Xerolycosa miniata mitochondrial 12S rRNA gene//0.013:228:63//AJ008020

- R-HEMBA1002954//HS_3246_A2_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=18 Row=M, genomic survey sequence.//5.8e-42:258:91//AQ218005
- R-HEMBA1002968//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//4.2e-38:300:83//AC005553
- 5 R-HEMBA1002970//Slime mold (D.discoideum) prestalk D11 gene, complete cds.//5.0e-05:541:57//M11012
- R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds.//7.2e-29:162:99//AB014579
- R-HEMBA1002973//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//9.1e-36:520:69//AC006128
- R-nnnnnnnnnnnn//Homo Sapiens Chromosome X clone bWXD691, complete sequence.//0.00040:504:59//AC004386
- 10 R-HEMBA1002999//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.7e-66:556:79//U19614
- R-HEMBA1003021//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-44:530:70//AC000406
- 15 R-HEMBA1003033//Homo sapiens full-length insert cDNA clone ZC34B10.//4.6e-78:414:94//AF086194
- R-HEMBA1003034//Homo sapiens chromosome 19, cosmid R29351, complete sequence.//9.0e-52:322:75//AC004026
- R-HEMBA1003035//HS_2008_A2_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=16 Row=M, genomic survey sequence.//4.0e-68:343:97//AQ269839
- 20 R-HEMBA1003037//347G15.TVB CIT978SKA1 Homo sapiens genomic clone A-347G15, genomic survey sequence.//0.57:188:58//B17694
- R-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//6.3e-30:350:72//AC004983
- R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//4.1e-118:578:97//AF054182
- 25 R-HEMBA1003064//Human cosmid LL12NC01-N-136B11, located centromeric to the ETV6 gene, chromosome 12p12-13.//0.0018:271:60//U59962
- R-HEMBA1003067//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 633019, WORKING DRAFT SEQUENCE.//5.3e-48:464:76//AL022302
- 30 R-HEMBA1003071//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.19:48:87//AQ110136
- R-HEMBA1003077//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.9e-69:494:84//U42975
- R-HEMBA1003078//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.1e-11:331:64//Z97054
- 35 R-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//4.6e-116:576:98//AC004673
- R-HEMBA1003083//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-43:280:83//AC005798
- 40 R-HEMBA1003086//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3-unordered pieces.//1.2e-43:281:88//AC006039
- R-HEMBA1003096//Human DNA sequence from clone J506G21, WORKING DRAFT SEQUENCE.//0.00037:421:59//Z82213
- 45 R-HEMBA1003098//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.4e-30:303:78//AC005598
- R-HEMBA1003117
- R-HEMBA1003129//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 407F11, WORKING DRAFT SEQUENCE.//7.9e-11:109:85//AL022329
- 50 R-HEMBA1003133//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.9e-99:484:98//AC004472
- R-HEMBA1003136//CIT-HSP-2281L22.TF CIT-HSP Homo sapiens genomic clone 2281L22, genomic survey sequence.//2.0e-10:93:92//B99861
- R-HEMBA1003142//Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.8e-40:270:87//AC004024
- 55 R-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//1.1e-116:586:96//AJ005670
- R-HEMBA1003166//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//6.4e-35:364:70//Z83822

R-HEMBA1003175//Human IFNAR gene for interferon alpha/beta receptor.//1.9e-30:282:77//X60459
 R-HEMBA1003197
 R-HEMBA1003199//HS_2166_A1_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2166 Col=23 Row=I, genomic survey sequence.//0.00026:271:61//AQ164162
 5 R-HEMBA1003202//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//
 5.4e-44:291:83//AC005480
 R-HEMBA1003204//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//3.1e-10:293:62//
 AC000118
 R-HEMBA1003212//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.0:
 10 118:69//AC006148
 R-HEMBA1003220//HS_3092_B1_F09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3092 Col=17 Row=L, genomic survey sequence.//0:00014:59:91//AQ128202
 R-HEMBA1003222//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y43F8,
 WORKING DRAFT SEQUENCE.//0.84:214:62//Z95393
 15 R-HEMBA1003229//RPCI11-16F15.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16F15, genomic survey
 sequence.//0.42:167:64//B83610
 R-HEMBA1003235//CIT-HSP-2320G19.TF CIT-HSP Homo sapiens genomic clone 2320G19, genomic survey se-
 quence.//3.6e-36:195:81//AQ037231
 R-HEMBA1003250//HS_2168_A2_C09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2168 Col=18 Row=E, genomic survey sequence.//1.4e-22:158:89//AQ125356
 20 R-HEMBA1003257//Human PCP4 gene, exon 3 and complete cds.//0.96:268:61//U53709
 R-HEMBA1003273//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete se-
 quence.//1.0e-32:255:84//AC002549
 R-HEMBA1003276//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING
 DRAFT SEQUENCE, 5 unordered pieces.//0.0044:212:60//AC005308
 25 R-HEMBA1003278//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Rqswell Park Cancer Institute Human PAC library)
 complete sequence.//1.1e-34:286:74//AC002395
 R-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1
 ordered pieces.//1.8e-53:428:83//AC005840
 30 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//3.0e-115:551:99//AB011109
 R-HEMBA1003296//CIT-HSP-2196L16.TR CIT-HSP Homo sapiens genomic clone 2196L16, genomic survey se-
 quence.//2.9e-20:337:65//AQ003073
 R-HEMBA1003304//Sequence 23 from patent US 5552281.//1.8e-31:179:97//I25662
 R-HEMBA1003309//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete se-
 35 quence.//0.00019:334:60//AB017061
 R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//2.8e-111:545:97//
 AB001872
 R-HEMBA1003322//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS,
 GSS, complete sequence.//0.60:274:61//AL022153
 40 R-HEMBA1003327//Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.//0.00028:172:65//
 AC005099
 R-HEMBA1003328//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//
 2.2e-44:268:90//AC005081
 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds.//2.7e-61:312:97//
 45 AF026029
 R-HEMBA1003348//***ALU WARNING: Human Alu-J subfamily consensus sequence.//7.2e-38:186:83//U14567
 R-HEMBA1003369//Caenorhabditis elegans cosmid F59C6, complete sequence.//0.00012:465:59//Z79600
 R-HEMBA1003370//Homo sapiens chromosome 17, clone hRPC867C24, complete sequence.//3.2e-42:301:87//
 AC002558
 50 R-HEMBA1003373//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alter-
 natively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a
 PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta,
 PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs,
 STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.4e-34:375:74//AL022721
 55 R-HEMBA1003376//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//1.6e-46:
 309:88//AC004651
 R-HEMBA1003380//HS_3184_B2_E06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3184 Col=12 Row=J, genomic survey sequence.//1.0e-35:237:88//AQ189144

EP 1 074 617 A2

R-HEMBA1003384//HS_2193_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=16 Row=P, genomic survey sequence.//0.00029:96:76//AQ032212
R-HEMBA1003395//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.6e-21:139:86//AC002993
5 R-HEMBA1003402//CIT-HSP-2166E19.TR CIT-HSP Homo sapiens genomic clone 2166E19, genomic survey sequence.//0.99:144:61//B91549
R-nnnnnnnnnnnnn
R-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//2.5e-112:547:98//AL031321
10 R-HEMBA1003418//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//0.082:352:59//AC004879
R-HEMBA1003433//Homo sapiens cell cycle regulatory protein p95 (NBS1) mRNA, complete cds.//9.9e-114:544:98//AF058696
R-HEMBA1003461
15 R-HEMBA1003463
R-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//9.1e-106:533:96//AC005041
R-HEMBA1003528
R-HEMBA1003531//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//3.4e-08:333:64//AC002454
20 R-HEMBA1003538//Human mRNA for complement component C1r.//1.4e-23:333:68//X04701
R-HEMBA1003545//Zebrafish mRNA for zflsl-2 (insulin gene enhancer binding protein homolog), complete cds.//0.030:144:68//D38453
R-HEMBA1003548//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0017:487:57//AC004153
25 R-HEMBA1003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 371H6, WORKING DRAFT SEQUENCE.//2.8e-99:503:96//AL031718
R-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//1.6e-114:574:97//AC005913
R-HEMBA1003560//Diplolepis rosae microsatellite clone DR04096.//0.24:116:67//AF034416
30 R-HEMBA1003568//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.9e-05:422:63//AC006036
R-HEMBA1003569//Homo sapiens full-length insert cDNA clone ZD82D06.//8.7e-108:545:95//AF086450
R-HEMBA1003571//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//4.6e-51:570:71//AC004914
35 R-HEMBA1003579//HS_3237_B2_E05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237 Col=10 Row=J, genomic survey sequence.//8.5e-97:495:95//AQ209302
R-HEMBA1003581//Mouse mRNA for talin.//8.3e-12:128:82//X56123
R-HEMBA1003591//Homo sapiens chromosome 16, BAC clone 2603 (LANL), complete sequence.//2.9e-87:251:95//AC005774
40 R-HEMBA1003595//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a ggtt repeat polymorphism, complete sequence.//4.5e-52:384:83//AL008715
R-HEMBA1003597//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.6e-41:442:74//Z84480
45 R-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.8e-23:177:88//AC005153
R-HEMBA1003615
R-HEMBA1003617//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:494:57//AC005139
50 R-HEMBA100362111*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0052I22; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.3e-26:309:75//AC004599
R-HEMBA1003622//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//7.1e-56:545:75//AC002980
55 R-HEMBA1003630//Homo sapiens CC chemokine gene cluster, complete sequence.//2.8e-32:546:68//AF088219
R-HEMBA1003637//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//8.0e-25:457:68//AC002454
R-HEMBA1003640//Homo sapiens chromosome X, PAC 671D9, complete sequence.//2.8e-40:280:86//AF031078

EP 1 074 617 A2

R-HEMBA1003645//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE //1.7e-33:297:82//AL023693

R-HEMBA1003646//Plasmodium falciparum MAL3P7, complete sequence //0.44:319:59//AL034559

5 R-HEMBA1003656//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence //6.9e-36:242:80//AC004382

R-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence //8.6e-117:588:96//AC005746

R-HEMBA1003667//Sequence 8 from patent US 5420245 //1.8e-21:170:88//I12222

10 R-HEMBA1003679//Homo sapiens BAC clone RG114B19, from 7q31.1, complete sequence //1.6e-22:180:87//AC005065

R-HEMBA1003680//C. elegans cosmid ZK353 //1.1e-06:270:61//L15313

R-HEMBA1003684//Colias alexandra alexandra cytochrome oxidase subunit I (cox1) gene, mitochondrial gene encoding mitochondrial protein, partial cds //0.77:171:66//AF044872

15 R-HEMBA1003690//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence //1.6e-104:523:97//AC004466

R-HEMBA1003692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE //1.7e-41:414:77//AL021707

R-HEMBA1003711//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces //1.6e-29:304:77//AC000406

20 R-HEMBA1003714

R-HEMBA1003715//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-685D8, WORKING DRAFT SEQUENCE, 16 unordered pieces //1.4e-63:578:77//AC005136

R-HEMBA1003720//Homo sapiens, WORKING DRAFT SEQUENCE, 135 unordered pieces //2.4e-36:350:78//AC002353

25 R-HEMBA1003725//Homo sapiens chromosome 19, cosmid R31973, complete sequence //6.3e-42:250:75//AC004699

R-HEMBA1003729//RPCI11-22D14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22D14, genomic survey sequence //1.0:234:62//B86158

R-HEMBA1003733//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence //7.7e-80:558:83//AL008634

30 R-HEMBA1003742//HS_3080_B2_H06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=12 Row=P, genomic survey sequence //3.4e-55:331:91//AQ139179

R-HEMBA1003758//Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains ESTs, CA repeat, STS and CpG island //4.5e-59:521:75//Z97876

35 R-HEMBA1003760

R-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds //2.6e-72:467:86//U17343

R-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds //1.0e-77:557:81//AF084259

40 R-HEMBA1003784

R-HEMBA1003799//Homo sapiens PAC clone DJ1032B10 from 7p15.3-p21, complete sequence //2.1 e-49:390:72//AC004455

R-HEMBA1003803

R-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence //9.4e-99:359:99//AC004596

45 R-HEMBA1003805//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence //8.0e-113:567:96//AL031781

50 R-HEMBA1003807//Bovine dinucleotide microsatellite HUJII77 //5.4e-18:194:78//M96348

R-HEMBA1003836//Human DNA from overlapping chromosome 19 cosmids R31396, F2545L and R31076 containing COX6B and UPKA, genomic sequence, complete sequence //3.4e-40:256:85//AC002115

R-HEMBA1003838//CIT-HSP-2380F18.TF CIT-HSP Homo sapiens genomic clone 2380F18, genomic survey sequence //9.7e-25:150:96//AQ196624

55 R-HEMBA1003856//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence //4.8e-33:486:68//Z93929

R-HEMBA1003864//, complete sequence //4.4e-100:531:94//AC005300

R-HEMBA1003866//HS_3203_B2_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=2 Row=F, genomic survey sequence.//2.6e-05:206:64//AQ180298
R-HEMBA1003879//Homo sapiens chromosome 10 clone CIT987SK-1119P3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.7e-17:170:79//U82207
5 R-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//7.8e-103:526:96//AP000036
R-HEMBA1003885//Human apolipoprotein apoC-IV (APOC4) gene, complete cds.//3.5e-45:299:87//U32576
R-HEMBA1003893//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1137F22, WORKING DRAFT SEQUENCE.//1.1e-41:386:77//AL034421
10 R-HEMBA1003902//HS_3031_B2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3031 Col=14 Row=J, genomic survey sequence.//5.3e-50:293:93//AQ165549
R-HEMBA1003908//CIT-HSP-2367K7.TR CIT-HSP Homo sapiens genomic clone 2367K7, genomic survey sequence.//1.2e-32:220:92//AQ076795
R-HEMBA1003926//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//3.1e-58:294:85//AC005368
15 R-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//8.0e-111:590:93//AF109718
R-HEMBA1003939
R-HEMBA1003942//Homo sapiens clone DJ0828F13, complete sequence.//2.2e-08:474:58//AC004904
R-HEMBA1003950//Plasmodium vivax from Brazil cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.034:258:62//AF069619
20 R-HEMBA1003953//Plasmodium falciparum MAL3P8, complete sequence.//0.096:492:57//AL034560
R-HEMBA1003958//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//7.3e-40:382:78//AL031668
R-HEMBA1003959//Amaranthus hypochondriacus betaine aldehyde dehydrogenase (ahybadh4) gene, complete cds.//0.11:428:60//AF000132
25 R-HEMBA1003976//Homo sapiens PAC clone DJ0724E13 from 7p11.2-p12, complete sequence.//1.0:222:62//AC004414
R-HEMBA1003978//Sequence 31 from patent US 5708157.//1.9e-14:159:77//I80060
R-HEMBA1003985//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.6e-14:136:83//AC004804
30 R-HEMBA1003987//Human chromosome 12p13 sequence, complete sequence.//3.2e-26:268:79//U47924
R-HEMBA1003989//RPCI11-52K22.TJ RPCI11 Homo sapiens genomic clone R-52K22, genomic survey sequence.//2.2e-86:443:95//AQ052484
R-HEMBA1004000
35 R-HEMBA1004011
R-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//4.7e-38:284:85//AC005670
R-HEMBA1004015//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//0.48:460:58//AL023575
40 R-HEMBA1004024//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.5e-21:159:80//AC005081
R-HEMBA1004038//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.9e-10:231:66//AC006054
R-HEMBA1004042//Homo sapiens clone DJ0968I16, complete sequence.//0.00071:263:68//AC006016
45 R-HEMBA1004045//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//8.8e-23:196:69//AC006143
R-HEMBA1004048//CIT-HSP-2288N20.TF CIT-HSP Homo sapiens genomic clone 2288N20, genomic survey sequence.//0.013:162:67//AQ007283
R-HEMBA1004049//Human hsp 70 gene 3' region for 70 kDa heat shock protein.//7.7e-30:176:96//X04677
50 R-HEMBA1004055//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.4e-05:395:63//AC005504
R-HEMBA1004056//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-61:551:77//AC005484
R-HEMBA1004074//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.98:275:63//AC004952
55 R-HEMBA1004086//Sequence 65 from patent US 5691147.//2.8e-54:313:92//I76237
R-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//1.8e-11:323:63//AF091234
R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds.//9.3e-42:534:69//D50918

- R-HEMBA1004132//Homo sapiens chromosome 17, clone hCIT.211_P_7, complete sequence//6.0e-49:491:76//AC003665
- R-HEMBA1004133//HS_3229_B2_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=18 Row=J, genomic survey sequence//1.1e-72:374:97//AQ192003
- 5 R-HEMBA1004138//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE//3.1e-09:277:66//AL024498
- R-HEMBA1004143//Plasmodium falciparum MAL3P4, complete sequence//0.53:239:61//AL008970
- R-HEMBA1004146//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces//3.0e-35:165:88//AC004820
- 10 R-HEMBA1004150//CITBI-E1-2517I2.TR CITBI-E1 Homo sapiens genomic clone 2517I2, genomic survey sequence//0.56:379:59//AQ277616
- R-HEMBA1004164//Human BAC clone GS200K05 from 7q21-q22, complete sequence//4.6e-49:448:77//AC002429
- R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//2.4e-110:563:96//AF067855
- 15 R-HEMBA1004199//S.pombe chromosome I cosmid c8A4//0.73:187:64//Z66569
- R-HEMBA1004200//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence//6.3e-30:293:77//AC004552
- R-HEMBA1004202//rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt]//3.0e-64:517:80//S72304
- 20 R-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces//1.0e-97:303:98//AC005488
- R-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds//3.6e-116:573:97//U50748
- R-HEMBA1004225//Drosophila melanogaster mitochondrial DNA with 12 tRNAs and 7 genes//5.4e-11:493:60//M37275
- 25 R-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds//6.1e-76:443:86//AF095927
- R-HEMBA1004238//Homo sapiens chromosome 19, cosmid R28341, complete sequence//1.1e-42:330:83//AC005763
- R-HEMBA1004241
- 30 R-HEMBA1004246//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE//1.1e-45:288:85//AP000011
- R-HEMBA1004248//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence//5.2e-09:516:61//AC004903
- R-HEMBA1004264
- 35 R-HEMBA1004267//HS_2255_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=24 Row=O, genomic survey sequence//8.6e-59:318:95//AQ068854
- R-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCIS-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence//1.1e-113:576:96//AC005831
- R-nnnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence//4.4e-110:553:96//AF091081
- 40 R-HEMBA1004276
- R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//1.9e-106:538:97//AF022795
- R-HEMBA1004289//RPCI11-74010.TJ RPCI11 Homo sapiens genomic clone R-74010, genomic survey sequence//2.3e-37:248:76//AQ266668
- 45 R-HEMBA1004295//Baboon apolipoprotein A-VI mRNA, 3' end//0.0016:273:64//L13174
- R-HEMBA1004306//HS_3175_B2_F01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3175 Col=2 Row=L, genomic survey sequence//1.6e-28:190:77//AQ169206
- R-HEMBA1004312//Human BAC clone RG119P24 from 7q31, complete sequence//6.3e-36:267:82//AC003088
- 50 R-HEMBA1004321//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 10155, WORKING DRAFT SEQUENCE//4.1e-111:576:95//AJ009611
- R-HEMBA1004323//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence//2.7e-42:136:91//AQ114933
- R-HEMBA1004327//CIT-HSP-2303L24.TF CIT-HSP Homo sapiens genomic clone 2303L24, genomic survey sequence//1.0:78:67//AQ017600
- 55 R-HEMBA1004330//Homo sapiens clone DJ1173120, WORKING DRAFT SEQUENCE, 5 unordered pieces//2.3e-119:580:98//AC004987
- R-HEMBA1004334//Pimpinella brachycarpa Phybl mRNA, complete cds//3.3e-14:238:69//AF082024
- R-HEMBA1004335//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence//1.8e-

- 21:291:71//AC004638
 R-HEMBA1004341
 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds.//4.1e-74:444:90//D89667
 R-HEMBA1004354//Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.//7.0e-38:287:82//AC003002
 5 R-HEMBA1004356//Sequence 2 from patent US 5652144.//3.7e-108:588:92//I58611
 R-HEMBA1004366//WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-14:446:63//AC005949
 R-HEMBA1004372//CIT-HSP-2005C13.TF CIT-HSP Homo sapiens genomic clone 2005C13, genomic survey sequence.//0.010:334:61//B55811
 10 R-HEMBA1004389//Homo sapiens full-length insert cDNA clone ZE09A11.//1.5e-19:170:83//AF086540
 R-HEMBA1004394//Human (D21S198) DNA segment containing (TG)23 repeat.//1.0:50:84//X58124
 R-HEMBA1004396//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//8.2e-34:459:69//AC004057
 R-HEMBA1004405//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//2.8e-42:314:84//AC005030
 15 R-HEMBA1004408
 R-HEMBA1004429//M.musculus of DNA encoding DNA-binding protein.//1.6e-66:449:82//Z54200
 R-HEMBA1004433//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//7.2e-32:460:68//AJ011930
 20 R-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.9e-113:581:96//AC004846
 R-HEMBA1004461//HS_3244_A2_F12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=24 Row=K, genomic survey sequence.//8.0e-83:397:99//AQ220876
 R-HEMBA1004479//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-40:485:70//AC006012
 25 R-HEMBA1004482//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//2.2e-11:513:59//AE001370
 R-HEMBA1004502//Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.//2.0e-08:245:66//AC005951
 30 R-HEMBA1004506//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34606, WORKING DRAFT SEQUENCE.//4.2e-81:582:83//Z84487
 R-HEMBA1004507//Caenorhabditis elegans cosmid C40C9, complete sequence.//0.56:235:64//Z70266
 R-HEMBA1004509
 R-HEMBA1004534//Sequence 58 from patent US 5691147.//1.9e-61:430:83//I76230
 35 R-HEMBA1004538//HS_3189_B2_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=6 Row=F, genomic survey sequence.//6.1e-21:140:92//AQ170330
 R-HEMBA1004554//CIT-HSP-712K9.TP CIT-HSP Homo sapiens genomic clone 712K9, genomic survey sequence.//1.7e-16:116:93//B73329
 40 R-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//2.2e-14:213:71//D87457
 R-HEMBA1004573
 R-HEMBA1004577//Human DNA sequence from cosmid L247F6, Huntington's Disease Region, chromosome 4p16.3 contains protein similar to Mouse SH3 binding protein 3BP2, multiple ESTs and a CpG island.//1.0:352:60//Z68279
 R-HEMBA1004586
 45 R-nnnnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.0012:359:60//Z98551
 R-HEMBA1004610//S.pombe chromosome II cosmid c354.//0.0011:362:62//AL022071
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1, specific transcript KIAA0501.//1.4e-50:327:85//AB007970
 R-HEMBA1004629//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human BAC Library) complete sequence.//4.4e-13:527:63//AC004805
 50 R-HEMBA1004631//Rattus norvegicus Nclone10 mRNA.//2.9e-24:364:71//U31866
 R-HEMBA1004632
 R-HEMBA1004637//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-117:573:98//AC005534
 55 R-HEMBA1004638//H.sapiens mRNA for DGCR2.//3.8e-19:118:99//X84076
 R-HEMBA1004666//Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence.//0.00013:501:58//AC005171
 R-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel

- genes, ESTs, GSSs and CpG islands, complete sequence.//1.5e-120:571:98//AL031432
 R-HEMBA1004670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//4.4e-12:110:88//Z93241
- 5 R-HEMBA1004672//Human DNA sequence from PAC 308I13 on chromosome 1p35-1p36.3.//3.4e-38:324:81//Z99291
 R-HEMBA1004693//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//0.86:309:57//AB006702
 R-HEMBA1004697//T33B22TF TAMU Arabidopsis thaliana genomic clone T33B22, genomic survey sequence.//0.29:331:61//B97342
- 10 R-HEMBA1004705//Plasmodium falciparum MAL3P7, complete sequence.//0.051:424:58//AL034559
 R-HEMBA1004709//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.7e-49:497:76//AC004638
 R-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//1.6e-38:362:79//AC005562
- 15 R-HEMBA1004725
 R-HEMBA1004730//Homo sapiens Chromosome 17p13 Cosmid Clone cos26, complete sequence.//1.1e-58:489:79//AC002085
 R-HEMBA1004733
 R-HEMBA1004734//Human DNA sequence from clone 273N12 on chromosome 6q16.1-16.3. Contains the gene for the N-Oct5a (N-Oct3, N-Oct5b) POU domain proteins and an unknown gene. Contains a putative CpG island, ESTs, STS; and GSSs, complete sequence.//0.0030:362:61//AL022395
- 20 R-HEMBA1004736//Homo sapiens clone DJ0981O07, complete sequence.//1.9e-58:282:87//AC006017
 R-HEMBA1004748//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//3.6e-34:287:81//AC004953
- 25 R-HEMBA1004751//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//5.3e-40:266:89//Z98950
 R-HEMBA1004752//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 495010, WORKING DRAFT SEQUENCE.//3.3e-39:281:85//AL031121
 R-HEMBA1004753//Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.//2.6e-65:475:84//L06498
- 30 R-HEMBA1004756//Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A/1, H2B.1A, H4, H2A.1b, H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island.//1.8e-08:516:59//AL021807
 R-HEMBA1004758//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//5.1e-45:577:72//AC004057
- 35 R-HEMBA1004763
 R-HEMBA1004768//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Amino transferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-60:435:78//AL022310
- 40 R-HEMBA1004770//Plasmodium falciparum chromosome 2, section 8 of 73 of the complete sequence.//8.7e-05:476:61//AE001371
 R-HEMBA1004771//Homo sapiens Xp22 Cosmid U152D7 (Lawrence Livermore human cosmid library) complete sequence.//5.0e-08:113:80//AC003047
- 45 R-HEMBA1004776
 R-HEMBA1004778//**ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-35:288:84//U14567
 R-nnnnnnnnnnnn/HS_3192_B1_F09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3192 Col=17 Row=L, genomic survey sequence.//1.9e-44:233:98//AQ155855
- 50 R-HEMBA1004803//Homo sapiens minisatellite ms31 repeat region.//3.0e-67:318:87//AF048728
 R-HEMBA1004806
 R-HEMBA1004807//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-20:333:69//AC005015
- 55 R-HEMBA1004816//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//6.3e-13:148:77//Z92545
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds.//1.5e-12:141:85//M74002
 R-HEMBA1004847//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//7.6e-80:297:85//X53744

- R-HEMBA1004850
 R-HEMBA1004863//Human DNA sequence from PAC 345P10 on chromosome 22q12-qter contains ESTs and STS and polymorphic CA repeat D22S927.//2.0e-14:159:79//Z82201
 R-HEMBA1004864
- 5 R-HEMBA1004865//Homo sapiens Xp22-149 BAC RPC111-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.90:76:76//AC005297
 R-HEMBA1004880//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-49:551:73//AC004826
 R-HEMBA1004889//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 223B1, WORKING DRAFT SEQUENCE.//0.0021:189:65//AL031943
- 10 R-HEMBA1004900//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence.//6.6e-11:144:7711AC005972
 R-HEMBA1004909//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//7.6e-46:341:83//Z98052
- 15 R-HEMBA1004918//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 994L9, WORKING DRAFT SEQUENCE.//1.6e-54:301:89//AL034554
 R-HEMBA1004923//Homo sapiens 47kB DNA fragment from Xq28, proximal to MTM1 gene.//2.0e-07:182:69//Y15994
 R-HEMBA1004929
- 20 R-HEMBA1004930//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.7e-66:547:79//AC005848
 R-HEMBA1004933//H. sapiens Humig mRNA.//0.13:233:62//X72755
 R-HEMBA1004934//CIT-HSP-2021116.TF CIT-HSP Homo sapiens genomic-clone 2021116, genomic survey sequence.//0.66:268:62//B65345
- 25 R-HEMBA1004944//CIT-HSP-2281L12.TR CIT-HSP Homo sapiens genomic clone 2281L12, genomic survey sequence.//3.8e-20:104:82//B99849
 R-HEMBA1004954//Homo sapiens chromosome 17, clone hRPK.146_P_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00082:385:60//AC005341
 R-HEMBA1004956//CIT-HSP-2305H22.TF CIT-HSP Homo sapiens genomic clone 2305H22, genomic survey sequence.//1.6e-84:411:99//AQ020408
- 30 R-HEMBA1004960//Human DNA sequence from PAC 358H7 on chromosome X.//3.3e-22:249:74//Z77249
 R-HEMBA1004972//nbxb0003aF01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003K01f, genomic survey sequence.//0.52:171:64//AQ049982
 R-HEMBA1004973//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.69:179:64//AC003656
- 35 R-HEMBA1004977//Caenorhabditis elegans cosmid F08G2, complete sequence.//7.6e-07:492:58//Z81495
 R-HEMBA1004978//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.20:427:60//AL024509
 R-HEMBA1004980//CIT-HSP-2379K5.TF CIT-HSP Homo sapiens genomic clone 2379K5, genomic survey sequence.//1.6e-53:331:88//AQ108614
- 40 R-HEMBA1004983//Genomic sequence from Human 17, complete sequence.//0.00061:473:58//AC000389
 R-HEMBA1004995//Homo sapiens chromosome 16, cosmid clone 306E5 (LANL), complete sequence.//1.6e-90:527:89//AC004224
 R-HEMBA10050087//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//5.4e-65:357:83//AL031663
- 55 R-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//5.6e-107:550:96//AF041474
 R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//6.3e-104:542:94//AB014548
 R-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c).

- H4FFP (H4/I pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence//3.1e-67:493:83//AL009179
R-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence//7.4e-101:537:94//AC004596
- 5 R-HEMBA1005039//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE//9.5e-30:446:68//AL031650
R-HEMBA1005047//Mus musculus mRNA for Rab24 protein//1.4e-34:229:88//Z22819
R-HEMBA1005050//Human Chromosome X PAC RPC11-290C9 from the Pieter de Jong Human PAC library; complete sequence//4.0e-43:371:80//AC002404
- 10 R-HEMBA1005062//Homo sapiens chromosome 17, clone hCIT.186_H_2, complete sequence//2.3e-15:269:66//AC004675
R-HEMBA1005066//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces//4.0e-30:305:74//AC006030
R-HEMBA1005075
- 15 R-HEMBA1005079//Homo sapiens clone HS 19.11 Alu-Ya5 sequence//6.5e-48:245:91//AF015156
R-HEMBA1005083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE//1.3e-15:142:83//AL034423
R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//5.3e-110:545:96//AF080561
- 20 R-HEMBA1005113//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53C10, WORKING DRAFT SEQUENCE//0.026:252:64//Z93340
R-HEMBA1005123//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence//7.1e-55:306:82//AL022336
- 25 R-HEMBA1005133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE//6.4e-45:309:87//AL022345
R-HEMBA1005149//Human cosmid LL12NC01-95H4, ETV6 gene, exon 2 and partial cds//3.2e-31:310:76//U81834
R-HEMBA1005152//Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island//1.4e-33:361:79//AL021407
- 30 R-HEMBA1005159//Human DNA sequence from clone 163016 on chromosome 1p35.1-36.13 Contains CA repeat, STS, complete sequence//2.7e-22:440:66//AL031279
R-HEMBA1005185//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE//0.0017:381:58//AL022594
- 35 R-HEMBA1005201//P.falciparum complete gene map of plastid-like DNA (IR-B)//8.5e-05:457:57//X95276
R-HEMBA1005202//Human 18S ribosomal RNA//4.7e-38:236:91//X03205
R-HEMBA1005219
R-HEMBA1005223//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces//1.0:209:65//AC004854
- 40 R-HEMBA1005232//Homo-sapiens chromosome Y, clone 264.M.20, complete sequence//0.0040:439:58//AC004617
R-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence//4.2e-111:568:96//AC005154
R-HEMBA1005244//HS_3092_B2_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=22 Row=F, genomic survey sequence//4.9e-12:116:84//AQ127947
- 45 R-HEMBA1005251//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence//3.2e-27:210:84//AC004548
R-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence//4.6e-105:437:97//AC005837
- 50 R-HEMBA1005274//Slime mold mitochondrial DNA, binding region to the membrane system//0.011:339:59//D86630
R-HEMBA1005275//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence//3.4e-17:269:71//AC004914
R-HEMBA1005293//Human DNA sequence from PAC 130N4, BRCA2 gene region chromosome 13q12-13 contains xs7 mRNA, ESTs//6.9e-20:193:73//Z75887
- 55 R-HEMBA1005296//HS_3037_B1_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=1 Row=H, genomic survey sequence//0.26:184:64//AQ117120
R-HEMBA1005304//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces//

- 1.5e-58:445:78//AC006146
 R-HEMBA1005311//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796E4, WORKING DRAFT SEQUENCE.//9.3e-42:383:78//AL022337
 R-HEMBA1005314//Caenorhabditis elegans cosmid F23H11.//0.80:179:65//AF003389
 5 R-HEMBA1005315//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-40:409:71//AC006030
 R-HEMBA1005318//S.pombe chromosome I cosmid c2E11.//0.97:370:61//AL031181
 R-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214_C_8, complete sequence.//1.9e-112:577:95//AC005803
 10 R-HEMBA1005353//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 429E7, WORKING DRAFT SEQUENCE.//8.9e-80:406:97//AL031722
 R-HEMBA1005359//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-50:320:84//AC005412
 R-HEMBA1005367//RPC111-85E23.TV RPC111 Homo sapiens genomic clone R-85E23, genomic survey sequence.//0.39:148:67//AQ281915
 15 R-HEMBA1005372//Homo sapiens full-length insert cDNA YH93B03.//2.6e-108:557:95//AF074997
 R-HEMBA1005374//Homo sapiens full-length insert cDNA clone ZA95D11.//1.9e-110:531:98//AF086142
 R-HEMBA1005389//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Tsp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RS (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//6.0e-41:432:75//Z92542
 20 R-HEMBA1005394//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 681N20, WORKING DRAFT SEQUENCE.//4.9e-107:585:93//AL031670
 R-HEMBA1005403//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//5.1e-118:586:97//AL034379
 25 R-HEMBA1005408//Bos taurus retina membrane guanylate cyclase ROS-GC2 mRNA, complete cds.//1.6e-06:204:68//U95958
 R-HEMBA1005410//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//1.2e-23:452:66//AL008722
 30 R-HEMBA1005411//RPC111-66N19.TK RPC111 Homo sapiens genomic clone R-66N19, genomic survey sequence.//2.2e-38:222:79//AQ237442
 R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//5.6e-117:453:99//AF041248
 R-HEMBA1005426//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//0.86:278:60//Z97196
 35 R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment.//5.4e-46:305:87//L40391
 R-HEMBA1005447//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//3.3e-79:531:86//AL031054
 R-HEMBA1005468//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//4.0e-27:469:66//AC004894
 40 R-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//7.2e-40:410:76//AC005212
 R-HEMBA1005472//Human DNA Sequence *** SEQUENCING IN PROGRESS *** from clone 1090E8, WORKING DRAFT SEQUENCE.//3.1e-40:296:85//AL033524
 45 R-HEMBA1005475//HS_2266_B2_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=8 Row=F, genomic survey sequence.//0.49:209:61//AQ069377
 R-HEMBA1005497
 R-HEMBA1005500//Homo sapiens PAC clone DJ1093O17 from 7q11.23-q21, complete sequence.//4.5e-116:580:97//AC004957
 50 R-HEMBA1005506//Arabidopsis thaliana BAC T26D22.//0.0050:442:59//AF058826
 R-HEMBA1005508//Sigalphus sp. 16S ribosomal RNA gene, partial sequence.//0.020:391:59//AF003509
 R-HEMBA1005511//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.44:195:63//Z96811
 R-HEMBA1005517//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.44:470:57//L14320
 55 R-HEMBA1005518//M.musculus mRNA for paladin gene.//6.2e-29:183:81//X99384
 R-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-40:281:86//AC004913

- R-HEMBA1005526//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE //3.9e-40:482:73//Z97985
- R-HEMBA1005528//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11 //3.8e-84:309:99//AB020860
- 5 R-HEMBA1005530//Homo sapiens PAC clone 946B23 SCA2 region, SP6 end, genomic sequence, genomic survey sequence //8.1e-25:154:94//U84091
- R-HEMBA1005548//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 970A17, WORKING DRAFT SEQUENCE //5.3e-105:534:96//AL034431
- 10 R-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence //2.8e-69:432:88//AC004743
- R-HEMBA1005558
- R-HEMBA1005568//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence //5.9e-33:367:74//AC004087
- R-HEMBA1005570//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence //2.2e-67:399:91//AL020989
- 15 R-HEMBA1005576//Homo sapiens chromosome 16, BAC clone 97H22 (LANL), complete sequence //1.0:156:631//AC005737
- R-HEMBA1005577
- R-HEMBA1005581//Homo sapiens mRNA for MEGFS, partial cds //9.7e-27:561:64//AB011538
- 20 R-HEMBA1005582//Torulopsis glabrata mitochondrial intergenic region ATPase 9 -cytochrome oxidase 2 genes //2.3e-10:404:62//X02171
- R-HEMBA1005583//HS_3014_B1_D05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=9 Row=H, genomic survey sequence //3.0e-81:442:94//AQ154499
- R-HEMBA1005588//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence //1.8e-54:490:77//Z98046
- 25 R-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence //2.2e-28:262:79//AC005746
- R-HEMBA1005595//HS_2224_A2_G03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2224 Col=6 Row=M, genomic survey sequence //3.6e-48:263:95//AQ033446
- R-HEMBA1005606//Human PAC clone DJ0093I03 from Xq23, complete sequence //2.5e-08:355:63//AC003983
- R-HEMBA1005609//HS_2182_B1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=P, genomic survey sequence //2.2e-82:400:99//AQ023130
- 35 R-HEMBA1005616//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 124K22, WORKING DRAFT SEQUENCE //0.80:308:60//AL031176
- R-HEMBA1005621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE //7.4e-76:338:98//AL031731
- R-HEMBA1005627//Homo sapiens full-length insert cDNA clone ZD53D02 //4.5e-72:398:93//AF086321
- 40 R-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence //3.8e-17:548:60//AC004460
- R-HEMBA1005632//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence //1.4e-13:172:75//AL022069
- R-HEMBA1005634//RPCI11-13015.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-13015, genomic survey sequence //1.0e-28:153:82//B73293
- 45 R-HEMBA1005666//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs //4.5e-51:343:87//AL021786
- R-HEMBA1005670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE //2.5e-33:288:78//AL020995
- R-HEMBA1005679//Human esterase D mRNA, 3'end //4.2e-49:322:88//M13450
- 50 R-HEMBA1005680//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence //3.0e-36:285:83//AC005924
- R-HEMBA1005685//H.sapiens (MAR8) chromosome 19 DNA, 343bp //0.022:65:86//Z35281
- R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds //5.4e-46:376:84//U66406
- 55 R-HEMBA1005705//RPCI11-13014.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13014, genomic survey sequence //0.071:182:59//B76186
- R-HEMBA1005717//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.